



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 126127

TO: Dave Nguyen
Location: REM-2D31/2C18
Art Unit: 1632
Friday, July 02, 2004

Case Serial Number: 10/068160

From: Barb O'Bryen
Location: Biotech-Chem Library
Remsen 1A69
Phone: 571-272-2518 *BOB*

barbara.obryen@uspto.gov

Search Notes

Ex. Nguyen,

Part 1 of your search could only be done in the Registry file. Results are expensive to display there, so I pulled out the GenBank hits & printed those records ~~def~~ directly from GenBank. The Gen Bank printouts are behind the STN printouts.

Please let me know if you have any questions.

Barb



STIC SEARCH RESULTS FEEDBACK FORM

Biotech-Chem Library

Questions about the scope or the results of the search? Contact *the searcher or contact:*

Mary Hale, Information Branch Supervisor
Remsen Bldg. 01 D86
571-272-2507

Voluntary Results Feedback Form

➤ I am an examiner in Workgroup: Example: 1610

➤ Relevant prior art **found**, search results used as follows:

- ☐ 102 rejection
- ☐ 103 rejection
- ☐ Cited as being of interest.
- ☐ Helped examiner better understand the invention.
- ☐ Helped examiner better understand the state of the art in their technology.

Types of relevant prior art found:

- ☐ Foreign Patent(s)
- ☐ Non-Patent Literature
(journal articles, conference proceedings, new product announcements etc.)

➤ Relevant prior art **not found**:

- ☐ Results verified the lack of relevant prior art (helped determine patentability).
- ☐ Results were not useful in determining patentability or understanding the invention.

Comments:

Drop off or send completed forms to STIC-Biotech-Chem Library Remsen Bldg.



GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 2, 2004, 08:11:05 ; Search time 138.732 Seconds
(without alignments)
625.926 Million cell updates/sec

Title: US-10-068-160-20

Perfect score: 18

Sequence: 1 tgcgtcggtgcaggggg 18

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 3163042 seqs, 2412103800 residues

Total number of hits satisfying chosen parameters: 6326084

Minimum DB seq length: 0

Maximum DB seq length: 2080000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:*

- 1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/ptodata/2/pubpna/PTC_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
- 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
- 6: /cgn2_6/ptodata/2/pubpna/PTC_PUBCOMB.seq:*
- 7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
- 8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
- 10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
- 12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
- 13: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
- 14: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
- 15: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
- 16: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
- 17: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
- 18: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
- 19: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	18	100.0	18	15	US-10-068-160-20
2	18	100.0	20	17	US-10-068-022-8
3	17	94.4	19	15	US-10-194-035-79
4	16.4	91.1	18	15	US-10-068-160-16
5	16.4	91.1	20	15	US-10-068-160-7
6	16.4	91.1	20	15	US-10-194-035-40
7	16.4	91.1	20	15	US-10-194-035-81
8	16.4	91.1	20	15	US-10-194-035-82
9	16.4	91.1	20	17	US-10-666-022-4
10	16.4	91.1	20	17	US-10-666-022-16
11	16	88.9	840	9	US-09-960-631A-1
12	16	88.9	1392	9	US-09-822-830A-199
13	16	88.9	2487	17	US-10-416-314-99
14	15.4	85.6	19	15	US-10-194-035-75

15	15.4	85.6	19	15	US-10-194-035-83	Sequence 83, Appl
16	15.4	85.6	303	13	US-10-424-599-125602	Sequence 125602, A
c 17	15.4	85.6	570	13	US-10-424-599-82230	Sequence 82230, A
18	15.4	85.6	765	9	US-09-974-300-7185	Sequence 7185, Ap
c 19	15.4	85.6	815	13	US-10-424-599-97884	Sequence 97884, A
c 20	15.4	85.6	1842	17	US-10-437-963-10345	Sequence 10345, A
c 21	15.4	85.6	2772	17	US-10-437-963-14876	Sequence 14876, A
22	15.4	85.6	2859	13	US-10-282-1228-27811	Sequence 27811, A
c 23	15.4	85.6	3162	13	US-10-027-632-114523	Sequence 114523, A
c 24	15.4	85.6	3162	16	US-10-027-632-114523	Sequence 114523, A
25	15	83.3	476	17	US-10-437-963-98704	Sequence 98704, A
26	15	83.3	1007	16	US-10-369-493-32802	Sequence 32802, A
27	15	83.3	1463	17	US-10-437-963-45745	Sequence 45745, A
c 28	15	83.3	1590	17	US-10-437-963-90205	Sequence 90205, A
c 29	15	83.3	1868	17	US-10-437-963-84855	Sequence 84855, A
c 30	15	83.3	1923	17	US-10-437-963-90203	Sequence 90203, A
31	15	83.3	2000	16	US-10-260-238-2666	Sequence 2666, Ap
32	15	83.3	2448	15	US-10-349-836-13	Sequence 13, Appl
33	15	83.3	2450	9	US-09-892-985-9	Sequence 9, Appl
34	15	83.3	18435	15	US-10-156-761-412	Sequence 412, App
35	15	83.3	100000	15	US-10-156-761-15103	Sequence 15103, A
c 36	15	83.3	9025608	15	US-10-156-761-1	Sequence 1, Appl
37	14.8	82.2	18	13	US-09-874-991C-503	Sequence 503, App
38	14.8	82.2	18	13	US-09-874-991C-513	Sequence 513, App
39	14.8	82.2	18	13	US-09-874-991C-551	Sequence 551, App
40	14.8	82.2	18	15	US-10-068-160-12	Sequence 12, Appl
41	14.8	82.2	18	15	US-10-068-160-13	Sequence 13, Appl
42	14.8	82.2	18	15	US-10-068-160-14	Sequence 14, Appl
43	14.8	82.2	18	15	US-10-068-160-17	Sequence 17, Appl
44	14.8	82.2	18	15	US-10-068-160-18	Sequence 18, Appl
45	14.8	82.2	20	13	US-09-874-991C-494	Sequence 494, App

ALIGNMENTS

RESULT 1
US-10-068-160-20
; Sequence 20, Application US/10068160
; Publication No. US2003006040A1
; GENERAL INFORMATION:
; APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA, REPRESENTED BY THE SECRETARY, DEPARTMENT OF HEALTH AND HUMAN SERVICES
; APPLICANT: SECRETARY, DEPARTMENT OF HEALTH AND HUMAN SERVICES
; APPLICANT: KLINMAN, Dennis
; APPLICANT: ISHII, Ken
; APPLICANT: VERTHELYI, Daniela
; TITLE OF INVENTION: OLIGODEOXYNUCLEOTIDE AND ITS USE TO INDUCE AN IMMUNE RESPONSE
; FILE REFERENCE: 4239-61999
; CURRENT APPLICATION NUMBER: US/10/068.160
; CURRENT FILING DATE: 2002-02-06
; PRIOR APPLICATION NUMBER: 60/128,898
; PRIOR FILING DATE: 1999-04-12
; NUMBER OF SEQ ID NOS: 120
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 20
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide
US-10-068-160-20

Query Match 100.0% Score 18; DB 15; Length 18;
Best Local Similarity 100.0%; Pred. No; 40;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGCCTCGGTGCAGGGGG 18
| | | | | | | | | | | | | | | | | | | | | |
Db 1 TGCCTCGGTGCAGGGGG 18

RESULT 2
US-10-666-022-8

```

; Sequence 8, Application US/10666022
; Publication No. US20040105872A1
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America, as represented by the
; APPLICANT: Secretary of the Department of Health and Human Services
; APPLICANT: Klimman, Dennis M.
; APPLICANT: Verthelyi, Daniela
; TITLE OF INVENTION: METHOD OF TREATING AND PREVENTING INFECTIONS IN IMMUNOCOMPROMISED
; TITLE OF INVENTION: SUBJECTS WITH IMMUNOSTIMULATORY CPG
; FILE REFERENCE: 4239-66899
; CURRENT APPLICATION NUMBER: US/10/666,022
; CURRENT FILING DATE: 2003-09-17
; PRIOR APPLICATION NUMBER: US 60/411,944
; PRIOR FILING DATE: 2002-09-18
; NUMBER OF SEQ ID NOS: 181
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic
; NAME/KEY: misc feature
; LOCATION: (1)-(20)
; OTHER INFORMATION: n is a, c, g, or t, or no nucleotide
US-10-666-022-8

```

```

Query Match 100.0%; Score 18; DB 17; Length 20;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 1 TGGCTCGGTGCAGGGGG 18
Db 3 TGGCTCGGTGCAGGGGG 20

```

```

RESULT 3
US-10-194-035-79
; Sequence 79, Application US/10194035
; Publication No. US2003014229A1
; GENERAL INFORMATION:
; APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS REPRESENTED BY THE
; APPLICANT: SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES
; APPLICANT: KLIMMAN, Dennis
; APPLICANT: ISHII, Ken
; APPLICANT: VERTHELYI, Daniela
; TITLE OF INVENTION: OLIGODEOXYNUCLEOTIDE AND ITS USE TO INDUCE AN IMMUNE RESPONSE
; FILE REFERENCE: 4239-63317
; CURRENT APPLICATION NUMBER: US/10/194,035
; CURRENT FILING DATE: 2002-07-12
; PRIOR APPLICATION NUMBER: PCT/US01/01122
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: US 60/176,115
; PRIOR FILING DATE: 2000-01-14
; NUMBER OF SEQ ID NOS: 119
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 79
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
US-10-194-035-79

```

```

Query Match 94.4%; Score 17; DB 15; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 1 TGGCTCGGTGCAGGGGG 17
Db 3 TGGCTCGGTGCAGGGGG 19

```

```

RESULT 4
US-10-068-160-16
; Sequence 16, Application US/10068160
; Publication No. US20030060440A1
; GENERAL INFORMATION:
; APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA, REPRESENTED BY THE
; APPLICANT: SECRETARY, DEPARTMENT OF HEALTH AND HUMAN SERVICES
; APPLICANT: KLIMMAN, Dennis
; APPLICANT: ISHII, Ken
; APPLICANT: VERTHELYI, Daniela
; TITLE OF INVENTION: OLIGODEOXYNUCLEOTIDE AND ITS USE TO INDUCE AN IMMUNE RESPONSE
; FILE REFERENCE: 4239-61999
; CURRENT APPLICATION NUMBER: US/10/068,160
; CURRENT FILING DATE: 2002-02-06
; PRIOR APPLICATION NUMBER: 60/128,898
; PRIOR FILING DATE: 1999-04-12
; NUMBER OF SEQ ID NOS: 120
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide
US-10-068-160-16

```

```

Query Match 91.1%; Score 16.4; DB 15; Length 18;
Best Local Similarity 94.4%; Pred. No. 2.3e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

Qy 1 TGGCTCGGTGCAGGGGG 18
Db 1 TGGCTCGGTGCAGGGGG 18

```

```

RESULT 5
US-10-068-160-7
; Sequence 7, Application US/10068160
; Publication No. US20030060440A1
; GENERAL INFORMATION:
; APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA, REPRESENTED BY THE
; APPLICANT: SECRETARY, DEPARTMENT OF HEALTH AND HUMAN SERVICES
; APPLICANT: KLIMMAN, Dennis
; APPLICANT: ISHII, Ken
; APPLICANT: VERTHELYI, Daniela
; TITLE OF INVENTION: OLIGODEOXYNUCLEOTIDE AND ITS USE TO INDUCE AN IMMUNE RESPONSE
; FILE REFERENCE: 4239-61999
; CURRENT APPLICATION NUMBER: US/10/068,160
; CURRENT FILING DATE: 2002-02-06
; PRIOR APPLICATION NUMBER: 60/128,898
; PRIOR FILING DATE: 1999-04-12
; NUMBER OF SEQ ID NOS: 120
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide
US-10-068-160-7

```

```

Query Match 91.1%; Score 16.4; DB 15; Length 20;
Best Local Similarity 94.4%; Pred. No. 2.3e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

Qy 1 TGGCTCGGTGCAGGGGG 18
Db 3 TGGCTCGGTGCAGGGGG 20

```

```

RESULT 6
US-10-194-035-40

```

```

; Sequence 40, Application US/10194035
; Publication No. US20030144229A1
; GENERAL INFORMATION:
; APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS REPRESENTED BY THE
; SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES
; APPLICANT: KLIMAN, Dennis
; APPLICANT: ISHIL, Ken
; APPLICANT: VERHEL, Daniela
; TITLE OF INVENTION: OLIGODEOXYNUCLEOTIDE AND ITS USE TO INDUCE AN IMMUNE RESPONSE
; CURRENT APPLICATION NUMBER: US/10/194,035
; PRIOR FILING DATE: 2002-07-12
; PRIOR APPLICATION NUMBER: PCT/US01/01122
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: US 60/176,115
; PRIOR FILING DATE: 2000-01-14
; NUMBER OF SEQ ID NOS: 119
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 40
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
US-10-194-035-40

Query Match          91.1%; Score 16.4; DB 15; Length 20;
Best Local Similarity 94.4%; Pred. No. 2.3e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TCGTCGGTGCAGGGGG 18
   ||||| ||||| ||||| |||||
Db 3 TCGTCGATGCAGGGGG 20

RESULT 7
US-10-194-035-81
; Sequence 81, Application US/10194035
; Publication No. US20030144229A1
; GENERAL INFORMATION:
; APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS REPRESENTED BY THE
; SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES
; APPLICANT: KLIMAN, Dennis
; APPLICANT: ISHIL, Ken
; APPLICANT: VERHEL, Daniela
; TITLE OF INVENTION: OLIGODEOXYNUCLEOTIDE AND ITS USE TO INDUCE AN IMMUNE RESPONSE
; CURRENT APPLICATION NUMBER: US/10/194,035
; PRIOR FILING DATE: 2002-07-12
; PRIOR APPLICATION NUMBER: PCT/US01/01122
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: US 60/176,115
; PRIOR FILING DATE: 2000-01-14
; NUMBER OF SEQ ID NOS: 119
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 81
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
US-10-194-035-81

Query Match          91.1%; Score 16.4; DB 15; Length 20;
Best Local Similarity 94.4%; Pred. No. 2.3e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TCGTCGGTGCAGGGGG 18
   ||||| ||||| ||||| |||||
Db 3 TCGTCGATGCAGGGGG 20

```

RESULT 8

```

US-10-194-035-82
; Sequence 82, Application US/10194035
; Publication No. US20030144229A1
; GENERAL INFORMATION:
; APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS REPRESENTED BY THE
; SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES
; APPLICANT: KLIMAN, Dennis
; APPLICANT: ISHIL, Ken
; APPLICANT: VERHEL, Daniela
; TITLE OF INVENTION: OLIGODEOXYNUCLEOTIDE AND ITS USE TO INDUCE AN IMMUNE RESPONSE
; CURRENT APPLICATION NUMBER: US/10/194,035
; PRIOR FILING DATE: 2002-07-12
; PRIOR APPLICATION NUMBER: PCT/US01/01122
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: US 60/176,115
; PRIOR FILING DATE: 2000-01-14
; NUMBER OF SEQ ID NOS: 119
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 82
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
US-10-194-035-82

Query Match          91.1%; Score 16.4; DB 15; Length 20;
Best Local Similarity 94.4%; Pred. No. 2.3e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TCGTCGGTGCAGGGGG 18
   ||||| ||||| ||||| |||||
Db 3 TCGTCGATGCAGGGGG 20

RESULT 9
US-10-666-022-4
; Sequence 4, Application US/10666022
; Publication No. US20040105872A1
; GENERAL INFORMATION:
; APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA, as represented by the
; SECRETARY of the Department of Health and Human Services
; APPLICANT: Kliman, Dennis M.
; APPLICANT: Verchelyi, Daniela
; TITLE OF INVENTION: METHOD OF TREATING AND PREVENTING INFECTIONS IN IMMUNOCOMPROMISED
; SUBJECTS WITH IMMUNOSTIMULATORY CPG
; FILE REFERENCE: 4239-66899
; CURRENT APPLICATION NUMBER: US/10/666,022
; CURRENT FILING DATE: 2003-09-17
; PRIOR APPLICATION NUMBER: US 60/411,944
; PRIOR FILING DATE: 2002-09-18
; NUMBER OF SEQ ID NOS: 181
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 4
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic
; NAME/KEY: misc feature
; LOCATION: (1)-(20)
; OTHER INFORMATION: n is a, c, g, or t, or no nucleotide
US-10-666-022-4

Query Match          91.1%; Score 16.4; DB 17; Length 20;
Best Local Similarity 94.4%; Pred. No. 2.3e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TCGTCGGTGCAGGGGG 18
   ||||| ||||| ||||| |||||
Db 3 TCGTCGATGCAGGGGG 20

```

RESULT 10

US-10-666-022-16
; Sequence 16, Application US/10666022
; Publication No. US20040105872A1
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America, as represented by the
; APPLICANT: Secretary of the Department of Health and Human Services
; APPLICANT: Kliman, Dennis M.
; APPLICANT: Verhellyi, Daniela
; TITLE OF INVENTION: METHOD OF TREATING AND PREVENTING INFECTIONS IN IMMUNOCOMPROMISED
; TITLE OF INVENTION: SUBJECTS WITH IMMUNOSTIMULATORY CPG
; FILE REFERENCE: 4239-66899
; CURRENT APPLICATION NUMBER: US/10/666,022
; CURRENT FILING DATE: 2003-09-17
; PRIOR APPLICATION NUMBER: US 60/411,944
; PRIOR FILING DATE: 2002-09-18
; NUMBER OF SEQ ID NOS: 181
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic
US-10-666-022-16

Query Match 91.1%; Score 16.4; DB 17; Length 20;
Best Local Similarity 94.4%; Pred. No. 2.3e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TGGTCGGTGCAGGGGG 18
| | | | | | | | | | | | | | | | | | | | | |
Db 3 TGGTCGATGCAGGGGG 20

RESULT 11

US-09-960-631A-1
; Sequence 1, Application US/09960631A
; Patent No. US20020160495A1
; GENERAL INFORMATION:
; APPLICANT: MIROCHNITCHENKO, Oleg
; APPLICANT: WEI, Jiang
; APPLICANT: INOUE, Masayori
; TITLE OF INVENTION: SOLUBLE ISCHEMIA ACTIVATED PROTEIN
; FILE REFERENCE: 266/171
; CURRENT APPLICATION NUMBER: US/09/960,631A
; CURRENT FILING DATE: 2001-09-20
; PRIOR APPLICATION NUMBER: US 60/233,819
; PRIOR FILING DATE: 2000-09-20
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 840
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-960-631A-1

Query Match 88.9%; Score 16; DB 9; Length 840;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GCGTCGGTGCAGGGGG 17
| | | | | | | | | | | | | | | | | | | | | |
Db 12 GCGTCGGTGCAGGGGG 27

RESULT 12

US-09-822-830A-199/c
; Sequence 199, Application US/09822830A
; Patent No. US20020142952A1
; GENERAL INFORMATION:

; APPLICANT: Genetics Institute, Inc.
; APPLICANT: Wong, Gordon G.
; APPLICANT: Clark, Hilary
; APPLICANT: Fechtel, Kim
; APPLICANT: Agostino, Michael J.
; APPLICANT: Howes, Steven H.
; APPLICANT: Resnick, Richard J.
; APPLICANT: Gulukota, Kamalakr
; APPLICANT: Graham, James R.
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING NOVEL SECRETED PROTEINS
; FILE REFERENCE: GIN 6402
; CURRENT APPLICATION NUMBER: US/09/822,830A
; CURRENT FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: 60/195,604
; PRIOR FILING DATE: 2000-04-06
; NUMBER OF SEQ ID NOS: 631
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 199
; LENGTH: 1192
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-822-830A-199

Query Match 88.9%; Score 16; DB 9; Length 1192;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GCGTCGGTGCAGGGGG 17
| | | | | | | | | | | | | | | | | | | | | |
Db 376 GCGTCGGTGCAGGGGG 361

RESULT 13

US-10-416-314-99
; Sequence 99, Application US/10416314
; Publication No. US20040082508A1
; GENERAL INFORMATION:
; APPLICANT: YUE, Henry
; APPLICANT: YAO, Monique G.
; APPLICANT: GANDHI, Ameena R.
; APPLICANT: BAUGHN, Mariah R.
; APPLICANT: SWARNAKAR, Anita
; APPLICANT: CHAWLA, Narinder K.
; APPLICANT: SANJANWALA, Madhusudan M.
; APPLICANT: THORNTON, Michael B.
; APPLICANT: ELLIOTT, Vicki S.
; APPLICANT: LU, Yan
; APPLICANT: GIETZEN, Kimberly J.
; APPLICANT: BURFORD, Neil
; APPLICANT: DING, Li
; APPLICANT: TANG, Y. Tom
; APPLICANT: HAFALIA, April J.A.
; APPLICANT: BANDMAN, Olga
; APPLICANT: WARREN, Bridget A.
; APPLICANT: HONCHELL, Cynthia D.
; APPLICANT: LU, Dyung Aina W.
; APPLICANT: THANGAVELU, Kavitha
; APPLICANT: LEE, Sally
; APPLICANT: XU, Yuming
; APPLICANT: YANG, Junning
; APPLICANT: LAL, Preeti G.
; APPLICANT: TRAN, Bao
; APPLICANT: ISON, Craig H.
; APPLICANT: DUGGAN, Brendan M.
; APPLICANT: KAREHT, Stephanie K.
; TITLE OF INVENTION: SECRETED PROTEINS
; FILE REFERENCE: PI-0287 USN
; CURRENT APPLICATION NUMBER: US/10/416,314
; CURRENT FILING DATE: 2003-05-08
; PRIOR APPLICATION NUMBER: US 60/247,505
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: US 60/249,642
; PRIOR FILING DATE: 2000-11-09

; PRIOR APPLICATION NUMBER: US 60/249,824
; PRIOR FILING DATE: 2000-11-16
; PRIOR APPLICATION NUMBER: US 60/252,824
; PRIOR FILING DATE: 2000-11-21
; PRIOR APPLICATION NUMBER: US 60/254,305
; PRIOR FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: US 60/256,448
; PRIOR FILING DATE: 2000-12-18
; NUMBER OF SEQ ID NOS: 130
; SOFTWARE: PERL Program
; SEQ ID NO 99
; LENGTH: 2487
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No: 1545079CB1
US-10-416-314-99

Query Match 88.9%; Score 16; DB 17; Length 2487;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GCGTCGTCGACGGGG 17
|||||
DB 675 GCGTCGTCGACGGGG 690

RESULT 14
US-10-194-035-75
; Sequence 75, Application US/10194035
; Publication No. US20030144229A1
; GENERAL INFORMATION:
; APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS REPRESENTED BY THE
; APPLICANT: SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES
; APPLICANT: KLINMAN, Dennis
; APPLICANT: ISHII, Ken
; APPLICANT: VERTHELYI, Daniela
; TITLE OF INVENTION: OLIGODEOXYNUCLEOTIDE AND ITS USE TO INDUCE AN IMMUNE RESPONSE
; FILE REFERENCE: 4239-63317
; CURRENT APPLICATION NUMBER: US/10/194,035
; CURRENT FILING DATE: 2002-07-12
; PRIOR APPLICATION NUMBER: PCT/US01/01122
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: US 60/176,115
; PRIOR FILING DATE: 2000-01-14
; NUMBER OF SEQ ID NOS: 119
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 75
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
US-10-194-035-75

Query Match 85.6%; Score 15.4; DB 15; Length 19;
Best Local Similarity 94.1%; Pred. No. 6.9e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TCGTCGTCGACGGGG 17
|||||
DB 3 TCGTCGTCGACGGGG 19

RESULT 15
US-10-194-035-83
; Sequence 83, Application US/10194035
; Publication No. US20030144229A1
; GENERAL INFORMATION:
; APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS REPRESENTED BY THE
; APPLICANT: SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES
; APPLICANT: KLINMAN, Dennis

; APPLICANT: ISHII, Ken
; APPLICANT: VERTHELYI, Daniela
; TITLE OF INVENTION: OLIGODEOXYNUCLEOTIDE AND ITS USE TO INDUCE AN IMMUNE RESPONSE
; FILE REFERENCE: 4239-63317
; CURRENT APPLICATION NUMBER: US/10/194,035
; CURRENT FILING DATE: 2002-07-12
; PRIOR APPLICATION NUMBER: PCT/US01/01122
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: US 60/176,115
; PRIOR FILING DATE: 2000-01-14
; NUMBER OF SEQ ID NOS: 119
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 83
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
US-10-194-035-83

Query Match 85.6%; Score 15.4; DB 15; Length 19;
Best Local Similarity 94.1%; Pred. No. 6.9e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TCGTCGTCGACGGGG 17
|||||
DB 3 TCGTCGTCGACGGGG 19

Search completed: July 2, 2004, 13:58:31
Job time : 143.732 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OK nucleic - nucleic search, using sw model

Run on: July 2, 2004, 07:38:45 ; Search time 1348.02 seconds

(without alignments)
398.746 Million cell updates/sec

Title: US-10-068-160-20

Perfect score: 18

Sequence: 1 tgcgtcgtgcaggggg 18

Scoring table: IDENTITY NUC

Gapop 10_0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estnu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_hcc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: gb_estfun:*
16: em_estom:*
17: em_gss_fum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_nam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_phg:*
27: em_gss_vrl:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
c 1	16.4	91.1	245	10 AW325275	AW325275 TENU4637
c 2	16.4	91.1	271	29 CE174729	CE174729 tigr-gss-
c 3	16.4	91.1	277	28 AQ444154	AQ444154 GSSTC0207
c 4	16.4	91.1	323	9 AL898002	AL898002 AL898002

5	16.4	91.1	400	12	BJ216073
6	16.4	91.1	421	9	AL897989
c 7	16.4	91.1	429	28	BH746584
c 8	16.4	91.1	1018	12	BG913279
c 9	16.4	91.1	1110	29	AG082246
10	16.4	91.1	1173	29	AG121475
11	16.4	91.1	1404	28	BZ554593
c 12	16	88.9	415	12	BM068740
c 13	16	88.9	453	12	BM055266
c 14	16	88.9	490	12	BM792946
c 15	16	88.9	519	12	BM820521
c 16	16	88.9	677	10	BF983122
c 17	16	88.9	697	12	BG493894
c 18	16	88.9	762	10	BE275117
c 19	16	88.9	787	14	CB990992
c 20	16	88.9	788	14	CB961467
c 21	16	88.9	791	29	CG343610
c 22	16	88.9	808	29	CG284584
c 23	16	88.9	809	14	CB988391
c 24	16	88.9	815	10	BE910177
c 25	16	88.9	826	29	CG316705
c 26	16	88.9	842	12	BG419606
c 27	16	88.9	853	14	CB997838
c 28	16	88.9	863	9	AL562129
c 29	16	88.9	867	14	CB988924
c 30	16	88.9	876	14	CD110248
c 31	16	88.9	880	13	BUI94354
c 32	16	88.9	923	29	CG284593
c 33	16	88.9	936	13	EX403217
c 34	16	88.9	945	29	CG316713
c 35	16	88.9	974	12	BG749183
c 36	16	88.9	996	13	EX339259
c 37	16	88.9	1005	13	EX384032
c 38	16	88.9	1026	13	BUI56800
c 39	16	88.9	1063	13	BQ921007
c 40	16	88.9	1085	14	CB992782
c 41	16	88.9	1088	14	CD107371
c 42	16	88.9	1098	13	EX377620
c 43	16	88.9	1099	13	BUI527443
c 44	16	88.9	1114	13	BQ439272
c 45	16	88.9	1132	12	BMS51929

ALIGNMENTS

RESULT 1
AW325275/c
LOCUS
DEFINITION
TENU4637 T.cruzi epimastigote normalized cDNA Library Trypanosoma
cruzi CDNA clone 25h9 5', mRNA sequence.
ACCESSION
AW325275
VERSION
AW325275.1
KEYWORDS
EST.
SOURCE
Trypanosoma cruzi
ORGANISM
Trypanosoma cruzi
REFERENCE
1 (bases 1 to 245)
AUTHORS
Porcel, B.M., Tran, A.-N., Tammi, M., Nyarady, Z., Rydaker, M.,
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
Trypanosoma; Schizotrypanum.

245 bp mRNA linear EST 21-SEP-2000
cruzi CDNA clone 25h9 5', mRNA sequence.

AW325275.1 GI:6761196

Trypanosoma cruzi

Trypanosoma cruzi

Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;

Trypanosoma; Schizotrypanum.

1 (bases 1 to 245)

Porcel, B.M., Tran, A.-N., Tammi, M., Nyarady, Z., Rydaker, M.,

Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;

Trypanosoma; Schizotrypanum.

Gene survey of the pathogenic protozoan Trypanosoma cruzi

Genome Res. 10 (8), 1103-1107 (2000)

20414748

10958628

COMMENT

Contact: Aslund L

Department of Medical Genetics

Uppsala University

Biomedical Center, Box 589, S-751 23 Uppsala, Sweden

Tel: 46 18 471 45 85

Fax: 46 18 52 68 49

Email: lena.aslund@medgen.uu.se

```

Seq primer: T7 primer
High quality sequence stop: 245.
Location/Qualifiers
1. .245
/organism="Trypanosoma cruzi"
/mol_type="mRNA"
/strain="Cl-Brenner"
/db_xref="taxon:5693"
/clone="25h9"
/cell_type="epimastigote"
/clone_lib="T. cruzi epimastigote normalized cDNA library"
/notes="cDNA library constructed with oligo dt primed
epimastigote mRNA and cloned in pT7318D phagemid with
modified polylinker (Pharmacia)"

ORIGIN
Query Match 91.1%; Score 16.4; DB 10; Length 245;
Best Local Similarity 94.4%; Pred. No. 1.5e+04;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TGGTCGGTGCAGGGGG 18
Db 65 TGCATCGGTGCAGGGGG 48

RESULT 2
CE174729
LOCUS 271 bp DNA linear GSS 25-SEP-2003
DEFINITION tigr-gss-dog-17000326716213 Dog Library Canis familiaris genomic,
genomic survey sequence.
ACCESSION CE174729
VERSION CE174729.1 GI:35318341
KEYWORDS GSS.
SOURCE Canis familiaris (dog)
ORGANISM Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE 1 (bases 1 to 271)
AUTHORS Kirkness, E.F., Bafna, V., Halpern, A.L., Levy, S., Remington, K.,
Rusch, D.B., Deicher, A.L., Pop, M., Wang, W., Fraser, C.M. and
Venter, J.C.
TITLE The dog genome: survey sequencing and comparative analysis
JOURNAL Science 301 (5641), 1898-1903 (2003)
MEDLINE 22875432
PUBMED 14512627
COMMENT Contact: Kirkness EF
The Institute for Genomic Research
Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
Rockville, MD 20850, USA
Tel: 301-838-0200
Fax: 301-838-0208
Email: ekirknes@tigr.org
Class: shotgun.
Location/Qualifiers
1. .271
/organism="Canis familiaris"
/mol_type="genomic DNA"
/strain="Standard Poodle"
/db_xref="taxon:9615"
/clone_lib="Dog Library"
/notes="Site 1: BstXI; Libraries were prepared from
peripheral blood"

FEATURES
source
Query Match 91.1%; Score 16.4; DB 29; Length 271;
Best Local Similarity 94.4%; Pred. No. 1.5e+04;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TGGTCGGTGCAGGGGG 18
Db 217 TGGTCGGTGCAGGGGG 234

ORIGIN
Query Match 91.1%; Score 16.4; DB 28; Length 277;
Best Local Similarity 94.4%; Pred. No. 1.5e+04;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TGGTCGGTGCAGGGGG 18
Db 238 TGCATCGGTGCAGGGGG 221

RESULT 3
AQ444154/c
LOCUS 277 bp DNA linear GSS 09-JAN-2001
DEFINITION GSS7c0207 Trypanosoma cruzi random genomic library Trypanosoma
cruzi genomic clone G10L7, genomic survey sequence.
ACCESSION AQ444154
VERSION AQ444154.3 GI:10130745
KEYWORDS GSS.
SOURCE Trypanosoma cruzi
ORGANISM Trypanosoma cruzi
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
Trypanosoma; Schizotrypanum.
1 (bases 1 to 277)
AUTHORS Agüero, F., Verdun, R., Frasch, A.C.C. and Sanchez, D.O.
TITLE A random sequencing approach for the analysis of the trypanosoma
cruzi genome: General structure, large gene and repetitive DNA
families, and gene discovery
JOURNAL Genome Res. 10 (12), 1996-2005 (2000)
MEDLINE 20568489
PUBMED 11116094
COMMENT On Sep 14, 2000 this sequence version replaced gi:9372108.
Contact: Sanchez D.O.
Instituto de Investigaciones Biotecnológicas (Univ. Nac. de Gral
San Martín)
Av. Gral Paz S/N, INTI, Edificio 24, B 1650 KNA, San Martín, Buenos
Aires, Argentina
Tel: (54-11) 4580/7255/7
Fax: (54-11) 4752-9639
Email: dsanchez@lib.unsam.edu.ar
Sequences were basecalled with phred and vector was masked with
crossmatch (see http://genome.washington.edu). Sequences were then
trimmed from both ends to remove low quality bases and masked
vector.
Seq primer: T7
Class: shotgun.
Location/Qualifiers
1. .277
/organism="Trypanosoma cruzi"
/mol_type="genomic DNA"
/strain="Cl-Brenner"
/db_xref="taxon:5693"
/clone="G10L7"
/cell_type="epimastigote"
/clone_lib="Trypanosoma cruzi random genomic library"
/notes="Vector: pBS(-) (Stratagene); T. cruzi DNA was
randomly sheared using a nebulizer and the 1 to 2 Kb range
was gel purified and cloned into the dephosphorylated
KincII site of the vector"

ORIGIN
Query Match 91.1%; Score 16.4; DB 28; Length 277;
Best Local Similarity 94.4%; Pred. No. 1.5e+04;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TGGTCGGTGCAGGGGG 18
Db 238 TGCATCGGTGCAGGGGG 221

RESULT 4
AL898002
LOCUS 323 bp mRNA linear EST 04-DEC-2003
DEFINITION AL898002 XGC-egg Silurana tropicalis cDNA clone TEGG043g16 5', mRNA
sequence.
ACCESSION AL898002
VERSION AL898002.2 GI:38697559
KEYWORDS EST.
SOURCE Silurana tropicalis (western clawed frog)
ORGANISM Silurana tropicalis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
Xenopodinae; Silurana.
1 (bases 1 to 323)
REFERENCE 1 (bases 1 to 323)

```

```

AUTHORS      Croning,M.D.R., Ashurst,J.L., Taylor,R., Zorn,A.M. and Rogers,J.
TITLE        Sanger Xenopus tropicalis EST project 2001 (11_2003)
JOURNAL      Unpublished (2003)
COMMENT      On Sep 16, 2002 this sequence version replaced gi:22950395.
Contact: Taylor R
Sanger Institute
Hinxton, Cambridgeshire, CB10 1SA, UK
Email: trop@sanger.ac.uk
Sanger Xenopus tropicalis EST project 2001
TROFICALIS_SEQUENCE_ID: TEGG043g16.plkSP6
Sequencing primer: SP6
This sequence is from a Xenopus Gene Collection (XGC) library
constructed by Aaron M. Zorn.
cDNA was oligo dt primed from 5ug of poly A+ RNA from egg.
EcoRI-NotI cut cDNA was then ligated into pCS107 with EcoRI at the
5' end and NotI at the 3' end.
Vector: pCS107; Site_1: EcoRI; Site_2: NotI
Host: Escherichia coli XL1-blue.
Location/Qualifiers
1..323
/organism="Silurana tropicalis"
/mol_type="mRNA"
/db_xref="taxon:8364"
/clone="TEGG043g16"
/dev_stage="egg"
/lab_host="Escherichia coli XL1-blue"
/clone_lib="XGC-egg"
/note="Vector: pCS107; Site_1: EcoRI; Site_2: NotI; cDNA
was oligo dt primed from 5ug of poly A+ RNA from egg.
EcoRI-NotI cut cDNA was then ligated into pCS107 with
EcoRI at the 5' end and NotI at the 3' end"

ORIGIN
Query Match      91.1%; Score 16.4; DB 9; Length 323;
Best Local Similarity 94.4%; Pred. No. 1.5e+04;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TCGTCGCGTGCAGGGGGG 18
    |||||
Db 79 TCGCGCGTGCAGGGGGG 96

RESULT 5
BJ216073
LOCUS      BJ216073 Y. Ogihara unpublished cDNA library, Wh Triticum aestivum
DEFINITION BJ216073.1 GI:23071352
ACCESSION  BJ216073
VERSION     BJ216073.1
KEYWORDS    EST
SOURCE      Triticum aestivum (bread wheat)
ORGANISM    Triticum aestivum
REFERENCE   1 (bases 1 to 400)
            Ogihara,Y. and Murai,K.
            Expressed genes in triticum aestivum
            Unpublished (2002)
            Contact: Tadasu Shin-i
            Center For Genetic Resource Information
            National Institute of Genetics
            1111 Yata, Mishima, Shizuoka 411-8540, Japan
            Tel: 81-559-81-6856
            Fax: 81-559-81-6855
            Email: tschini@genes.nig.ac.jp.
            Location/Qualifiers
            1..400
            /organism="Triticum aestivum"
            /mol_type="mRNA"
            /cultivar="Chinese Spring"
            /db_xref="taxon:4565"
            /clone="wh9n06"

FEATURES
source
/tissue_type="spike at meiosis"
/dev_stage="Feekes' scale 9"
/clone_lib="Y. Ogihara unpublished cDNA library, Wh"

AUTHORS      Croning,M.D.R., Ashurst,J.L., Taylor,R., Zorn,A.M. and Rogers,J.
TITLE        Sanger Xenopus tropicalis EST project 2001 (11_2003)
JOURNAL      Unpublished (2003)
COMMENT      On Sep 16, 2002 this sequence version replaced gi:22950395.
Contact: Taylor R
Sanger Institute
Hinxton, Cambridgeshire, CB10 1SA, UK
Email: trop@sanger.ac.uk
Sanger Xenopus tropicalis EST project 2001
TROFICALIS_SEQUENCE_ID: TEGG043g16.plkSP6
Sequencing primer: SP6
This sequence is from a Xenopus Gene Collection (XGC) library
constructed by Aaron M. Zorn.
cDNA was oligo dt primed from 5ug of poly A+ RNA from egg.
EcoRI-NotI cut cDNA was then ligated into pCS107 with EcoRI at the
5' end and NotI at the 3' end.
Vector: pCS107; Site_1: EcoRI; Site_2: NotI
Host: Escherichia coli XL1-blue.
Location/Qualifiers
1..421
/organism="Silurana tropicalis"
/mol_type="mRNA"
/db_xref="taxon:8364"
/clone="TEGG043e14"
/dev_stage="egg"
/lab_host="Escherichia coli XL1-blue"
/clone_lib="XGC-egg"
/note="Vector: pCS107; Site_1: EcoRI; Site_2: NotI; cDNA
was oligo dt primed from 5ug of poly A+ RNA from egg.
EcoRI-NotI cut cDNA was then ligated into pCS107 with
EcoRI at the 5' end and NotI at the 3' end"

ORIGIN
Query Match      91.1%; Score 16.4; DB 9; Length 421;
Best Local Similarity 94.4%; Pred. No. 1.5e+04;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TCGTCGCGTGCAGGGGGG 18
    |||||
Db 79 TCGCGCGTGCAGGGGGG 96

RESULT 6
AL897989
LOCUS      AL897989 XGC-egg Silurana tropicalis cDNA clone TEGG043e14 5', mRNA
DEFINITION AL897989.2 GI:38697548
ACCESSION  AL897989
VERSION     AL897989.2
KEYWORDS    EST
SOURCE      Silurana tropicalis (western clawed frog)
ORGANISM    Silurana tropicalis
REFERENCE   1 (bases 1 to 421)
            Croning,M.D.R., Ashurst,J.L., Taylor,R., Zorn,A.M. and Rogers,J.
            Sanger Xenopus tropicalis EST project 2001 (11_2003)
            Unpublished (2003)
            On Sep 16, 2002 this sequence version replaced gi:22950382.
            Contact: Taylor R
            Sanger Institute
            Hinxton, Cambridgeshire, CB10 1SA, UK
            Email: trop@sanger.ac.uk
            TROFICALIS_SEQUENCE_ID: TEGG043e14.plkSP6
            Sequencing primer: SP6
            This sequence is from a Xenopus Gene Collection (XGC) library
            constructed by Aaron M. Zorn.
            cDNA was oligo dt primed from 5ug of poly A+ RNA from egg.
            EcoRI-NotI cut cDNA was then ligated into pCS107 with EcoRI at the
            5' end and NotI at the 3' end.
            Vector: pCS107; Site_1: EcoRI; Site_2: NotI
            Host: Escherichia coli XL1-blue.
            Location/Qualifiers
            1..421
            /organism="Silurana tropicalis"
            /mol_type="mRNA"
            /db_xref="taxon:8364"
            /clone="TEGG043e14"
            /dev_stage="egg"
            /lab_host="Escherichia coli XL1-blue"
            /clone_lib="XGC-egg"
            /note="Vector: pCS107; Site_1: EcoRI; Site_2: NotI; cDNA
            was oligo dt primed from 5ug of poly A+ RNA from egg.
            EcoRI-NotI cut cDNA was then ligated into pCS107 with
            EcoRI at the 5' end and NotI at the 3' end"

ORIGIN
Query Match      91.1%; Score 16.4; DB 9; Length 421;
Best Local Similarity 94.4%; Pred. No. 1.5e+04;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TCGTCGCGTGCAGGGGGG 18
    |||||
Db 79 TCGCGCGTGCAGGGGGG 96

RESULT 7
BH746584/c
LOCUS      BH746584 429 bp DNA linear GSS 27-FEB-2002

```



```

DEFINITION SALK_044872.30.00.x Arabidopsis thaliana TDNA insertion lines
Arabidopsis thaliana genomic clone SALK_044872.30.00.x, genomic
survey sequence.
ACCESSION BH746584
VERSION BH746584.1 GI:18959699
SOURCE GSS.
ORGANISM Arabidopsis thaliana (thale cress)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 429)
Alonso,J.M., Leisse,T.J., Barajas,F., Chen,H., Cheuk,R.,
Gadrinab,C., Jeske,A., Karne,M., Kim,C.J., Parker,H., Prednis,L.,
Shinn,P., Zimmerman,J. and Ecker,J.R.
A Sequence-Indexed Library of Insertion Mutations in the
Arabidopsis Genome
Unpublished (2001)
Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
This is single pass sequence recovered from the left border of
TDNA. This sequence lies within an annotated exon of At1g42480.
Class: TDNA tagged.
FEATURES             Location/Qualifiers
     source           1..429
                     /organism="Arabidopsis thaliana"
                     /mol_type="genomic DNA"
                     /strain="Columbia 0"
                     /db_xref="taxon:3702"
                     /clone="SALK_044872.30.00.x"
                     /note="PCR was performed on Arabidopsis thaliana lines
                     each of which contains one or more TDNA insertion
                     elements. The resultant fragment for each line was
                     directly sequenced to determine the genomic sequence at
                     the site of insertion. Details of the protocols used can
                     be found at http://signal.salk.edu/tdna_protocols.html"

ORIGIN
Query Match          91.1%; Score 16.4; DB 28; Length 429;
Best Local Similarity 94.4%; Pred. No. 1.5e+04;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TGCCTCGTGCAGGGGG 18
    ||||| ||||| ||||| |||||
DB 414 TGCCTCGTGCAGGGGG 397

RESULT 8
BG913279/c
LOCUS BG913279 1018 bp mRNA linear EST 05-JUN-2001
DEFINITION 602811967F1 NCI CGAP_Brn67 Homo sapiens cDNA clone IMAGE:4943992
5', mRNA sequence.
ACCESSION BG913279
VERSION BG913279.1 GI:14293755
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1018)
NIH-WGC http://mgc.nci.nih.gov/.
NATIONAL INSTITUTES OF HEALTH, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabs-rc@mail.nih.gov
Tissue Procurement: David N. Louis, M.D.
CDNA Library Preparation: Life Technologies, Inc.

```

```

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Inyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10888 row: e column: 17
High quality sequence stop: 472.
FEATURES             Location/Qualifiers
     source           1..1018
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4943992"
                     /tissue_type="anaplastic oligodendroglioma with ip/19q
                     loss"
                     /lab_host="DH10B (T1 phage-resistant)"
                     /clone_lib="NCI CGAP Brn67"
                     /note="Organ: Brain; Vector: PCMV-SPORT6; Site 1: NotI;
                     Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
                     Average insert size 2.3 kb. Constructed by Life
                     Technologies. Note: this is a NCI CGAP Library."

ORIGIN
Query Match          91.1%; Score 16.4; DB 12; Length 1018;
Best Local Similarity 94.4%; Pred. No. 1.7e+04;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TCGCTCGGTGCAGGGGG 18
    ||||| ||||| ||||| |||||
DB 751 TCGCTCGGTGCAGGGGG 734

RESULT 9
AG082246/c
LOCUS AG082246 1110 bp DNA linear GSS 03-NOV-2001
DEFINITION Pan troglodytes DNA, clone: PTB-079B07.R, genomic survey sequence.
ACCESSION AG082246
VERSION AG082246.1 GI:16634048
KEYWORDS GSS.
SOURCE Pan troglodytes (chimpanzee)
ORGANISM Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
1
Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
Totoki,Y., Watanabe,H. and Sakaki,Y.
BAC end sequences of Library PTB
Unpublished
2 (bases 1 to 1110)
Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
Totoki,Y., Watanabe,H. and Sakaki,Y.
Direct Submission
Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-chou,Tsukumi-ku, Yokohama, Kanagawa 230-0045, Japan
(E-mail:chimpsgsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC end
was generated during the RED process and may have higher chance of
clone tracking errors.
PRIMERS
Sequencing: M13Rev
LIBRARY
Vector : pXS145
R.Site 1 : SacI
R.Site 2 : SacI.
Location/Qualifiers
1..1110
/organism="pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
/clone="PTB-079B07.R"
/sex="male"

```

```

/cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee Male BAC Library"

ORIGIN
Query Match          91.1%; Score 16.4; DB 29; Length 1110;
Best Local Similarity 94.4%; Pred. No. 1.7e+04;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TCGCTCGGTGCAGGGGG 18
||||| |||||||
Db 611 TGGCTGCTGCAGGGGG 594

RESULT 10
AG121475
LOCUS Pan troglodytes DNA, clone: PTB-130114.F, genomic survey sequence.
DEFINITION AG121475
ACCESSION AG121475.1 GI:16650640
VERSION
KEYWORDS
SOURCE
ORGANISM Pan troglodytes (chimpanzee)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
REFERENCE 1 Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
AUTHORS Totoki, Y., Watanabe, H. and Sakaki, Y.
TITLE BAC end sequences of library PTB
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1173)
AUTHORS Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
Totoki, Y., Watanabe, H. and Sakaki, Y.
TITLE Direct Submission
JOURNAL Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
(5-mail:chimpses@sc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
Tel:81-45-503-9111, Fax:81-45-503-9170)
COMMENT Clones are derived from the chimpanzee BAC library PTB This BAC end
clone tracking errors.
PRIMERS
Sequencing: -21M13
LIBRARY Vector : pKS145
R.Site 1 : SacI
R.Site 2 : SacI
FEATURES
Location/Qualifiers
1..1173
/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
/clone="PTB-130114.F"
/sex="male"
/cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee Male BAC Library"

ORIGIN
Query Match          91.1%; Score 16.4; DB 29; Length 1173;
Best Local Similarity 94.4%; Pred. No. 1.7e+04;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TCGCTCGGTGCAGGGGG 18
||||| |||||||
Db 910 TGGCTGCTGCAGGGGG 927

RESULT 11
BZ554593
LOCUS
DEFINITION
ACCESSION
BZ554593
pacsl-60 4763.x1 pacsl-60 Pseudomonas aeruginosa genomic clone
pacsl-60 4763, genomic survey sequence.
BZ554593

/cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee Male BAC Library"

ORIGIN
Query Match          91.1%; Score 16.4; DB 29; Length 1110;
Best Local Similarity 94.4%; Pred. No. 1.7e+04;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TCGCTCGGTGCAGGGGG 18
||||| |||||||
Db 611 TGGCTGCTGCAGGGGG 594

RESULT 10
AG121475
LOCUS Pan troglodytes DNA, clone: PTB-130114.F, genomic survey sequence.
DEFINITION AG121475
ACCESSION AG121475.1 GI:16650640
VERSION
KEYWORDS
SOURCE
ORGANISM Pan troglodytes (chimpanzee)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
REFERENCE 1 Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
AUTHORS Totoki, Y., Watanabe, H. and Sakaki, Y.
TITLE BAC end sequences of library PTB
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1173)
AUTHORS Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
Totoki, Y., Watanabe, H. and Sakaki, Y.
TITLE Direct Submission
JOURNAL Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
(5-mail:chimpses@sc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
Tel:81-45-503-9111, Fax:81-45-503-9170)
COMMENT Clones are derived from the chimpanzee BAC library PTB This BAC end
clone tracking errors.
PRIMERS
Sequencing: -21M13
LIBRARY Vector : pKS145
R.Site 1 : SacI
R.Site 2 : SacI
FEATURES
Location/Qualifiers
1..1173
/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
/clone="PTB-130114.F"
/sex="male"
/cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee Male BAC Library"

ORIGIN
Query Match          91.1%; Score 16.4; DB 29; Length 1173;
Best Local Similarity 94.4%; Pred. No. 1.7e+04;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TCGCTCGGTGCAGGGGG 18
||||| |||||||
Db 910 TGGCTGCTGCAGGGGG 927

RESULT 11
BZ554593
LOCUS
DEFINITION
ACCESSION
BZ554593
pacsl-60 4763.x1 pacsl-60 Pseudomonas aeruginosa genomic clone
pacsl-60 4763, genomic survey sequence.
BZ554593

/cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee Male BAC Library"

ORIGIN
Query Match          91.1%; Score 16.4; DB 28; Length 1404;
Best Local Similarity 94.4%; Pred. No. 1.7e+04;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TCGCTCGGTGCAGGGGG 18
||||| |||||||
Db 760 TCGCTCGGTGCAGGGGG 777

RESULT 12
BM068740/c
LOCUS
DEFINITION
ACCESSION
VERSION
SOURCE
KEYWORDS
EST.
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 415)
AUTHORS Melton, D., Brown, J., Kent, G., Permut, A., Lee, C., Kaestner, K.,
Lemishka, I., Searce, M., Brestelli, J., Gradwohl, G., Clifton, S.,
Hillier, L., Marra, M., Pape, D., Wylie, T., Martin, J., Blisstein, A.,
Schmitt, A., Theising, B., Ritter, E., Ronko, I., Bennett, J.,
Cardenas, M., Gibbons, M., McCann, R., Cole, R., Teagareishvili, R.,
Williams, T., Jackson, Y. and Bowers, Y.
TITLE Endocrine Pancreas Consortium
JOURNAL Unpublished (2000)
COMMENT Other ESTs: ie84c05.x1
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
MA 02138
Tel: 617-495-1812
Fax: 617-495-8557
Email: dmelton@bioh.harvard.edu
Library was constructed by Dr. Douglas Melton DNA sequencing by:
Washington University Genome Sequencing Center For information on

```

BZ554593.1 GI:27162271

GSS.
Pseudomonas aeruginosa
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
1 (bases 1 to 1404)
Spencer, D.H., Raymond, C.K., Smith, E.E., Sims, E.E., Hastings, M.,
Burns, J.L., Kaul, R. and Olsen, M.V.
Whole-Genome-Sequence variation among multiple isolates of
Pseudomonas aeruginosa library
J. Bacteriol. (2002) In press
Contact: Chris K. Raymond
Genome Center
University of Washington
Box 352145, Seattle, WA 98105-2145, USA
Tel: 2062216954
Fax: 2066857244
Email: craymond@u.washington.edu
Class: shotgun.

Location/Qualifiers
1..1404
/organism="Pseudomonas aeruginosa"
/mol_type="genomic DNA"
/strain="1-60"
/db_xref="taxon:287"
/clone="pacsl-60 4763"
/clone_lib="pacsl-60"
/note="clinical isolate 1-60 Whole genomic shotgun
library."

Query Match 91.1%; Score 16.4; DB 28; Length 1404;
Best Local Similarity 94.4%; Pred. No. 1.7e+04;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 TCGCTCGGTGCAGGGGG 18
||||| |||||||
Db 760 TCGCTCGGTGCAGGGGG 777

RESULT 12
BM068740/c
LOCUS
DEFINITION
ACCESSION
VERSION
SOURCE
KEYWORDS
EST.
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 415)
AUTHORS Melton, D., Brown, J., Kent, G., Permut, A., Lee, C., Kaestner, K.,
Lemishka, I., Searce, M., Brestelli, J., Gradwohl, G., Clifton, S.,
Hillier, L., Marra, M., Pape, D., Wylie, T., Martin, J., Blisstein, A.,
Schmitt, A., Theising, B., Ritter, E., Ronko, I., Bennett, J.,
Cardenas, M., Gibbons, M., McCann, R., Cole, R., Teagareishvili, R.,
Williams, T., Jackson, Y. and Bowers, Y.
TITLE Endocrine Pancreas Consortium
JOURNAL Unpublished (2000)
COMMENT Other ESTs: ie84c05.x1
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
MA 02138
Tel: 617-495-1812
Fax: 617-495-8557
Email: dmelton@bioh.harvard.edu
Library was constructed by Dr. Douglas Melton DNA sequencing by:
Washington University Genome Sequencing Center For information on

RESULT 12
BM068740/c
LOCUS
DEFINITION
ACCESSION
VERSION
SOURCE
KEYWORDS
EST.
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 415)
AUTHORS Melton, D., Brown, J., Kent, G., Permut, A., Lee, C., Kaestner, K.,
Lemishka, I., Searce, M., Brestelli, J., Gradwohl, G., Clifton, S.,
Hillier, L., Marra, M., Pape, D., Wylie, T., Martin, J., Blisstein, A.,
Schmitt, A., Theising, B., Ritter, E., Ronko, I., Bennett, J.,
Cardenas, M., Gibbons, M., McCann, R., Cole, R., Teagareishvili, R.,
Williams, T., Jackson, Y. and Bowers, Y.
TITLE Endocrine Pancreas Consortium
JOURNAL Unpublished (2000)
COMMENT Other ESTs: ie84c05.x1
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
MA 02138
Tel: 617-495-1812
Fax: 617-495-8557
Email: dmelton@bioh.harvard.edu
Library was constructed by Dr. Douglas Melton DNA sequencing by:
Washington University Genome Sequencing Center For information on

obtaining a clone please contact: Juliana Brown
(brown@fas.harvard.edu) This sequence now available from the IMAGE
consortium, for clone orders contact: info@image.llnl.gov
High quality sequence stop: 413.

FEATURES

source
1. .415
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5673585"
/sex="Both"
/tissue_type="Islets of Langerhans"
/dev_stage="Adult"
/lab_host="DH10B"
/clone_lib="Melton Normalized Human Islet 4 M4-HIS 1"
/note="Organ: Pancreas; Vector: pSPORT1; Site: 1; Not 1;
Site 2: Sal 1; Starting library constructed using
SuperScript Plasmid Library kit (Life Technologies). cDNA
made by oligo-dT priming. Size-selected by column
fractionation; average insert size 1.08 kb. Library was
amplified once on solid support and plasmid DNA from
library was prepared. The library DNA was normalized by
method #4 from Bonaldo, Lennon, and Soares 1996 Genome
Research 6:791-806; 0.5 microgram single-stranded library
plasmid DNA was mixed with 5 micrograms PCR product
representing library inserts and hybridized to an Ecot of
20. Single-stranded (unhybridized) plasmids were isolated
by hydroxyapatite chromatography and used to make this
library."

ORIGIN

Query Match 88.9%; Score 16; DB 12; Length 415;
Best Local Similarity 100.0%; Pred. No. 2.2e+04;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 GCGTCGTCGACGGGG 17
|||||
DB 101 GCGTCGTCGACGGGG 86

RESULT 13
BM055266/c
LOCUS
DEFINITION
cDNA clone IMAGE:5674507 5', mRNA sequence.
BM055266
BM055266.1 GI:16813022
EST.
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 453)
Melton, D., Brown, J., Kenty, G., Permutt, A., Lee, C., Kaestner, K.,
Lemishka, I., Searce, M., Brestelli, J., Gradwohl, G., Clifton, S.,
Hillier, L., Marra, M., Pape, D., Wylie, T., Martin, J., Blistain, A.,
Schmitt, A., Theising, B., Ritter, E., Renko, I., Bennett, J.,
Cardenas, M., Gibbons, M., McCann, R., Cole, R., Tsagarishvili, R.,
Williams, T., Jackson, Y., and Bowers, Y.
Endocrine Pancreas Consortium
Unpublished (2000)
Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
MA 02138
Tel: 617-495-1812
Fax: 617-495-8557
Email: dmelton@biohp.harvard.edu
Library was constructed by Dr. Douglas Melton DNA sequencing by:
Washington University Genome Sequencing Center For information on
obtaining a clone please contact: Juliana Brown
(brown@fas.harvard.edu) This sequence now available from the IMAGE

consortium, for clone orders contact: info@image.llnl.gov
High quality sequence stop: 429.

FEATURES

source
1. .453
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5674507"
/sex="Both"
/tissue_type="Islets of Langerhans"
/dev_stage="Adult"
/lab_host="DH10B"
/clone_lib="Melton Normalized Human Islet 4 M4-HIS 1"
/note="Organ: Pancreas; Vector: pSPORT1; Site: 1; Not 1;
Site 2: Sal 1; Starting library constructed using
SuperScript Plasmid Library kit (Life Technologies). cDNA
made by oligo-dT priming. Size-selected by column
fractionation; average insert size 1.08 kb. Library was
amplified once on solid support and plasmid DNA from
library was prepared. The library DNA was normalized by
method #4 from Bonaldo, Lennon, and Soares 1996 Genome
Research 6:791-806; 0.5 microgram single-stranded library
plasmid DNA was mixed with 5 micrograms PCR product
representing library inserts and hybridized to an Ecot of
20. Single-stranded (unhybridized) plasmids were isolated
by hydroxyapatite chromatography and used to make this
library."

ORIGIN

Query Match 88.9%; Score 16; DB 12; Length 453;
Best Local Similarity 100.0%; Pred. No. 2.2e+04;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 GCGTCGTCGACGGGG 17
|||||
DB 325 GCGTCGTCGACGGGG 310

RESULT 14
BM792946/c
LOCUS
DEFINITION
K-EST0073583 S22SNU16n1 Homo sapiens cDNA clone S22SNU16n1-4-D03
5', mRNA sequence.
BM792946
BM792946.1 GI:19141178
EST.
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 490)
Kim, N.S., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R.,
Oh, K.J., Cheong, J.E., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and
Kim, Y.S.
21C Frontier Korean EST Project 2001
Unpublished (2002)
Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 4 row: D column: 03
High quality sequence stop: 490.

FEATURES

source
1. .490
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="S22SNU16n1-4-D03"
/sex="F"
/tissue_type="Ascites"

/cell_type="Lymphoblast-like"
 /cell_line="SNU-16"
 /lab_host="DH10B"
 /clone_lib="S22SNU16n1"
 /notes="Organ: Stomach; Vector: pT7T3-Pac; Site 1: ECORI;
 Site 2: NotI; The S22SNU16 library was contributed by the
 Soares laboratory and it was constructed as described by
 Bonaldi, M.F., Lennon, G. and Soares, M.B. (1996), genome
 Research 6(9): 791-806. RNA was prepared from harvested
 cells of SNU-16 culture. SNU-16 cell was obtained from
 Korean Cell Line Bank (KCLB). SNU-16 was established from
 ascitic fluids of Korean patients by Park J.G. et al.
 (1990), Cancer Res 50: 2773-2780."

ORIGIN

Query Match 88.9%; Score 16; DB 12; Length 490;
 Best Local Similarity 100.0%; Pred. No. 2.2e+04;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GCGTCGGTGCAGGGG 17
 |||||
 DB 41 GCGTCGGTGCAGGGG 26

RESULT 15

BM820521/c
 LOCUS K-EST0089071 S20T665307 Homo sapiens cDNA clone S20T665307-7-H11
 DEFINITION 519 bp mRNA linear EST 06-MAR-2002

ACCESSION BM820521

VERSION BM820521.1 GI:19176934

KEYWORDS EST.

SOURCE Homo sapiens

ORGANISM Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 519)

Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,

Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and

Kim,Y.S.

21C Frontier Korean EST Project 2001

Unpublished (2002)

Contact: Kim YS

Genome Research Center

Korea Research Institute of Bioscience & Biotechnology

52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea

Tel: +82-42-860-4470

Fax: +82-42-860-4409

Email: yongsung@mail.kribb.re.kr

Plate: 7 row: H column: 11

High quality sequence stop: 519.

Location/Qualifiers

1..519

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="S20T665307-7-H11"

/sex="M"

/lab_host="Top10F"

/clone_lib="S20T665307"

/notes="Organ: Stomach; Vector: pCNS; Site 1: ECORI;

Site 2: NotI; The poly (A)+ RNA was dephosphorylated with

bacterial alkaline phosphatase (BAP) and then decapped

with tobacco acid pyrophosphatase (TAP). The decapped

intact mRNA was ligated with DNA-RNA linker including EcoR

I site by treatment of T4 RNA ligase and the first strand

cDNA was synthesized from oligo dt-selected mRNA by

priming with dt-tailed vector. The dt-tailed vector was

adjusted to have about 60nt. The cDNA vector was

circularized with E. coli DNA ligase after digestion of

EcoRI which site is also included in vector. An RNA strand

converted to a DNA strand by Okayama-Berg method. The

obtained cDNA vectors were used for transformation of

competent cells E. coli Top10F' by electroporation method.
 The cDNA libraries constructed by this method are
 full-length enriched cDNA library."

ORIGIN

Query Match 88.9%; Score 16; DB 12; Length 519;
 Best Local Similarity 100.0%; Pred. No. 2.2e+04;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GCGTCGGTGCAGGGG 17
 |||||

DB 414 GCGTCGGTGCAGGGG 399
 |||||

ORIGIN

Search completed: July 2, 2004, 13:33:13
 Job time : 1350.14 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 2, 2004, 08:09:30 ; Search time 28.2073 Seconds
(without alignments)
354.132 Million cell updates/sec

Title: US-10-068-160-20

Perfect score: 18
Sequence: 1 tgcgtcggtcagggggg 18

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA:
1: /cgn2_6/ptodata/2/ina/5A_COMB.seq.*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq.*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq.*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq.*
5: /cgn2_6/ptodata/2/ina/PTUS_COMB.seq.*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
C 1	15.4	85.6	885	4	US-09-252-991A-7532
C 2	15.4	85.6	912	4	US-09-252-991A-7811
C 3	15.4	85.6	1242	4	US-09-252-991A-7949
C 4	15.4	85.6	1392	4	US-09-489-039A-4664
C 5	15.4	85.6	1794	4	US-09-252-991A-7681
C 6	15.4	83.3	1521	1	US-08-496-855A-3
C 7	15.4	83.3	1521	2	US-07-938-154-9
C 8	15.4	83.3	1521	5	PCT-US91-02311-9
C 9	15.4	83.3	2448	4	US-08-487-596-13
C 10	15.4	83.3	2448	4	US-08-660-451A-13
C 11	15.4	83.3	2450	2	US-08-466-589-9
C 12	15.4	83.3	2450	2	US-08-700-636-9
C 13	15.4	83.3	2450	3	US-08-467-574-9
C 14	15.4	83.3	2450	4	US-09-217-345-9
C 15	15.4	83.3	2450	4	US-09-892-985-9
C 16	14.8	82.2	1814	4	US-09-702-705-319
C 17	14.8	82.2	1814	4	US-09-736-457-319
C 18	14.8	82.2	1814	4	US-09-614-124B-319
C 19	14.8	82.2	1814	4	US-09-671-325-319
C 20	14.8	82.2	1814	4	US-09-589-184-319
C 21	14.4	80.0	1584	4	US-09-489-039A-2524
C 22	14.4	80.0	43360	4	US-09-453-702B-206
C 23	14.4	80.0	45325	4	US-09-453-702B-261
C 24	14.4	77.8	227	1	US-08-337-268A-40
C 25	14.4	77.8	227	1	US-08-484-570A-40
C 26	14.4	77.8	876	4	US-09-252-991A-12753
C 27	14.4	77.8	36800	4	US-08-311-731A-139

C 28	13.8	76.7	402	4	US-09-252-991A-1377	Sequence 1877, Ap
C 29	13.8	76.7	423	4	US-09-252-991A-13029	Sequence 13029, A
C 30	13.8	76.7	552	4	US-09-252-991A-6091	Sequence 6091, Ap
C 31	13.8	76.7	609	4	US-09-252-991A-6173	Sequence 6173, Ap
C 32	13.8	76.7	633	4	US-09-489-039A-2752	Sequence 2752, Ap
C 33	13.8	76.7	642	4	US-09-252-991A-6014	Sequence 6014, Ap
C 34	13.8	76.7	822	4	US-09-252-991A-6377	Sequence 6377, Ap
C 35	13.8	76.7	861	4	US-09-252-991A-1336	Sequence 1336, Ap
C 36	13.8	76.7	883	3	US-08-943-731-171	Sequence 171, Appl
C 37	13.8	76.7	903	3	US-08-829-525-37	Sequence 37, Appl
C 38	13.8	76.7	903	3	US-08-609-583A-37	Sequence 37, Appl
C 39	13.8	76.7	903	3	US-08-937-399-37	Sequence 37, Appl
C 40	13.8	76.7	903	4	US-09-310-367-37	Sequence 37, Appl
C 41	13.8	76.7	903	4	US-09-032-337-37	Sequence 37, Appl
C 42	13.8	76.7	903	4	US-09-252-991A-8502	Sequence 8502, Ap
C 43	13.8	76.7	903	4	US-09-464-231-37	Sequence 37, Appl
C 44	13.8	76.7	1086	4	US-09-252-991A-8434	Sequence 8434, Ap
C 45	13.8	76.7	1110	4	US-09-252-991A-8962	Sequence 8962, Ap

ALIGNMENTS

RESULT 1
US-09-252-991A-7532/c
; Sequence 7532, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 7532
; LENGTH: 885
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-7532

Query Match 85.6%; Score 15.4; DB 4; Length 885;
Best Local Similarity 94.1%; Pred. No. 1.3e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GCGTCGTCACGGGGG 18
Db 642 GCGCGTCACGGGGG 626

RESULT 2
US-09-252-991A-7811
; Sequence 7811, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 7811
; LENGTH: 912
; TYPE: DNA

ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-7811

Query Match 85.6%; Score 15.4; DB 4; Length 912;
Best Local Similarity 94.1%; Pred. No. 1.3e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GCCTCGGTGCAGGGGG 18
||| ||||| ||||| |||||
DB 277 GCGGCGGTGCAGGGGG 293

RESULT 3
US-09-252-991A-7949
; Sequence 7949, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252.991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 7949
; LENGTH: 1242
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-7949

Query Match 85.6%; Score 15.4; DB 4; Length 1242;
Best Local Similarity 94.1%; Pred. No. 1.3e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GCCTCGGTGCAGGGGG 18
||| ||||| ||||| |||||
DB 509 GCGGCGGTGCAGGGGG 525

RESULT 4
US-09-489-039A-4664
; Sequence 4664, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489.039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 4664
; LENGTH: 1392
; TYPE: DNA
; ORGANISM: Klebsiella pneumoniae
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (876)
; OTHER INFORMATION: Identity of nucleotide at the above locations are unknown.
US-09-489-039A-4664

Query Match 85.6%; Score 15.4; DB 4; Length 1392;
Best Local Similarity 94.1%; Pred. No. 1.3e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GCCTCGGTGCAGGGGG 18
||| ||||| ||||| |||||

DB 335 GCTTCGGTGCAGGGGG 351

RESULT 5
US-09-252-991A-7681/c
; Sequence 7681, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252.991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 7681
; LENGTH: 1794
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-7681

Query Match 85.6%; Score 15.4; DB 4; Length 1794;
Best Local Similarity 94.1%; Pred. No. 1.3e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GCCTCGGTGCAGGGGG 18
||| ||||| ||||| |||||
DB 259 GCGGCGGTGCAGGGGG 243

RESULT 6
US-08-496-855A-3
; Sequence 3, Application US/08496855A
; Patent No. 5801232
; GENERAL INFORMATION:
; APPLICANT: Elliot, Kathryn J.
; APPLICANT: Ellis, Steven B.
; APPLICANT: Harpold, Michael M.
; TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE
; TITLE OF INVENTION: RECEPTOR COMPOSITIONS AND METHODS EMPLOYING SAME
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brown, Martin, Haller & McClain
; STREET: 1660 Union Street
; CITY: San Diego
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 92101-2926
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/496,855A
; FILING DATE: 20-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/149,503
; FILING DATE: 08-NOV-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/028,031
; FILING DATE: 08-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 6362-9369B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-238-0999
; TELEFAX: 619-238-0062

; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1521 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1..1521
; OTHER INFORMATION: /note= "Human neuronal NACHR beta-2
; OTHER INFORMATION: cDNA shown as top nucleotide sequence in
; OTHER INFORMATION: Figure..."
US-08-496-855A-3

Query Match 83.3%; Score 15; DB 1; Length 1521;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GCGTCGGTGCAGGG 16
Db 1192 GCGTCGGTGCAGGG 1206

RESULT 7

US-07-938-154-9
; Sequence 9, Application US/07938154
; Patent No. 5981193
; GENERAL INFORMATION:
; APPLICANT: Harpold, Michael M.
; APPLICANT: Ellis, Stephen B.
; APPLICANT: Brust, Paul
; APPLICANT: Velicelebi, Gonul
; TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pretty Schroeder Brueggemann & Clark
; STREET: 444 South Flower Street, Suite 2000
; CITY: Los Angeles
; STATE: CA
; COUNTRY: USA
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/938,154
; FILING DATE: 30-NOV-1992
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/US91/02311
; FILING DATE: 03-APR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/504,455
; FILING DATE: 03-APR-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Reiter, Stephen E.
; REGISTRATION NUMBER: 31,192
; REFERENCE/DOCKET NUMBER: 241 9380
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-546-4737
; TELEFAX: 619-546-9392
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1521 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cDNA

; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1..1521
; OTHER INFORMATION: /note= "Human neuronal NACHR beta-2
; OTHER INFORMATION: cDNA shown as top sequence in Fig 9."
US-07-938-154-9

Query Match 83.3%; Score 15; DB 2; Length 1521;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GCGTCGGTGCAGGG 16
Db 1192 GCGTCGGTGCAGGG 1206

RESULT 8

PCT-US91-02311-9
; Sequence 9, Application PC/TUS9102311
; GENERAL INFORMATION:
; APPLICANT: Harpold, Michael M.
; APPLICANT: Ellis, Stephen B.
; APPLICANT: Brust, Paul
; APPLICANT: Velicelebi, Gonul
; TITLE OF INVENTION: Human Neuronal Nicotinic Acetylcholine
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fitch, Even, Tabin & Flannery
; STREET: 135 S. LaSalle St.
; CITY: Chicago
; STATE: Ill.
; COUNTRY: USA
; ZIP: 60603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US91/02311
; FILING DATE: 19910403
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Feder, Scott B.
; REFERENCE/DOCKET NUMBER: 51247/PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-372-7842
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1521 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: DNA (genomic)
PCT-US91-02311-9
Query Match 83.3%; Score 15; DB 5; Length 1521;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GCGTCGGTGCAGGG 16
Db 1192 GCGTCGGTGCAGGG 1206

RESULT 9

US-08-487-596-13
; Sequence 13, Application US/08487596
; Patent No. 6440681
; GENERAL INFORMATION:
; APPLICANT: Elliot, Kathryn J.

APPLICANT: Ellis, Steven B.
APPLICANT: Harpold, Michael M.
TITLE OF INVENTION: METHODS FOR IDENTIFYING AGONISTS AND
TITLE OF INVENTION: ANTAGONISTS FOR HUMAN NEURONAL
TITLE OF INVENTION: NICOTINIC ACETYLCHOLINE RECEPTORS
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Brown, Martin, Haller & McClain
STREET: 1660 Union Street
CITY: San Diego
STATE: CA
COUNTRY: USA
ZIP: 92101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US 08/487,596
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO US94/02447
FILING DATE: 08-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/149,503
FILING DATE: 08-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/028,031
FILING DATE: 08-MAR-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/938,154
FILING DATE: 30-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/504,455
FILING DATE: 03-APR-1990
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L.
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 6362-9951
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-238-0999
TELEFAX: 619-238-0062
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 2448 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 265..1773
OTHER INFORMATION: /product= "BETA-2 SUBUNIT"

US-08-487-596-13
Query Match 83.3%; Score 15; DB 4; Length 2448;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GCGTCGGTGCAGGGG 16
|||||
Db 1444 GCGTCGGTGCAGGGG 1458

RESULT 10
US-08-660-451A-13
Sequence 13, Application US/08660451A
Patent No. 6524789
GENERAL INFORMATION:
APPLICANT: Elliott, Kathryn J.
APPLICANT: Harpold, Michael M.

TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE
TITLE OF INVENTION: RECEPTOR COMPOSITIONS AND METHODS EMPLOYING SAME
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Brown, Martin, Haller & McClain
STREET: 1660 Union Street
CITY: San Diego
STATE: CA
COUNTRY: USA
ZIP: 92101-2926
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US 08/660,451A
FILING DATE: June 7, 1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/484,722
FILING DATE: 06/07/95
ATTORNEY/AGENT INFORMATION:
NAME: Seidman, Stephanie L.
REGISTRATION NUMBER: 33,779
REFERENCE/DOCKET NUMBER: 6362-9370B
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-238-0999
TELEFAX: 619-238-0062
TELEX:
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 2448 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: Genomic DNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE:
ORIGINAL SOURCE:
FEATURE:
NAME/KEY: Coding Sequence
LOCATION: 265..1773
OTHER INFORMATION: beta2 human neuronal nicotinic
OTHER INFORMATION: acetylcholine receptor
NAME/KEY: 5'UTR
LOCATION: 1..264
OTHER INFORMATION:
NAME/KEY: 3'UTR
LOCATION: 1774..2448
OTHER INFORMATION:
US-08-660-451A-13

Query Match 83.3%; Score 15; DB 4; Length 2448;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GCGTCGGTGCAGGGG 16
|||||
Db 1444 GCGTCGGTGCAGGGG 1458

RESULT 11
US-08-466-589-9
Sequence 9, Application US/08466589
Patent No. 5837489
GENERAL INFORMATION:
APPLICANT: Elliott, Kathryn J.
APPLICANT: Ellis, Steven B.
APPLICANT: Harpold, Michael M.
TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE
TITLE OF INVENTION: RECEPTOR COMPOSITIONS AND METHODS EMPLOYING SAME


```
;
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brown, Martin, Haller & McClaim
; STREET: 1660 Union Street
; CITY: San Diego
; STATE: CA
; COUNTRY: USA
; ZIP: 92101-2926
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/466,589
; FILING DATE: June 5, 1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/028,031
; FILING DATE: March 8, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie L
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 6362-9950
; TELEPHONE: 619-238-0999
; TELEFAX: 619-238-0062
; TELEX:
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2450 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: CDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 267..1775
; US-08-466-589-9

Query Match      83.3%; Score 15; DB 2; Length 2450;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 GCGTCGGTGCAGGGG 16
Db      1446 GCGTCGGTGCAGGGG 1460
|||||
RESULT 12
US-08-700-636-9
; Sequence 9, Application US/08700636
; Patent No. 5910582
; GENERAL INFORMATION:
; APPLICANT: Elliot, Kathryn J.
; APPLICANT: Ellis, Steven B.
; APPLICANT: Harpold, Michael M.
; TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark
; STREET: 444 South Flower Street, Suite 2000
; CITY: Los Angeles
; STATE: CA
; COUNTRY: USA
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
```

```
;
; APPLICATION NUMBER: US/08/700,636
; FILING DATE: 16-JUL-1996
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/028,031
; FILING DATE: 08-MAR-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Reiter, Stephen E.
; REGISTRATION NUMBER: 31,192
; REFERENCE/DOCKET NUMBER: P41 9368
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-546-4737
; TELEFAX: 619-546-9392
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2450 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: CDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 267..1775
; US-08-700-636-9

Query Match      83.3%; Score 15; DB 2; Length 2450;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 GCGTCGGTGCAGGGG 16
Db      1446 GCGTCGGTGCAGGGG 1460
|||||
RESULT 13
US-08-467-574-9
; Sequence 9, Application US/08467574
; Patent No. 6022704
; GENERAL INFORMATION:
; APPLICANT: Elliot, Kathryn J.
; APPLICANT: Ellis, Steven B.
; APPLICANT: Harpold, Michael M.
; TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Brown, Martin, Haller & McClaim
; STREET: 1660 Union Street
; CITY: San Diego
; STATE: CA
; COUNTRY: USA
; ZIP: 92101-2926
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/467,574
; FILING DATE: June 5, 1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/028,031
; FILING DATE: March 8, 1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie L
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 6362-9949
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-238-0999
; TELEFAX: 619-238-0062
; TELEX:
; INFORMATION FOR SEQ ID NO: 9:
```

```

; SEQUENCE CHARACTERISTICS:
; LENGTH: 2450 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 267..1775
US-08-467-574-9

; Query Match
; Best Local Similarity 93.3%; Score 15; DB 3; Length 2450;
; Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps
;

QY 2 GCGTCGGTCAGGG 16
DB 1446 GCGTCGGTCAGGG 1450

RESULT 14
US-09-217-345-9
; Sequence 9, Application US/09217345
; Patent No. 6303753
; GENERAL INFORMATION:
; APPLICANT: Eliot, Kathryn J.
; APPLICANT: Ellis, Steven B.
; APPLICANT: Harpold, Michael M.
; TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE
; TITLE OF INVENTION: RECEPTOR COMPOSITIONS AND METHODS EMPLOYING SAME
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Heller Ehrman White & McAuliffe
; STREET: 4250 Executive Square, 7th Floor
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/217,345
; FILING DATE: 21-DEC-96
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/467,574
; FILING DATE: 05-JUN-95
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/466,589,
; FILING DATE: 05-JUN-95
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/028,031
; FILING DATE: 08-MAR-93
; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie L
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 24735-9949B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-450-8400
; TELEFAX: 619-587-5360
; TELEX:
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2450 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 267..1775

```

```

US-09-217-345-9
Query Match      83.3%; Score 15; DB 4; Length 2450;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 15; Conservative 0; Mismatches 0; Gaps 0;

QY      2 GCGTCGGTCGAGGG 16
      |||||
Db      1446 GCGTCGGTCGAGGG 1460
      |||||

RESULT 15
US-09-892-985-9
; Sequence 9, Application US/09892985
; Patent No. 6664375
; GENERAL INFORMATION:
; APPLICANT: Elliot, Kathryn J.
;           Ellis, Steven B.
;           Harpold, Michael M.
; TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE
; RECEPTOR COMPOSITIONS AND METHODS EMPLOYING SAME
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Heller Erman White & McAuliffe
; STREET: 4250 Executive Square, 7th Floor
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/892,985
; FILING DATE: 27-Jun-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/217,345
; FILING DATE: 21-DEC-98
; APPLICATION NUMBER: US 08/467,574
; FILING DATE: 05-JUN-95
; APPLICATION NUMBER: US 08/466,589,
; FILING DATE: 05-JUN-95
; APPLICATION NUMBER: US 08/028,031
; FILING DATE: 08-MAR-93
; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie L
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 24735-9949B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-450-8400
; TELEFAX: 619-587-5360
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2450 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 267..1775
; SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-09-892-985-9

Query Match      83.3%; Score 15; DB 4; Length 2450;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 15; Conservative 0; Mismatches 0; Gaps 0;

QY      2 GCGTCGGTCGAGGG 16
      |||||

```

```

US-09-217-345-9
Query Match      83.3%; Score 15; DB 4; Length 2450;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 15; Conservative 0; Mismatches 0; Gaps 0;

QY      2 GCGTCGGTCGAGGG 16
      |||||
Db      1446 GCGTCGGTCGAGGG 1460
      |||||

RESULT 15
US-09-892-985-9
; Sequence 9, Application US/09892985
; Patent No. 6664375
; GENERAL INFORMATION:
; APPLICANT: Elliot, Kathryn J.
;           Ellis, Steven B.
;           Harpold, Michael M.
; TITLE OF INVENTION: HUMAN NEURONAL NICOTINIC ACETYLCHOLINE
; RECEPTOR COMPOSITIONS AND METHODS EMPLOYING SAME
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Heller Erman White & McAuliffe
; STREET: 4250 Executive Square, 7th Floor
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/892,985
; FILING DATE: 27-Jun-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/217,345
; FILING DATE: 21-DEC-98
; APPLICATION NUMBER: US 08/467,574
; FILING DATE: 05-JUN-95
; APPLICATION NUMBER: US 08/466,589,
; FILING DATE: 05-JUN-95
; APPLICATION NUMBER: US 08/028,031
; FILING DATE: 08-MAR-93
; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie L
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 24735-9949B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-450-8400
; TELEFAX: 619-587-5360
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2450 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 267..1775
; SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-09-892-985-9

Query Match      83.3%; Score 15; DB 4; Length 2450;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 15; Conservative 0; Mismatches 0; Gaps 0;

QY      2 GCGTCGGTCGAGGG 16
      |||||

```

Db 1446 GCGTCGTCACAGGG 1460

Search completed: July 2, 2004, 13:37:54
Job time : 29.2073 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 2, 2004, 06:05:50 ; Search time 134.89 Seconds
(without alignments)
566.887 Million cell updates/sec

Title: US-10-068-160-20

Perfect score: 18

Sequence: 1 tgcgtcggtcagggggg 18

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 212409041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N.Geneseq_29Jan04:*

- 1: Geneseqn1980s:*
- 2: Geneseqn1990s:*
- 3: Geneseqn2000s:*
- 4: Geneseqn2001as:*
- 5: Geneseqn2001bs:*
- 6: Geneseqn2002s:*
- 7: Geneseqn2003as:*
- 8: Geneseqn2003bs:*
- 9: Geneseqn2003cs:*
- 10: Geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	18	100.0	20 7 ACC48318	Acc48318 CpG oligo
2	18	100.0	20 7 ACC48305	Acc48305 CpG oligo
3	18	100.0	20 8 ACC83123	Acc83123 D class C
4	17	94.4	19 4 AAC80659	Aac80659 Immunogen
5	17	94.4	19 4 AAC80629	Aac80629 Immunogen
6	17	94.4	19 6 ABK46507	Abk46507 Immunost
7	16.4	91.1	20 4 AAC80662	Aac80662 Immunogen
8	16.4	91.1	20 4 AAC80661	Aac80661 Immunogen
9	16.4	91.1	20 4 AAC80620	Aac80620 Immunogen
10	16.4	91.1	20 4 AAC80631	Aac80631 Immunore
11	16.4	91.1	20 4 AAC80590	Aac80590 Immunore
12	16.4	91.1	20 4 AAC80632	Aac80632 Immunore
13	16.4	91.1	20 6 ABK46510	Abk46510 Immunost
14	16.4	91.1	20 6 ABK46468	Abk46468 Immunost
15	16.4	91.1	20 6 ABK46509	Abk46509 Immunost
16	16.4	91.1	20 7 ACC48298	Acc48298 CpG oligo
17	16.4	91.1	20 7 ACC48320	Acc48320 CpG oligo
18	16.4	91.1	20 7 ACC48312	Acc48312 CpG oligo
19	16.4	91.1	20 7 ACC48306	Acc48306 CpG oligo
20	16.4	91.1	20 7 ACC48319	Acc48319 CpG oligo
21	16.4	91.1	20 7 ACC48321	Acc48321 CpG oligo
22	16.4	91.1	20 8 ACC83125	Acc83125 D class C
23	16.4	91.1	20 8 ACC83117	Acc83117 D class C

24	16.4	91.1	20 8 ACC83124	Acc83124 D class C
25	16.4	91.1	20 8 ACC83126	Acc83126 D class C
26	16.4	91.1	20 9 ADD01050	Add01050 CpG D oli
27	16	88.9	840 7 ABX12764	Abx12764 DNA encod
28	16	88.9	1192 6 AAS62412	Aas62412 cDNA sequ
29	16	88.9	2487 6 AAL39655	Aal39655 Human sec
30	15.4	85.6	19 4 AAC80655	Aac80655 Immunogen
31	15.4	85.6	19 4 AAC80663	Aac80663 Immunogen
32	15.4	85.6	19 4 AAS09633	Aas09633 Immunorea
33	15.4	85.6	19 4 AAS09625	Aas09625 Immunorea
34	15.4	85.6	19 6 ABK46503	Abk46503 Immunosti
35	15.4	85.6	19 6 ABK46511	Abk46511 Immunosti
36	15.4	85.6	337 6 ABNL9459	Abnl9459 Human ORF
37	15.4	85.6	765 6 ABK79894	Abk79894 Bacillus
38	15.4	85.6	1510 9 ADC30295	Adc30295 Human nov
39	15.4	85.6	2118 5 AAS82471	Aas82471 DNA encod
40	15.4	85.6	2118 5 AAS93017	Aas93017 DNA encod
41	15.4	85.6	2859 7 ACA39941	Aca39941 Prokaryot
42	15.4	85.6	3290 7 ACF16998	Acf16998 Human NOV
43	15.4	85.6	12423 9 ADS54082	Ads54082 Pretreate
44	15	83.3	21 4 AAH62282	Aah62282 CHRN82 po
45	15	83.3	1023 9 ADB78681	Adb78681 Human nic

ALIGNMENTS

RESULT 1
ACC48318
ID ACC48318 standard; DNA; 20 BP.

XX AC ACC48318;

XX AC ACC48318;

DT 11-AUG-2003 (first entry)

XX CpG oligodeoxynucleotide DV51.

CpG oligodeoxynucleotide; dendritic cell; tumour; immunotherapy; vaccine;
cytostatic; immunostimulant; gene therapy; ss.

XX Synthetic.

XX WO2003020884-A2.

XX 13-MAR-2003.

XX 13-AUG-2002; 2002WO-US025732.

XX 14-AUG-2001; 2001US-0312190P.

XX (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX Klimman DM, Gursel M, Verthelyi D;

XX WPI; 2003-300874/29.

Generating mature dendritic cells for tumor immunotherapy or as vaccines
for activating the immune system to treat diseases such as cancer,
comprise contacting a dendritic cell precursor with a D type
oligodeoxynucleotide.

XX Disclosure; Fig 8; 69pp; English.

The present sequence is that of CpG oligodeoxynucleotide DV51 of the
invention. A claimed method for generating dendritic cells involves
contacting a dendritic cell precursor, especially a monocyte, with a D
type oligodeoxynucleotide (see ACC48294) containing a central
unmethylated CpG motif. The method is useful for generating mature
dendritic cells and enhancing T cell responses, thus enhancing antigen
presentation. Mature dendritic cells are useful for tumour immunotherapy,
for augmenting an immune response to an infectious agent or to a vaccine,
and as vaccines to prevent future infection or to activate the immune
system to treat diseases such as cancer. Mature dendritic cells may also

CC be used to produce activated T lymphocytes
 XX Sequence 20 BP; 1 A; 3 C; 13 G; 3 T; 0 U; 0 Other;
 SQ Query Match 100.0%; Score 18; DB 7; Length 20;
 Best Local Similarity 100.0%; Pred. No. 68;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGGCTCGGTGCAGGGGG 18
 |||||
 Db 3 TGGCTCGGTGCAGGGGG 20

RESULT 2
 ACC48305
 ID ACC48305 standard; DNA; 20 BP.
 XX AC ACC48305;
 XX DT 11-AUG-2003 (first entry)
 XX DE CpG oligodeoxynucleotide used for dendritic cell maturation.
 XX KW CpG oligodeoxynucleotide; dendritic cell; tumour; immunotherapy; vaccine;
 XX KW cytotatic; immunostimulant; gene therapy; ss.
 XX OS Synthetic.
 XX FH Key Location/Qualifiers
 FT misc_difference 1 /tag= a
 FT /note= "N is any base (especially G) or no base"
 FT misc_difference 2 /tag= b
 FT /note= "N is any base (especially G) or no base"
 FT WO2003020884-A2.
 XX PN 13-MAR-2003.
 XX PD 13-AUG-2002; 2002WO-US025732.
 XX PF 14-AUG-2001; 2001US-0312190P.
 XX PR (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX PA Klinman DM, Gursel M, Verthelyi D;
 XX PI WPI; 2003-300874/29.
 XX DR
 XX PT Generating mature dendritic cells for tumor immunotherapy or as vaccines
 XX PT for activating the immune system to treat diseases such as cancer,
 XX PT comprises contacting a dendritic cell precursor with a D type
 XX PT oligodeoxynucleotide.
 XX PS Disclosure; Page 26; 69pp; English.
 XX CC The present sequence is that of a D type CpG oligodeoxynucleotide that is
 XX CC an example of claimed D type oligodeoxynucleotides (see ACC48294) of the
 XX CC invention. Mature dendritic cells are obtained by contacting a dendritic
 XX CC cell precursor, such as a monocyte, with such an oligodeoxynucleotide.
 XX CC The method is useful for generating mature dendritic cells and enhancing
 XX CC T cell responses, thus enhancing antigen presentation. Mature dendritic
 XX CC cells are useful for tumour immunotherapy, for augmenting an immune
 XX CC response to an infectious agent or to a vaccine, and as vaccines to
 XX CC prevent future infection or to activate the immune system to treat
 XX CC diseases such as cancer. Mature dendritic cells may also be used to
 XX CC produce activated T lymphocytes
 XX SQ Sequence 20 BP; 1 A; 3 C; 11 G; 3 T; 0 U; 2 Other;

Query Match 100.0%; Score 18; DB 7; Length 20;
 Best Local Similarity 100.0%; Pred. No. 68;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGGCTCGGTGCAGGGGG 18
 |||||
 Db 3 TGGCTCGGTGCAGGGGG 20

RESULT 3
 ACC83123
 ID ACC83123 standard; DNA; 20 BP.
 XX AC ACC83123;
 XX DT 27-AUG-2003 (first entry)
 XX DE D class CpG ODN sequence useful for encapsulating in SSCL, DV51.
 XX KW Sterically stabilised cationic liposome; SSCL; ODN; oligodeoxynucleotide;
 XX KW tuberculosis; cytokine; leishmaniasis; AIDS-associated Kaposi's tumour;
 XX KW thyroid; cancer; allergy; eczema; allergic rhinitis; coryza; hay fever;
 XX KW schistosomiasis; interferon gamma; lupus erythematosus; antimicrobial;
 XX KW asthma; urticaria; autoimmune disease; diabetes; rheumatoid arthritis;
 XX KW CpG motif; interleukin-13; cytostatic; tularemia; malaria; psoriasis;
 XX KW multiple sclerosis; infection; tumour; ss.
 XX OS Unidentified.
 XX PN WO2003040308-A2.
 XX PD 15-MAY-2003.
 XX PF 29-JUL-2002; 2002WO-US024235.
 XX PR 27-JUL-2001; 2001US-0308283P.
 XX PR 25-JUL-2002; 2002US-00206407.
 XX PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX PI Klinman DM, Gursel I, Ishii KJ, Kawakami K, Joshi BH, Puri RK;
 XX PI WPI; 2003-482260/45.
 XX DR
 XX FT Cationic liposome composition for delivering oligodeoxynucleotides
 XX FT including a CpG motif in clinical applications, comprises a cationic
 XX FT lipid, a co-lipid, stabilizing agent and an encapsulated oligonucleotide.
 XX PS Disclosure; Fig 10C; 110pp; English.
 XX CC The invention relates to sterically stabilised cationic liposomes (SSCL)
 XX CC which comprises a cationic lipid, a co-lipid, stabilising agent and
 XX CC encapsulating a K type oligodeoxynucleotide (ODN) including a CpG motif.
 XX CC The invention is useful in pharmaceutical composition for impairing
 XX CC growth of a solid tumour cell (e.g. human tumour cell) bearing an
 XX CC interleukin-13 receptor in a subject; for stimulating an immune response,
 XX CC which is expression of a cytokine (e.g. interferon gamma), particularly
 XX CC immunotherapeutic response against tumours or stimulating an in vivo or
 XX CC an in vitro immune cell, and for inducing an immune response against an
 XX CC infectious agent e.g. virus, bacteria and fungus. It is also useful for
 XX CC delivering oligodeoxynucleotides including a CpG motif in clinical
 XX CC applications; for treating infectious diseases (e.g. tularemia, malaria,
 XX CC francisella, schistosomiasis, tuberculosis and leishmaniasis), cancer
 XX CC (e.g. solid tumours, AIDS-associated Kaposi's tumour, thyroid cancer
 XX CC etc), allergy (e.g. eczema, allergic rhinitis or coryza, hay fever,
 XX CC bronchial or allergic asthma, urticaria, food allergies), autoimmune
 XX CC diseases (e.g. diabetes, rheumatoid arthritis, lupus erythematosus and
 XX CC multiple sclerosis) and psoriasis. The present sequence is a D class CpG
 XX CC ODN potentially useful for encapsulating in SSCL
 XX SQ Sequence 20 BP; 1 A; 3 C; 13 G; 3 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 8; Length 20;
 Best Local Similarity 100.0%; Pred. No. 69;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCGCTCGGTGCAGGGGG 18
 DB 3 TCGCTCGGTGCAGGGGG 20

RESULT 4

AAC80659
 ID AAC80659 standard; DNA; 19 BP.

XX AAC80659;

DT 14-FEB-2001 (first entry)

DE Immunogenic CpG oligodeoxynucleotide, SEQ ID NO:79.

KW CpG oligodeoxynucleotide; unmethylated; antigen-presenting cell;
 KW immunogenic; cytokine release; natural killer cell; NK cell activation;
 KW cell-mediated immune response; T-cell response; humoral response;
 KW B-cell response; antibody production; immune response induction; vaccine;
 KW allergy; asthma; infection; bacterial; viral; fungal; protozoal;
 KW parasitic; tuberculosis; AIDS; autoimmune disease; lupus erythematosus;
 KW rheumatoid arthritis; multiple sclerosis; solid tumour; cancer;
 KW immune deficiency; biological warfare agent; cytostatic; antiarthritic;
 KW antimicrobial; anti-allergic; protozoicide; tuberculostatic;
 KW antiasthmatic; dermatological; phosphorothioate; ss.

OS Synthetic.

XX WO200061151-A2.

PN 19-OCT-2000.

PD 12-APR-2000; 2000WO-US009839.

PF 12-APR-1999; 99US-0128898P.

PR (KLIN/) KLINMAN D.

PA (ISHI/) ISHII K.

PA (VERT/) VERTHELYI D.

PI Klinman D, Ishii K, Verthelyi D;

DR WPI; 2001-006880/01.

XX Novel oligonucleotides useful for the prevention and treatment of

PT allergies, cancer, and autoimmune disorders and for ameliorating symptoms

PT resulting from exposure to a bio-warfare agent.

XX Claim 4; Page 36; 46pp; English.

XX The invention relates to novel immunogenic CpG oligodeoxynucleotides
 CC (AAC80591-C80723). The oligonucleotide are at least 10 bases long and
 CC comprise one of the generic sequences 5'-NNNT-CpG-WNNN-3' or 5'-RY-CpG-RY
 CC -3'. The central CpG motif is unmethylated, and the oligonucleotides
 CC optionally have phosphorothioate linkages which make them more resistant
 CC to degradation. The invention also relates to an oligonucleotide delivery
 CC complex comprising an oligonucleotide of the invention and a targeting
 CC agent, and a pharmaceutical composition comprising the oligonucleotide
 CC delivery complex. The oligonucleotides are able to induce either a cell-
 CC mediated (T-cell) response or a humoral (B-cell, antibody) response, with
 CC oligonucleotides of the sequence 5'-RY-CpG-RY-3' being able to induce a
 CC cell-mediated response, and those of the sequence 5'-NNNT-CpG-WNNN-3'
 CC being able to induce a humoral response. It is thought that after
 CC administration, the oligonucleotide acts on antigen-presenting cells
 CC (e.g., macrophages and dendritic cells), which then release cytokines,
 CC leading to activation of natural killer (NK) cells. A cell-mediated or
 CC humoral response can then occur by activation of T- or B-cells. The
 CC induction of an immune response is useful for treating, preventing or
 CC ameliorating an allergic reaction (preferably asthma), or an infection,
 CC where an immunogenic CpG oligonucleotide is administered either alone or
 CC in combination with an anti-allergic agent or anti-infectious agent.
 CC The allergic conditions which may be treated include eczema, allergic

CC rhinitis, hayfever, urticaria, food allergies and other atopic
 CC conditions, and the infections which may be treated include viral,
 CC bacterial, fungal and protozoal infections such as tuberculosis, AIDS,
 CC leishmania and schistosomiasis. Immune response induction may also be
 CC used in the treatment of an autoimmune disorder (e.g., lupus
 CC erythematosus, rheumatoid arthritis and multiple sclerosis), a disease
 CC associated with immune system deficiency, and symptoms resulting from
 CC exposure to an agent of biological warfare. An immunogenic CpG
 CC oligonucleotide, either alone or in combination with an anti-cancer
 CC agent, is useful for treating solid tumour cancer. The induction of an
 CC immune response is used in antineoplastic therapy and to improve the efficacy
 CC of a vaccine. The oligonucleotide is preferably administered to
 CC lymphocytes ex vivo, producing activated lymphocytes which are then
 CC administered to the host. The present sequence represents an immunogenic
 CC CpG oligodeoxynucleotide of the invention

XX Sequence 19 BP; 1 A; 3 C; 12 G; 3 T; 0 U; 0 Other;

QY Query Match 94.4%; Score 17; DB 4; Length 19;
 DB Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCGCTCGGTGCAGGGGG 17

DB 3 TCGCTCGGTGCAGGGGG 19

RESULT 5

AAS09629

ID AAS09629 standard; DNA; 19 BP.

XX AAS09629;

XX 26-SEP-2001 (first entry)

XX Immunoreactive CpG sequence-containing oligonucleotide #79.

KW CpG sequence; immune response; non-B cell activation; interferon gamma;
 KW IFN-gamma; humoral; antibody production; interleukin-6 production;
 KW therapeutic; allergic; asthma; cancer; autoimmune disorder; infection;
 KW bio-warfare; vaccine; antineoplastic therapy; eczema; allergic rhinitis;
 KW coryza; hay fever; urticaria; hives; food allergy; atopic condition;
 KW hepatitis; human immunodeficiency virus; HIV; malaria; Francisella;
 KW lupus erythematosus; rheumatoid arthritis; multiple sclerosis;
 KW schistosomiasis; tuberculosis; acquired immunodeficiency syndrome; AIDS;
 KW leishmania; Ebola; Anthrax; Listeria; ss.

OS Synthetic.

XX WO200151500-A1.

XX 19-JUL-2001.

XX 12-JAN-2001; 2001WO-US001122.

XX 14-JAN-2000; 2000US-0176115P.

XX (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX Klinman D, Ishii K, Verthelyi D;

XX WPI; 2001-442129/47.

XX Oligodeoxynucleotides for inducing an immune response to treat and
 PT prevent an allergic reaction, cancer, an autoimmune disorder and symptoms
 PT resulting from exposure to bio-warfare agents, comprise multiple CpG
 PT sequences.

XX Claim 5; Page 40; 48pp; English.

XX AAS09551-AAS09562 represent oligodeoxynucleotides (ODN) of at least 10
 CC nucleotides comprising multiple CpG sequences, where one of the CpG
 CC sequences is different from another of the multiple CpG sequences. The

CC ODN are useful for inducing an immune response, preferably a cell-mediated immune response, involving non-B cell activation, interferon gamma (IFN-gamma) production or a humoral immune response involving B cell activation, antibody and interleukin-6 production in a host, for treating, preventing or ameliorating an allergic reaction, e.g. asthma, cancer, e.g. solid tumour cancer, a disease associated with the immune system e.g. autoimmune disorder or an immune system deficiency, infection or a symptom resulting from exposure to bio-warfare agent in a human. The induction of immune response improves the efficacy of a vaccine and is used in antiseize therapy. The ODN are useful for treating, preventing or ameliorating allergic reactions, including eczema, allergic rhinitis or coryza, hay fever, bronchial asthma, urticaria (hives), food allergies and other atopic conditions, for improving the efficacy of vaccines against hepatitis A, B and C, human immunodeficiency virus (HIV) and malaria, for treating immune system deficiencies, e.g. lupus erythematosus and autoimmune diseases such as rheumatoid arthritis and multiple sclerosis, infections including Francisella, schistosomiasis, tuberculosis, acquired immunodeficiency syndrome (AIDS), Leishmania and symptoms resulting from exposure of bio-warfare agent, including Ebola, Anthrax and Listeria

XX Sequence 19 BP; 1 A; 3 C; 12 G; 3 T; 0 U; 0 Other;

Query Match 94.4%; Score 17; DB 4; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCGTCGCGTCGACGGGG 17
| | | | | | | | | | | | | | | | | |
Db 3 TCGTCGCGTCGACGGGG 19

RESULT 6

ABK46507
ID ABK46507 standard; DNA; 19 BP.

AC ABK46507;

XX 05-JUN-2002 (first entry)

XX Immunostimulatory unmethylated CpG oligodeoxynucleotide #97.

XX unmethylated CpG; oligidideoxynucleotide; ODN; virucide; vaccine;
XX Paramyxoviridae; P protein; respiratory syncytial virus; RSV;
XX viral bronchiolitis; pneumonia; infectious pulmonary disease;
XX bronchopulmonary dysplasia; congenital heart condition; ss.

XX Synthetic.

XX WO200211761-A2.

XX 14-FEB-2002.

XX 09-AUG-2001; 2001WO-US041633.

XX 10-AUG-2000; 2000US-0224011P.

XX 01-SEP-2000; 2000US-0229307P.

XX (JACK-) JACKSON FOUND ADVANCEMENT MILITARY MED.

XX Mond JU, Prince G, Klinman DM;

XX WPI; 2002-227118/28.

XX Vaccine for immunizing patient against respiratory syncytial virus, has epitopes of paramyxoviridae F protein, and cytosine followed by guanine linked by phosphate bond-oligodeoxynucleotides.

XX Claim 4; Page 9; 30pp; English.

XX The invention describes a vaccine comprising one or more epitopes of a Paramyxoviridae F protein, and one or more CpG (cytosine followed by Guanine linked by phosphate bond)-oligodeoxynucleotides (ODNs). The

CC vaccine is useful for vaccinating a patient especially against viruses of the Paramyxoviridae family e.g. respiratory syncytial virus (RSV), the primary cause of viral bronchiolitis and pneumonia in infants and children, and infectious pulmonary disease in infants. RSV has been particularly implicated in death of infants that are premature, have bronchopulmonary dysplasia, or congenital heart conditions. This sequence CC represents an oligodeoxynucleotide that can be used in the creation of the vaccine

XX Sequence 19 BP; 1 A; 3 C; 12 G; 3 T; 0 U; 0 Other;

Query Match 94.4%; Score 17; DB 6; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCGTCGCGTCGACGGGG 17
| | | | | | | | | | | | | | | | | |
Db 3 TCGTCGCGTCGACGGGG 19

RESULT 7

AAC80662
ID AAC80662 standard; DNA; 20 BP.

XX AAC80662;

XX 14-FEB-2001 (first entry)

XX Immunogenic CpG oligodeoxynucleotide, SEQ ID NO:82.

XX CpG oligodeoxynucleotide; unmethylated; antigen-presenting cell;
XX immunogenic; cytokine release; natural killer cell; NK cell activation;
XX cell-mediated immune response; T-cell response; humoral response;
XX B-cell response; antibody production; immune response induction; vaccine;
XX allergy; asthma; infection; bacterial; viral; fungal; protozoal;
XX parasitic; tuberculosis; AIDS; autoimmune disease; lupus erythematosus;
XX rheumatoid arthritis; multiple sclerosis; solid tumour; cancer;
XX immune deficiency; biological warfare agent; cytostatic; antiarthritic;
XX antimicrobial; antiallergic; protozoacide; tuberculostatic;
XX antiasthmatic; dermatological; phosphorothioate; ss.

XX Synthetic.

XX WO200061151-A2.

XX 19-OCT-2000.

XX 12-APR-2000; 2000WO-US009839.

XX 12-APR-1999; 99US-0128898P.

XX (KLIN/) KLINMAN D.

XX (ISHI/) ISHII K.

XX (VERT/) VERTHELYI D.

XX Klinman D, Ishii K, Verthelyi D;

XX WPI; 2001-006880/01.

XX Novel oligonucleotides useful for the prevention and treatment of

XX allergies, cancer, and autoimmune disorders and for ameliorating symptoms

XX resulting from exposure to a bio-warfare agent.

XX Claim 4; Page 36; 46pp; English.

XX The invention relates to novel immunogenic CpG oligodeoxynucleotides (AAC80581-C80723). The oligonucleotides are at least 10 bases long and comprise one of the generic sequences 5'-NNN-CpG-WNNN-3' or 5'-RP-CpG-RY-3'. The central CpG motif is unmethylated, and the oligonucleotides optionally have phosphorothioate linkages which make them more resistant to degradation. The invention also relates to an oligonucleotide delivery complex comprising an oligonucleotide of the invention and a targeting agent, and a pharmaceutical composition comprising the oligonucleotide

CC delivery complex. The oligonucleotides are able to induce either a cell-mediated (T-cell) response or a humoral (B-cell, antibody) response, with CC oligonucleotides of the sequence 5'-RV-CpG-RV-3', being able to induce a CC cell-mediated response, and those of the sequence 5'-NNNT-CpG-WNNN-3' being able to induce a humoral response. It is thought that after CC administration, the oligonucleotide acts on antigen-presenting cells (e.g., macrophages and dendritic cells), which then release cytokines, CC leading to activation of natural killer (NK) cells. A cell-mediated or CC humoral response can then occur by activation of T- or B-cells. The CC induction of an immune response is useful for treating, preventing or CC ameliorating an allergic reaction (preferably asthma), or an infection, CC where an immunogenic CpG oligonucleotide is administered either alone or CC in combination with an anti-allergenic agent or anti-infectious agent. CC The allergic conditions which may be treated include eczema, allergic CC rhinitis, hayfever, urticaria, food allergies and other atopic CC conditions, and the infections which may be treated include viral, CC bacterial, fungal and protozoal infections such as tuberculosis, AIDS, CC leishmania and schistosomiasis. Immune response induction may also be CC used in the treatment of an autoimmune disorder (e.g., lupus, CC erythematosus, rheumatoid arthritis and multiple sclerosis), a disease CC associated with immune system deficiency, and symptoms resulting from CC exposure to an agent of biological warfare. An immunogenic CpG CC oligonucleotide, either alone or in combination with an anti-cancer CC agent, is useful for treating solid tumour cancer. The induction of an CC immune response is used in antineoplastic therapy and to improve the efficacy CC of a vaccine. The oligonucleotide is preferably administered to CC lymphocytes ex vivo, producing activated lymphocytes which are then CC administered to the host. The present sequence represents an immunogenic CC CpG oligodeoxynucleotide of the invention

XX Sequence 20 BP; 2 A; 3 C; 12 G; 3 T; 0 U; 0 Other;

Query Match 91.1%; Score 16.4; DB 4; Length 20;
Best Local Similarity 94.4%; Pred. No. 3.7e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TGGCTCGGTGCAGGGGGG 18
|||||
DB 3 TGGCTCGATGCAGGGGG 20

RESULT 8

AAC80661

ID AAC80661 standard; DNA; 20 BP.

AC AAC80661;

DT 14-FEB-2001 (first entry)

DE Immunogenic CpG oligodeoxynucleotide, SEQ ID NO:81.

XX CpG oligodeoxynucleotide; unmethylated; antigen-presenting cell;
XX immunogenic; cytokine release; natural killer cell; NK cell activation;
KW cell-mediated immune response; T-cell response; humoral response;
KW B-cell response; antibody production; immune response induction; vaccine;
KW allergy; asthma; infection; bacterial; viral; fungal; protozoal;
KW parasitic; tuberculosis; AIDS; autoimmune disease; lupus erythematosus;
KW rheumatoid arthritis; multiple sclerosis; solid tumour; cancer;
KW immune deficiency; biological warfare agent; cytostatic; antiarthritic;
KW antimicrobial; antiallergic; protozoacide; tuberculostatic;
KW antiasthmatic; dermatological; phosphorothioate; ss.

OS Synthetic.

XX WO200061151-A2.

XX 19-OCT-2000.

XX 12-APR-2000; 2000WO-US0009839.

XX 12-APR-1999; 99US-0128988P.

XX (KLIN/) KLINMAN D.

PA (ISHI/) ISHII K.
XX (VERT/) VERTHELYI D.
PI KLINMAN D, Ishii K, Verthelyi D;
XX WPI; 2001-006880/01.

XX Novel oligonucleotides useful for the prevention and treatment of
XX allergies, cancer, and autoimmune disorders and for ameliorating symptoms
XX resulting from exposure to a bio-warfare agent.

XX Claim 4; Page 36; 46pp; English.

XX The invention relates to novel immunogenic CpG oligodeoxynucleotides
XX (AAC80581-C80723). The oligonucleotide are at least 10 bases long and
XX comprise one of the generic sequences 5'-NNNT-CpG-WNNN-3' or 5'-RV-CpG-RV-
XX -3'. The central CpG motif is unmethylated, and the oligonucleotides
XX optionally have phosphorothioate linkages which make them more resistant
XX to degradation. The invention also relates to an oligonucleotide delivery
XX complex comprising an oligonucleotide of the invention and a targeting
XX agent, and a pharmaceutical composition comprising the oligonucleotide
XX delivery complex. The oligonucleotides are able to induce either a cell-
XX mediated (T-cell) response or a humoral (B-cell, antibody) response, with
XX oligonucleotides of the sequence 5'-RV-CpG-RV-3', being able to induce a
XX cell-mediated response, and those of the sequence 5'-NNNT-CpG-WNNN-3'
XX being able to induce a humoral response. It is thought that after
XX administration, the oligonucleotide acts on antigen-presenting cells
XX (e.g., macrophages and dendritic cells), which then release cytokines,
XX leading to activation of natural killer (NK) cells. A cell-mediated or
XX humoral response can then occur by activation of T- or B-cells. The
XX induction of an immune response is useful for treating, preventing or
XX ameliorating an allergic reaction (preferably asthma), or an infection,
XX where an immunogenic CpG oligonucleotide is administered either alone or
XX in combination with an anti-allergenic agent or anti-infectious agent. CC
XX The allergic conditions which may be treated include eczema, allergic
XX rhinitis, hayfever, urticaria, food allergies and other atopic
XX conditions, and the infections which may be treated include viral,
XX bacterial, fungal and protozoal infections such as tuberculosis, AIDS,
XX leishmania and schistosomiasis. Immune response induction may also be
XX used in the treatment of an autoimmune disorder (e.g., lupus, CC
XX erythematosus, rheumatoid arthritis and multiple sclerosis), a disease
XX associated with immune system deficiency, and symptoms resulting from
XX exposure to an agent of biological warfare. An immunogenic CpG
XX oligonucleotide, either alone or in combination with an anti-cancer
XX agent, is useful for treating solid tumour cancer. The induction of an
XX immune response is used in antineoplastic therapy and to improve the efficacy
XX of a vaccine. The oligonucleotide is preferably administered to
XX lymphocytes ex vivo, producing activated lymphocytes which are then
XX administered to the host. The present sequence represents an immunogenic
XX CpG oligodeoxynucleotide of the invention

XX Sequence 20 BP; 2 A; 3 C; 12 G; 3 T; 0 U; 0 Other;

Query Match 91.1%; Score 16.4; DB 4; Length 20;
Best Local Similarity 94.4%; Pred. No. 3.7e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TGGCTCGGTGCAGGGGGG 18

|||||
DB 3 TGGCTCGATGCAGGGGGG 20

RESULT 9

AAC80620

ID AAC80620 standard; DNA; 20 BP.

XX AAC80620;

DT 14-FEB-2001 (first entry)

XX Immunogenic CpG oligodeoxynucleotide, SEQ ID NO:40.

XX CpG oligodeoxynucleotide; unmethylated; antigen-presenting cell;

immunogenic; cytokine release; natural killer cell; NK cell activation;
 cell-mediated immune response; T-cell response; humoral response;
 B-cell response; antibody production; immune response induction; vaccine;
 allergy; asthma; infection; bacterial; viral; fungal; protozoal;
 parasitic; tuberculosis; AIDS; autoimmune disease; lupus erythematosus;
 rheumatoid arthritis; multiple sclerosis; solid tumour; cancer;
 immune deficiency; biological warfare agent; cytostatic; antiarthritic;
 antimicrobial; antiallergic; protozoicide; tuberculostatic;
 antiasthmatic; dermatological; phosphorothioate; ss.

XX Synthetic.

OS AAS09631

PN WO200061151-A2.

PD 19-OCT-2000.

XX 12-APR-2000; 2000WO-US009839.

XX 12-APR-1999; 99US-0128898P.

XX (KLIN/) KLINMAN D.

PA (ISHI/) ISHII K.

PA (VERT/) VERTHELYI D.

XX Klinman D, Ishii K, Verthelyi D;

PI WPI; 2001-006880/01.

Novel oligonucleotides useful for the prevention and treatment of
 allergies, cancer, and autoimmune disorders and for ameliorating symptoms
 resulting from exposure to a bio-warfare agent.

XX Claim 4; Page 30; 46pp; English.

XX The invention relates to novel immunogenic CpG oligodeoxynucleotides
 (AAC90581-C80723). The oligonucleotide are at least 10 bases long and
 comprise one of the generic sequences 5'-NNNT-CpG-WNNN-3' or 5'-RY-CpG-RY
 -3'. The central CpG motif is unmethylated, and the oligonucleotides
 optionally have phosphorothioate linkages which make them more resistant
 to degradation. The invention also relates to an oligonucleotide delivery
 complex comprising an oligonucleotide of the invention and a targeting
 agent, and a pharmaceutical composition comprising the oligonucleotide
 delivery complex. The oligonucleotides are able to induce either a cell-
 mediated (T-cell) response or a humoral (B-cell, antibody) response, with
 oligonucleotides of the sequence 5'-RY-CpG-RY-3' being able to induce a
 cell-mediated response, and those of the sequence 5'-NNNT-CpG-WNNN-3'
 being able to induce a humoral response. It is thought that after
 administration the oligonucleotide acts on antigen-presenting cells
 (e.g., macrophages and dendritic cells), which then release cytokines,
 leading to activation of natural killer (NK) cells. A cell-mediated or
 humoral response can then occur by activation of T- or B-cells. The
 induction of an immune response is useful for treating, preventing or
 ameliorating an allergic reaction (preferably asthma), or an infection,
 where an immunogenic CpG oligonucleotide is administered either alone or
 in combination with an anti-allergenic agent or anti-infectious agent.
 The allergic conditions which may be treated include eczema, allergic
 rhinitis, hayfever, urticaria, food allergies and other atopic
 conditions, and the infections which may be treated include viral,
 bacterial, fungal and protozoal infections such as tuberculosis, AIDS,
 leishmania and schistosomiasis. Immune response induction may also be
 used in the treatment of an autoimmune disorder (e.g., lupus
 erythematosus, rheumatoid arthritis and multiple sclerosis), a disease
 associated with immune system deficiency, and symptoms resulting from
 exposure to an agent of biological warfare. An immunogenic CpG
 oligonucleotide, either alone or in combination with an anti-cancer
 agent, is useful for treating solid tumour cancer. The induction of an
 immune response is used in antitumor therapy and to improve the efficacy
 of a vaccine. The oligonucleotide is preferably administered to
 lymphocytes ex vivo, producing activated lymphocytes which are then
 administered to the host. The present sequence represents an immunogenic
 CpG oligodeoxynucleotide of the invention

XX Sequence 20 BP; 2 A; 3 C; 12 G; 3 T; 0 U; 0 Other;

Query Match 91.1%; Score 16.4; DB 4; Length 20;
 Best Local Similarity 94.4%; Pred. No. 3.7e+02;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TCGTCGCTGTCAGCGGGG 18
 DB 3 TCGTCGATGTCAGCGGGG 20

RESULT 10

AAS09631

ID AAS09631 standard; DNA; 20 BP.

XX AAS09631;

XX 26-SEP-2001 (first entry)

XX Immunoreactive CpG sequence-containing oligonucleotide #81.

XX CpG sequence; immune response; non-B cell activation; interferon gamma;
 IFN-gamma; humoral; antibody production; interleukin-6 production;
 therapeutic; allergy; asthma; cancer; autoimmune disorder; infection;
 bio-warfare; vaccine; antisense therapy; eczema; allergic rhinitis;
 coryza; hay fever; urticaria; hives; food allergy; atopic condition;
 hepatitis; human immunodeficiency virus; HIV; malaria; Francisella;
 lupus erythematosus; rheumatoid arthritis; multiple sclerosis;
 schistosomiasis; tuberculosis; acquired immunodeficiency syndrome; AIDS;
 leishmania; Ebola; Anthrax; Listeria; ss.

XX Synthetic.

XX WO200151500-A1.

XX 19-JUL-2001.

XX 12-JAN-2001; 2001WO-US001122.

XX 14-JAN-2000; 2000US-0176115P.

XX (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX Klinman D, Ishii K, Verthelyi D;

XX WPI; 2001-442129/47.

XX Oligodeoxynucleotides for inducing an immune response to treat and
 prevent an allergic reaction, cancer, an autoimmune disorder and symptoms
 resulting from exposure to bio-warfare agents, comprise multiple CpG
 sequences.

XX Claim 5; Page 40; 48pp; English.

XX AAS09551-AAS09662 represent oligodeoxynucleotides (ODN) of at least 10
 nucleotides comprising multiple CpG sequences, where one of the CpG
 sequences is different from another of the multiple CpG sequences. The
 ODN are useful for inducing an immune response, preferably a cell-
 mediated immune response, involving non-B cell activation, interferon
 gamma (IFN-gamma) production or a humoral immune response involving B
 cell activation, antibody and interleukin-6 production in a host, for
 treating, preventing or ameliorating an allergic reaction, e.g. asthma,
 cancer, e.g. solid tumour cancer, a disease associated with the immune
 system e.g. autoimmune disorder or an immune system deficiency, infection
 or a symptom resulting from exposure to bio-warfare agent in a human. The
 induction of immune response improves the efficacy of a vaccine and is
 used in antitumor therapy. The ODN are useful for treating, preventing or
 ameliorating allergic reactions, including eczema, allergic rhinitis or
 coryza, hay fever, bronchial asthma, urticaria (hives), food allergies
 and other atopic conditions, for improving the efficacy of vaccines
 against hepatitis A, B and C, human immunodeficiency virus (HIV) and
 malaria, for treating immune system deficiencies, e.g. lupus
 erythematosus and autoimmune diseases such as rheumatoid arthritis and
 multiple sclerosis, infections including Francisella, schistosomiasis,

CC tuberculosis, acquired immunodeficiency syndrome (AIDS), Leishmania and
 CC symptoms resulting from exposure of bio-warfare agent, including Ebola,
 CC Anthrax and Listeria

XX SQ Sequence 20 BP; 2 A; 3 C; 12 G; 3 T; 0 U; 0 Other;
 Query Match 91.1%; Score 16.4; DB 4; Length 20;
 Best Local Similarity 94.4%; Pred. No. 3.7e+02;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TGGCTCGGTCGAGGGGG 18
 ||||| ||||| |||||
 Db 3 TGGCTCGATCGAGGGGG 20

RESULT 11
 AAS09590
 ID AAS09590 standard; DNA; 20 BP.
 XX AC AAS09590;

DT 26-SEP-2001 (first entry)

XX Immunoreactive CpG sequence-containing oligonucleotide #40.

CpG sequence; immune response; non-B cell activation; interferon gamma;
 IFN-gamma; humoral; antibody production; interleukin-6 production;
 therapeutic; allergy; asthma; cancer; autoimmune disorder; infection;
 bio-warfare; vaccine; antisense therapy; eczema; allergic rhinitis;
 coryza; hay fever; urticaria; hives; food allergy; atopic condition;
 hepatitis; human immunodeficiency virus; HIV; malaria; Francisella;
 lupus erythematosus; rheumatoid arthritis; multiple sclerosis;
 schistosomiasis; tuberculosis; acquired immunodeficiency syndrome; AIDS;
 Leishmania; Ebola; Anthrax; Listeria; ss.

XX Synthetic.

XX WO200151500-A1.

XX 19-JUL-2001.

XX 12-JAN-2001; 2001WO-US001122.

XX 14-JAN-2000; 2000US-0176115P.

XX (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX Klinman D, Ishii K, Verthelyi D;

XX WPI; 2001-442129/47.

XX Oligodeoxynucleotides for inducing an immune response to treat and
 PT prevent an allergic reaction, cancer, an autoimmune disorder and symptoms
 PT resulting from exposure to bio-warfare agents, comprise multiple CpG
 PT sequences.

XX Claim 5; Page 33; 48pp; English.

XX AAS09551-AAS09662 represent oligodeoxynucleotides (ODN) of at least 10
 CC nucleotides comprising multiple CpG sequences, where one of the CpG
 CC sequences is different from another of the multiple CpG sequences. The
 CC ODN are useful for inducing an immune response, preferably a cell-
 CC mediated immune response, involving non-B cell activation, interferon
 CC gamma (IFN-gamma) production or a humoral immune response involving B
 CC cell activation, antibody and interleukin-6 production in a host, for
 CC treating, preventing or ameliorating an allergic reaction, e.g. asthma,
 CC cancer, e.g. solid tumour cancer, a disease associated with the immune
 CC system e.g. autoimmune disorder or an immune system deficiency, infection
 CC or a symptom resulting from exposure to bio-warfare agent in a human. The
 CC induction of immune response improves the efficacy of a vaccine and is
 CC used in antisense therapy. The ODN are useful for treating, preventing or
 CC ameliorating allergic reactions, including eczema, allergic rhinitis or
 CC coryza, hay fever, bronchial asthma, urticaria (hives), food allergies

CC and other atopic conditions, for improving the efficacy of vaccines
 CC against hepatitis A, B and C, human immunodeficiency virus (HIV) and
 CC malaria, for treating immune system deficiencies, e.g. lupus
 CC erythematosus and autoimmune diseases such as rheumatoid arthritis and
 CC multiple sclerosis, infections including Francisella, schistosomiasis,
 CC tuberculosis, acquired immunodeficiency syndrome (AIDS), Leishmania and
 CC symptoms resulting from exposure of bio-warfare agent, including Ebola,
 CC Anthrax and Listeria

XX SQ Sequence 20 BP; 2 A; 3 C; 12 G; 3 T; 0 U; 0 Other;

Query Match 91.1%; Score 16.4; DB 4; Length 20;
 Best Local Similarity 94.4%; Pred. No. 3.7e+02;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TGGCTCGGTCGAGGGGG 18
 ||||| ||||| |||||
 Db 3 TGGCTCGATCGAGGGGG 20

RESULT 12

AAS09632

ID AAS09632 standard; DNA; 20 BP.

XX AC AAS09632;

XX 26-SEP-2001 (first entry)

DE Immunoreactive CpG sequence-containing oligonucleotide #82.

CpG sequence; immune response; non-B cell activation; interferon gamma;
 IFN-gamma; humoral; antibody production; interleukin-6 production;
 therapeutic; allergy; asthma; cancer; autoimmune disorder; infection;
 bio-warfare; vaccine; antisense therapy; eczema; allergic rhinitis;
 coryza; hay fever; urticaria; hives; food allergy; atopic condition;
 hepatitis; human immunodeficiency virus; HIV; malaria; Francisella;
 lupus erythematosus; rheumatoid arthritis; multiple sclerosis;
 schistosomiasis; tuberculosis; acquired immunodeficiency syndrome; AIDS;
 Leishmania; Ebola; Anthrax; Listeria; ss.

XX Synthetic.

XX WO200151500-A1.

XX 19-JUL-2001.

XX 12-JAN-2001; 2001WO-US001122.

XX 14-JAN-2000; 2000US-0176115P.

XX (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX Klinman D, Ishii K, Verthelyi D;

XX WPI; 2001-442129/47.

XX Oligodeoxynucleotides for inducing an immune response to treat and
 PT prevent an allergic reaction, cancer, an autoimmune disorder and symptoms
 PT resulting from exposure to bio-warfare agents, comprise multiple CpG
 PT sequences.

XX Claim 5; Page 40; 48pp; English.

XX AAS09551-AAS09662 represent oligodeoxynucleotides (ODN) of at least 10
 CC nucleotides comprising multiple CpG sequences, where one of the CpG
 CC sequences is different from another of the multiple CpG sequences. The
 CC ODN are useful for inducing an immune response, preferably a cell-
 CC mediated immune response, involving non-B cell activation, interferon
 CC gamma (IFN-gamma) production or a humoral immune response involving B
 CC cell activation, antibody and interleukin-6 production in a host, for
 CC treating, preventing or ameliorating an allergic reaction, e.g. asthma,
 CC cancer, e.g. solid tumour cancer, a disease associated with the immune
 CC system e.g. autoimmune disorder or an immune system deficiency, infection

or a symptom resulting from exposure to bio-warfare agent in a human. The induction of immune response improves the efficacy of a vaccine and is used in antiseptic therapy. The ODN are useful for treating, preventing or ameliorating allergic reactions, including eczema, allergic rhinitis or coryza, hay fever, bronchial asthma, urticaria (hives), food allergies and other atopic conditions, for improving the efficacy of vaccines against hepatitis A, B and C, human immunodeficiency virus (HIV) and malaria, for treating immune system deficiencies, e.g. lupus erythematosus and autoimmune diseases such as rheumatoid arthritis and multiple sclerosis, infections including Francisella, schistosomiasis, tuberculosis, acquired immunodeficiency syndrome (AIDS), Leishmania and symptoms resulting from exposure of bio-warfare agent, including Ebola, Anthrax and Listeria

CC the vaccine

XX Sequence 20 BP; 2 A; 3 C; 12 G; 3 T; 0 U; 0 Other;

SQ Query Match 91.1%; Score 16.4; DB 4; Length 20;

Best Local Similarity 94.4%; Pred. No. 3.7e+02;

Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TGGGTGGTGCAGGGGGG 18

Db 3 TGGGTGGTGCAGGGGGG 20

RESULT 13

ABK46510

ID ABK46510 standard; DNA; 20 BP.

XX ABK46510;

AC ABK46510;

XX 05-JUN-2002 (first entry)

DT Immunostimulatory unmethylated CpG oligodeoxynucleotide #100.

DE unmethylated CpG; oligodeoxynucleotide; ODN; virucide; vaccine;

KW Paramyxoviridae; F protein; respiratory syncytial virus; RSV;

KW viral bronchiolitis; pneumonia; infectious pulmonary disease;

KW bronchopulmonary dysplasia; congenital heart condition; ss.

XX Synthetic.

OS WO200211761-A2.

PN 14-FEB-2002.

XX 09-AUG-2001; 2001WO-US041633.

XX 10-AUG-2000; 2000US-0224011P.

XX 01-SEP-2000; 2000US-0229307P.

XX (JACK-) JACKSON FOUND ADVANCEMENT MILITARY MED.

PA Mond JJ, Prince G, Klinman DM;

PI WPI; 2002-227118/28.

XX Vaccine for immunizing patient against respiratory syncytial virus, has

PT epitopes of Paramyxoviridae F protein, and cytosine followed by guanine

PT linked by phosphate bond-oligodeoxynucleotides.

XX Claim 4; Page 9; 30pp; English.

XX The invention describes a vaccine comprising one or more epitopes of a

XX Paramyxoviridae F protein, and one or more CpG (cytosine followed by

XX guanine linked by phosphate bond)-oligodeoxynucleotides (ODNs). The

XX vaccine is useful for vaccinating a patient especially against viruses of

XX the Paramyxoviridae family e.g. respiratory syncytial virus (RSV), the

XX primary cause of viral bronchiolitis and pneumonia in infants and

XX children, and infectious pulmonary disease in infants. RSV has been

XX particularly implicated in death of infants that are premature, have

XX bronchopulmonary dysplasia, or congenital heart conditions. This sequence

XX represents an oligodeoxynucleotide that can be used in the creation of

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

CC the vaccine

XX Sequence 20 BP; 2 A; 3 C; 12 G; 3 T; 0 U; 0 Other;

SQ Query Match 91.1%; Score 16.4; DB 6; Length 20;

Best Local Similarity 94.4%; Pred. No. 3.7e+02;

Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TGGGTGGTGCAGGGGGG 18

Db 3 TGGGTGGTGCAGGGGGG 20

RESULT 14

ABK46468

ID ABK46468 standard; DNA; 20 BP.

XX ABK46468;

AC ABK46468;

XX 05-JUN-2002 (first entry)

DT Immunostimulatory unmethylated CpG oligodeoxynucleotide #58.

DE unmethylated CpG; oligodeoxynucleotide; ODN; virucide; vaccine;

KW Paramyxoviridae; F protein; respiratory syncytial virus; RSV;

KW viral bronchiolitis; pneumonia; infectious pulmonary disease;

KW bronchopulmonary dysplasia; congenital heart condition; ss.

XX Synthetic.

OS WO200211761-A2.

PN 14-FEB-2002.

XX 09-AUG-2001; 2001WO-US041633.

XX 10-AUG-2000; 2000US-0224011P.

XX 01-SEP-2000; 2000US-0229307P.

XX (JACK-) JACKSON FOUND ADVANCEMENT MILITARY MED.

PA Mond JJ, Prince G, Klinman DM;

PI WPI; 2002-227118/28.

XX Vaccine for immunizing patient against respiratory syncytial virus, has

PT epitopes of Paramyxoviridae F protein, and cytosine followed by guanine

PT linked by phosphate bond-oligodeoxynucleotides.

XX Claim 4; Page 8; 30pp; English.

XX The invention describes a vaccine comprising one or more epitopes of a

XX Paramyxoviridae F protein, and one or more CpG (cytosine followed by

XX guanine linked by phosphate bond)-oligodeoxynucleotides (ODNs). The

XX vaccine is useful for vaccinating a patient especially against viruses of

XX the Paramyxoviridae family e.g. respiratory syncytial virus (RSV), the

XX primary cause of viral bronchiolitis and pneumonia in infants and

XX children, and infectious pulmonary disease in infants. RSV has been

XX particularly implicated in death of infants that are premature, have

XX bronchopulmonary dysplasia, or congenital heart conditions. This sequence

XX represents an oligodeoxynucleotide that can be used in the creation of

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

RESULT 15
 ABK46509
 ID ABK46509 standard; DNA; 20 BP.
 XX
 AC ABK46509;
 XX
 DT 05-JUN-2002 (first entry)
 XX
 DE Immunostimulatory unmethylated CpG oligodeoxynucleotide #99.
 XX
 KW unmethylated CpG; oligodeoxynucleotide; ODN; virucide; vaccine;
 KW Paramyxoviridae; F protein; respiratory syncytial virus; RSV;
 KW viral bronchiolitis; pneumonia; infectious pulmonary disease;
 KW bronchopulmonary dysplasia; congenital heart condition; ss.
 XX
 OS Synthetic.
 XX
 PN WO200211761-A2.
 XX
 PD 14-FEB-2002.
 XX
 PF 09-AUG-2001; 2001WO-US041633.
 XX
 PR 10-AUG-2000; 2000US-0224011P.
 PR 01-SEP-2000; 2000US-0229307P.
 XX
 PA (JACK-) JACKSON FOUND ADVANCEMENT MILITARY MED.
 XX
 PI Mond JJ, Prince G, Klinman DM;
 XX
 DR WPI; 2002-227118/28.
 XX
 PT Vaccine for immunizing patient against respiratory syncytial virus, has
 PT epitopes of Paramyxoviridae F protein, and cytosine followed by guanine
 PT linked by phosphate bond-oligodeoxynucleotides.
 XX
 PS Claim 4; Page 9; 30pp; English.
 XX
 CC The invention describes a vaccine comprising one or more epitopes of a
 CC Paramyxoviridae F protein, and one or more CpG (cytosine followed by
 CC guanine linked by phosphate bond)-oligodeoxynucleotides (ODNs). The
 CC vaccine is useful for vaccinating a patient especially against viruses of
 CC the Paramyxoviridae family e.g. respiratory syncytial virus (RSV), the
 CC primary cause of viral bronchiolitis and pneumonia in infants and
 CC children, and infectious pulmonary disease in infants. RSV has been
 CC particularly implicated in death of infants that are premature, have
 CC bronchopulmonary dysplasia, or congenital heart conditions. This sequence
 CC represents an oligodeoxynucleotide that can be used in the creation of
 CC the vaccine
 XX
 SQ Sequence 20 BP; 2 A; 3 C; 12 G; 3 T; 0 U; 0 Other;
 Query Match 91.1%; Score 16.4; DB 6; Length 20;
 Best Local Similarity 94.4%; Pred. No. 3.7e+02;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Cg 1 TGGTCGGTGCAGGGGG 18
 Db 3 TGGTCGATGCAGGGGG 20
 Search completed: July 2, 2004, 08:31:39
 Job time : 135.89 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 2, 2004, 08:11:05 ; Search time 138.732 Seconds
(without alignments)
625.926 Million cell updates/sec

Title: US-10-068-160-19

Perfect score: 18
Sequence: 1 tgcacgcacgcagggggg 18

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 3163042 seqs, 2412103800 residues

Total number of hits satisfying chosen parameters: 6326084

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications NA:*
1: /cgm2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2: /cgm2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
3: /cgm2_6/ptodata/2/pubpna/US05_PUBCOMB.seq:*
4: /cgm2_6/ptodata/2/pubpna/US04_PUBCOMB.seq:*
5: /cgm2_6/ptodata/2/pubpna/US03_PUBCOMB.seq:*
6: /cgm2_6/ptodata/2/pubpna/US02_PUBCOMB.seq:*
7: /cgm2_6/ptodata/2/pubpna/US01_PUBCOMB.seq:*
8: /cgm2_6/ptodata/2/pubpna/US00_PUBCOMB.seq:*
9: /cgm2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
10: /cgm2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
11: /cgm2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
12: /cgm2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
13: /cgm2_6/ptodata/2/pubpna/US05_PUBCOMB.seq:*
14: /cgm2_6/ptodata/2/pubpna/US04_PUBCOMB.seq:*
15: /cgm2_6/ptodata/2/pubpna/US03_PUBCOMB.seq:*
16: /cgm2_6/ptodata/2/pubpna/US02_PUBCOMB.seq:*
17: /cgm2_6/ptodata/2/pubpna/US01_PUBCOMB.seq:*
18: /cgm2_6/ptodata/2/pubpna/US00_PUBCOMB.seq:*
19: /cgm2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	18	100.0	18	15	US-10-068-160-19
2	18	100.0	20	13	US-09-874-991C-498
3	18	100.0	20	13	US-09-874-991C-509
4	18	100.0	20	13	US-09-874-991C-542
5	18	100.0	20	15	US-10-068-160-35
6	18	100.0	20	15	US-10-194-035-100
7	18	100.0	20	17	US-10-666-022-7
8	18	100.0	28	13	US-09-874-991C-519
9	18	100.0	28	13	US-09-874-991C-531
10	17	94.4	19	15	US-10-194-035-88
11	16.4	91.1	18	13	US-09-874-991C-503
12	16.4	91.1	18	13	US-09-874-991C-513
13	16.4	91.1	18	13	US-09-874-991C-551
14	16.4	91.1	18	15	US-10-068-160-12

Sequence 14, Appl
Sequence 494, App
Sequence 502, App
Sequence 505, App
Sequence 512, App
Sequence 538, App
Sequence 546, App
Sequence 550, App
Sequence 1, Appl
Sequence 31, Appl
Sequence 38, Appl
Sequence 54, Appl
Sequence 64, Appl
Sequence 32, Appl
Sequence 34, Appl
Sequence 37, Appl
Sequence 38, Appl
Sequence 39, Appl
Sequence 41, Appl
Sequence 43, Appl
Sequence 72, Appl
Sequence 1, Appl
Sequence 3, Appl
Sequence 176, App
Sequence 177, App
Sequence 500, App
Sequence 544, App
Sequence 524, App
Sequence 536, App
Sequence 515, App
Sequence 523, App

US-10-068-160-14
US-09-874-991C-494
US-09-874-991C-502
US-09-874-991C-505
US-09-874-991C-512
US-09-874-991C-538
US-09-874-991C-546
US-09-874-991C-550
US-10-068-160-31
US-10-068-160-38
US-10-068-160-54
US-10-068-160-64
US-10-194-035-32
US-10-194-035-34
US-10-194-035-37
US-10-194-035-38
US-10-194-035-39
US-10-194-035-41
US-10-194-035-43
US-10-194-035-72
US-10-666-022-1
US-10-666-022-3
US-10-666-022-176
US-10-666-022-177
US-09-874-991C-500
US-09-874-991C-544
US-09-874-991C-524
US-09-874-991C-536
US-09-874-991C-515
US-09-874-991C-523

ALIGNMENTS

RESULT 1

US-10-068-160-19
Sequence 19, Application US/10068160
Publication No. US2003060440A1

GENERAL INFORMATION:
; APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA, REPRESENTED BY THE
; APPLICANT: SECRETARY, DEPARTMENT OF HEALTH AND HUMAN SERVICES
; APPLICANT: KLINMAN, Dennis
; APPLICANT: ISHII, Ken
; APPLICANT: VERTHELYI, Daniela

TITLE OF INVENTION: OLIGODEOXYNUCLEOTIDE AND ITS USE TO INDUCE AN IMMUNE RESPONSE
FILE REFERENCE: 4239-61999

CURRENT FILING DATE: 2002-02-06
PRIOR FILING DATE: 1999-04-12

NUMBER OF SEQ ID NOS: 120
SOFTWARE: Patent version 3.1

SEQ ID NO 19
LENGTH: 18
TYPE: DNA

ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Oligonucleotide

US-10-068-160-19

Query Match 100.0%; Score 18; DB 15; Length 18;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGCATCGACGCAGGGGGG 18

Db 1 TGCATCGACGCAGGGGGG 18

RESULT 2

US-09-874-991C-498

; Sequence 498, Application US/09874991C
; Publication No. US20040052763A1
; GENERAL INFORMATION:

; APPLICANT: MOND, JAMES J.
; APPLICANT: FLORA, MICHAEL
; APPLICANT: KLINMAN, DENNIS M.
; TITLE OF INVENTION: IMMUNOSTIMULATORY RNA/DNA HYBRID MOLECULES
; FILE REFERENCE: 07787.0042-0
; CURRENT APPLICATION NUMBER: US/09/874,991C
; CURRENT FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: 60/209,797
; PRIOR FILING DATE: 2000-06-07
; NUMBER OF SEQ ID NOS: 620
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 498
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic HDR
US-09-874-991C-498

Query Match 100.0%; Score 18; DB 13; Length 20;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGCATCGACGCGAGGGGG 18
|||
Db 3 TGCATCGACGCGAGGGGG 20
|||

RESULT 3

US-09-874-991C-509
; Sequence 509, Application US/09874991C
; Publication No. US20040052763A1
; GENERAL INFORMATION:

; APPLICANT: MOND, JAMES J.
; APPLICANT: FLORA, MICHAEL
; APPLICANT: KLINMAN, DENNIS M.
; TITLE OF INVENTION: IMMUNOSTIMULATORY RNA/DNA HYBRID MOLECULES
; FILE REFERENCE: 07787.0042-0
; CURRENT APPLICATION NUMBER: US/09/874,991C
; CURRENT FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: 60/209,797
; PRIOR FILING DATE: 2000-06-07
; NUMBER OF SEQ ID NOS: 620
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 509
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic HDR
US-09-874-991C-509

Query Match 100.0%; Score 18; DB 13; Length 20;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGCATCGACGCGAGGGGG 18
|||
Db 3 TGCATCGACGCGAGGGGG 20
|||

RESULT 4

US-09-874-991C-542
; Sequence 542, Application US/09874991C
; Publication No. US20040052763A1
; GENERAL INFORMATION:

; APPLICANT: MOND, JAMES J.
; APPLICANT: FLORA, MICHAEL
; APPLICANT: KLINMAN, DENNIS M.
; TITLE OF INVENTION: IMMUNOSTIMULATORY RNA/DNA HYBRID MOLECULES

; FILE REFERENCE: 07787.0042-0
; CURRENT APPLICATION NUMBER: US/09/874,991C
; CURRENT FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: 60/209,797
; PRIOR FILING DATE: 2000-06-07
; NUMBER OF SEQ ID NOS: 620
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 542
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic HDR
US-09-874-991C-542

Query Match 100.0%; Score 18; DB 13; Length 20;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGCATCGACGCGAGGGGG 18
|||
Db 3 TGCATCGACGCGAGGGGG 20
|||

RESULT 5

US-10-068-160-35
; Sequence 35, Application US/10068160
; Publication No. US20030060440A1
; GENERAL INFORMATION:

; APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA, REPRESENTED BY THE
; APPLICANT: SECRETARY, DEPARTMENT OF HEALTH AND HUMAN SERVICES
; APPLICANT: KLINMAN, DENNIS
; APPLICANT: ISHII, Ken
; APPLICANT: VERTHELYI, Daniela
; TITLE OF INVENTION: OLIGODEOXYNUCLEOTIDE AND ITS USE TO INDUCE AN IMMUNE RESPONSE
; FILE REFERENCE: 4239-61999
; CURRENT APPLICATION NUMBER: US/10/068,160
; CURRENT FILING DATE: 2002-02-06
; PRIOR APPLICATION NUMBER: 60/128,898
; PRIOR FILING DATE: 1999-04-12
; NUMBER OF SEQ ID NOS: 120
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 35
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide
US-10-068-160-35

Query Match 100.0%; Score 18; DB 15; Length 20;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGCATCGACGCGAGGGGG 18
|||
Db 3 TGCATCGACGCGAGGGGG 20
|||

RESULT 6

US-10-194-035-100
; Sequence 100, Application US/10194035
; Publication No. US20030144229A1
; GENERAL INFORMATION:

; APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS REPRESENTED BY THE
; APPLICANT: SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES
; APPLICANT: KLINMAN, DENNIS
; APPLICANT: ISHII, Ken
; APPLICANT: VERTHELYI, Daniela
; TITLE OF INVENTION: OLIGODEOXYNUCLEOTIDE AND ITS USE TO INDUCE AN IMMUNE RESPONSE
; FILE REFERENCE: 4239-63317
; CURRENT APPLICATION NUMBER: US/10/194,035
; CURRENT FILING DATE: 2002-07-12

```
; PRIOR APPLICATION NUMBER: PCT/US01/01122
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: US 60/176,115
; PRIOR FILING DATE: 2000-01-14
; NUMBER OF SEQ ID NOS: 119
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 100
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
US-10-194-035-100
Query Match 100.0%; Score 18; DB 15; Length 20;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGCATCGACGCGGGGG 18
DB 3 TGCATCGACGCGGGGG 20

RESULT 7
US-10-666-022-7
; Sequence 7, Application US/10666022
; Publication No. US20040105872A1
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America, as represented by the
; APPLICANT: Secretary of the Department of Health and Human Services
; APPLICANT: Klinman, Dennis M.
; APPLICANT: Vertelvi, Daniela
; TITLE OF INVENTION: METHOD OF TREATING AND PREVENTING INFECTIONS IN IMMUNOCOMPROMISED
; FILE REFERENCE: 4239-66999
; CURRENT APPLICATION NUMBER: US/10/666,022
; CURRENT FILING DATE: 2003-09-17
; PRIOR APPLICATION NUMBER: US 60/411,944
; PRIOR FILING DATE: 2002-09-18
; NUMBER OF SEQ ID NOS: 181
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic
; NAME/KEY: misc_feature
; LOCATION: (1)..(20)
; OTHER INFORMATION: n is a, c, g, or t, or no nucleotide
US-10-666-022-7
Query Match 100.0%; Score 18; DB 17; Length 20;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGCATCGACGCGGGGG 18
DB 3 TGCATCGACGCGGGGG 20

RESULT 8
US-09-874-991C-519
; Sequence 519, Application US/09874991C
; Publication No. US20040052763A1
; GENERAL INFORMATION:
; APPLICANT: MOND, JAMES J.
; APPLICANT: FLORA, MICHAEL
; APPLICANT: KLINMAN, DENNIS M.
; TITLE OF INVENTION: IMMUNOSTIMULATORY RNA/DNA HYBRID MOLECULES
; FILE REFERENCE: 07787.0042-0
; CURRENT APPLICATION NUMBER: US/09/874,991C
```

```
; CURRENT FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: 60/209,797
; PRIOR FILING DATE: 2000-06-07
; NUMBER OF SEQ ID NOS: 820
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 519
; LENGTH: 28
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic HDR
US-09-874-991C-519
Query Match 100.0%; Score 18; DB 13; Length 28;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGCATCGACGCGGGGG 18
DB 3 TGCATCGACGCGGGGG 20

RESULT 9
US-09-874-991C-531
; Sequence 531, Application US/09874991C
; Publication No. US20040052763A1
; GENERAL INFORMATION:
; APPLICANT: MOND, JAMES J.
; APPLICANT: FLORA, MICHAEL
; APPLICANT: KLINMAN, DENNIS M.
; TITLE OF INVENTION: IMMUNOSTIMULATORY RNA/DNA HYBRID MOLECULES
; FILE REFERENCE: 07787.0042-0
; CURRENT APPLICATION NUMBER: US/09/874,991C
; CURRENT FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: 60/209,797
; PRIOR FILING DATE: 2000-06-07
; NUMBER OF SEQ ID NOS: 620
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 531
; LENGTH: 28
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic HDR
US-09-874-991C-531
Query Match 100.0%; Score 18; DB 13; Length 28;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGCATCGACGCGGGGG 18
DB 11 TGCATCGACGCGGGGG 28

RESULT 10
US-10-194-035-88
; Sequence 88, Application US/10194035
; Publication No. US20030144229A1
; GENERAL INFORMATION:
; APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS REPRESENTED BY THE
; APPLICANT: SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES
; APPLICANT: KLINMAN, Dennis
; APPLICANT: VERTHELYI, Daniela
; APPLICANT: ISHII, Ken
; TITLE OF INVENTION: OLIGODEOXYNUCLEOTIDE AND ITS USE TO INDUCE AN IMMUNE RESPONSE
; FILE REFERENCE: 4239-63317
; CURRENT APPLICATION NUMBER: US/10/194,035
; CURRENT FILING DATE: 2002-07-12
; PRIOR APPLICATION NUMBER: PCT/US01/01122
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: US 60/176,115
; PRIOR FILING DATE: 2000-01-14
```

```
; NUMBER OF SEQ ID NOS: 119
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 88
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
US-10-10-035-88

Query Match          94.4%; Score 17; DB 15; Length 19;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGCATCGACGACGGGG 17
Db 3 TGCATCGACGACGGGG 19

RESULT 11
US-09-874-991C-503
; Sequence 503, Application US/09874991C
; Publication No. US20040052763A1
; GENERAL INFORMATION:
; APPLICANT: MOND, JAMES J.
; APPLICANT: FLORA, MICHAEL
; APPLICANT: KLINMAN, DENNIS M.
; TITLE OF INVENTION: IMMUNOSTIMULATORY RNA/DNA HYBRID MOLECULES
; FILE REFERENCE: 07787.0042-0
; CURRENT APPLICATION NUMBER: US/09/874,991C
; PRIOR FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: 60/209,797
; NUMBER OF SEQ ID NOS: 620
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 503
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic HDR
US-09-874-991C-503

Query Match          91.1%; Score 16.4; DB 13; Length 18;
Best Local Similarity 94.4%; Pred. No. 77;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TGCATCGACGACGGGG 18
Db 1 TGCATCGATCGACGGGG 18

RESULT 12
US-09-874-991C-513
; Sequence 513, Application US/09874991C
; Publication No. US20040052763A1
; GENERAL INFORMATION:
; APPLICANT: MOND, JAMES J.
; APPLICANT: FLORA, MICHAEL
; APPLICANT: KLINMAN, DENNIS M.
; TITLE OF INVENTION: IMMUNOSTIMULATORY RNA/DNA HYBRID MOLECULES
; FILE REFERENCE: 07787.0042-0
; CURRENT APPLICATION NUMBER: US/09/874,991C
; PRIOR FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: 60/209,797
; NUMBER OF SEQ ID NOS: 620
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 513
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic HDR
US-10-068-160-12
```

```
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic HDR
US-09-874-991C-513

Query Match          91.1%; Score 16.4; DB 13; Length 18;
Best Local Similarity 94.4%; Pred. No. 77;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TGCATCGACGACGGGG 18
Db 1 TGCATCGATCGACGGGG 18

RESULT 13
US-09-874-991C-551
; Sequence 551, Application US/09874991C
; Publication No. US20040052763A1
; GENERAL INFORMATION:
; APPLICANT: MOND, JAMES J.
; APPLICANT: FLORA, MICHAEL
; APPLICANT: KLINMAN, DENNIS M.
; TITLE OF INVENTION: IMMUNOSTIMULATORY RNA/DNA HYBRID MOLECULES
; FILE REFERENCE: 07787.0042-0
; CURRENT APPLICATION NUMBER: US/09/874,991C
; PRIOR FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: 60/209,797
; NUMBER OF SEQ ID NOS: 620
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 551
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic HDR
US-09-874-991C-551

Query Match          91.1%; Score 16.4; DB 13; Length 18;
Best Local Similarity 94.4%; Pred. No. 77;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TGCATCGACGACGGGG 18
Db 1 TGCATCGATCGACGGGG 18

RESULT 14
US-10-068-160-12
; Sequence 12, Application US/10068160
; Publication No. US2003006040A1
; GENERAL INFORMATION:
; APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA, REPRESENTED BY THE
; APPLICANT: SECRETARY, DEPARTMENT OF HEALTH AND HUMAN SERVICES
; APPLICANT: KLINMAN, DENNIS
; APPLICANT: ISHII, Ken
; APPLICANT: VERTHELYI, Daniela
; TITLE OF INVENTION: OLIGODEOXYNUCLEOTIDE AND ITS USE TO INDUCE AN IMMUNE RESPONSE
; FILE REFERENCE: 4239-61999
; CURRENT APPLICATION NUMBER: US/10/068,160
; CURRENT FILING DATE: 2002-02-06
; PRIOR APPLICATION NUMBER: 60/128,898
; PRIOR FILING DATE: 1999-04-12
; NUMBER OF SEQ ID NOS: 120
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide
US-10-068-160-12

Query Match          91.1%; Score 16.4; DB 15; Length 18;
Best Local Similarity 94.4%; Pred. No. 77;
```


Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TGCATCGACGACGGGGG 18
 |||||
 Db 1 TGCATCGATCGACGGGGG 18
 |||||

RESULT 15

US-10-068-160-14
 ; Sequence 14, Application US/10068160
 ; Publication No. US2003006040A1
 ; GENERAL INFORMATION:
 ; APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA, REPRESENTED BY THE
 ; APPLICANT: SECRETARY, DEPARTMENT OF HEALTH AND HUMAN SERVICES
 ; APPLICANT: KLIMAN, Dennis
 ; APPLICANT: ISHII, Ken
 ; APPLICANT: VERTHELYI, Daniela
 ; TITLE OF INVENTION: OLIGODEOXYNUCLEOTIDE AND ITS USE TO INDUCE AN IMMUNE RESPONSE
 ; FILE REFERENCE: 4239-61999
 ; CURRENT APPLICATION NUMBER: US/10/068,160
 ; CURRENT FILING DATE: 2002-02-05
 ; PRIOR APPLICATION NUMBER: 60/128,898
 ; PRIOR FILING DATE: 1999-04-12
 ; NUMBER OF SEQ ID NOS: 120
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 14
 ; LENGTH: 18
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Oligonucleotide
 US-10-068-160-14

Query Match 91.1%; Score 16.4; DB 15; Length 18;
 Best Local Similarity 94.4%; Pred. No. 77;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TGCATCGACGACGGGGG 18
 |||||
 Db 1 TGCATCGATCGACGGGGG 18
 |||||

Search completed: July 2, 2004, 13:58:26
 Job time : 138.732 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 2, 2004, 07:36:05 ; Search time 633.732 Seconds
(without alignments)
1231.080 Million cell updates/sec

Title: US-10-068-160-20
Perfect score: 18
Sequence: 1 tgcgtcggtgcagggggg 18

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues
Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenBankl: *
1: gb_ba: *
2: gb_htg: *
3: gb_in: *
4: gb_om: *
5: gb_ov: *
6: gb_pat: *
7: gb_ph: *
8: gb_pi: *
9: gb_pr: *
10: gb_ro: *
11: gb_sts: *
12: gb_sy: *
13: gb_un: *
14: gb_vi: *
15: em_ba: *
16: em_fun: *
17: em_hum: *
18: em_in: *
19: em_mu: *
20: em_om: *
21: em_or: *
22: em_ov: *
23: em_pat: *
24: em_ph: *
25: em_pl: *
26: em_ro: *
27: em_sts: *
28: em_un: *
29: em_vi: *
30: em_htg_hum: *
31: em_htg_inv: *
32: em_htg_other: *
33: em_htg_mus: *
34: em_htg_pin: *
35: em_htg_rod: *
36: em_htg_mam: *
37: em_htg_vrt: *
38: em_sy: *
39: em_htgo_hum: *
40: em_htgo_mus: *
41: em_htgo_other: *

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	17	94.4	19	6	AX194479	Sequence
2	17	94.4	19	6	AX465429	Sequence
3	16.4	91.1	20	6	AX194440	Sequence
4	16.4	91.1	20	6	AX194481	Sequence
5	16.4	91.1	20	6	AX194482	Sequence
6	16.4	91.1	20	6	AX465390	Sequence
7	16.4	91.1	20	6	AX465431	Sequence
8	16.4	91.1	20	6	AX465432	Sequence
9	16.4	91.1	10007	1	AE008951	Agrobacte
10	16.4	91.1	11009	1	AE007898	Continuation (23 o
11	16.4	91.1	110000	2	LMFLCHR32_22	Continuation (7 of
12	16.4	91.1	110000	2	LMFLCHR34_06	Continuation (7 of
13	16.4	91.1	178145	9	AC018559	Homo sapi
14	16.4	91.1	283100	1	SC0939110	Streptomy
15	16	88.9	1166	9	BC008984	Homo sapi
16	16	88.9	1182	9	AY286020	Homo sapi
17	16	88.9	1825	9	AY172561	Homo sapi
18	16	88.9	1851	9	AY286019	Homo sapi
19	16	88.9	134161	9	AC104336	Homo sapi
20	16	88.9	141567	2	AC133710	Homo sapi
21	16	88.9	143060	9	AL329472	Oryza sat
22	16	88.9	160402	2	AC136491	Human DNA
23	16	88.9	170908	2	AC022557	Oryza sat
24	16	88.9	190310	2	AC023225	Homo sapi
25	16	88.9	255952	2	AL513473	Homo sapi
26	16	88.9	302881	2	BX323850	Danio rer
27	15.4	85.6	19	6	AX194475	Sequence
28	15.4	85.6	19	6	AX194483	Sequence
29	15.4	85.6	19	6	AX465425	Sequence
30	15.4	85.6	19	6	AX465433	Sequence
31	15.4	85.6	262	11	G22208	human STS W
32	15.4	85.6	683	9	HS333016	Homo sapi
33	15.4	85.6	701	9	HS330295	Homo sapi
34	15.4	85.6	753	9	HS338993	Homo sapi
35	15.4	85.6	765	6	AX438770	Sequence
36	15.4	85.6	771	9	HS338994	Homo sapi
37	15.4	85.6	1392	6	AR387935	Sequence
38	15.4	85.6	1396	8	AX101989	Oryza sat
39	15.4	85.6	1716	9	HSU39195	Human clone
40	15.4	85.6	2722	8	AK100056	Oryza sat
41	15.4	85.6	2783	9	DS0134	Homo sapien
42	15.4	85.6	2968	9	HSU52154	Homo sapien
43	15.4	85.6	10440	1	AE000800	Methanoba
44	15.4	85.6	10942	1	AE004107	Vibriol ch
45	15.4	85.6	12092	1	AE004571	Pseudomon

ALIGNMENTS

RESULT 1	AX194479	AX194479	Sequence 79 from Patent WO0151500.	19 bp	DNA	linear	PAT 28-AUG-2001
LOCUS	AX194479	Sequence 79 from Patent WO0151500.					
DEFINITION	Sequence 79 from Patent WO0151500.						
ACCESSION	AX194479						
VERSION	AX194479.1	GI:15385135					
KEYWORDS							
SOURCE							
ORGANISM							
REFERENCE	1						
AUTHORS	Klinman, D., Ishii, K. and Verthelyi, D.						
TITLE	Oligodeoxynucleotide and its use to induce an immune response						
JOURNAL	Patent: WO 0151500-A 79 19-JUL-2001;						
	Secretary of the Department of Health and Human Services (US)						

```
FEATURES
source
  Location/Qualifiers
    1..19
      /organism="synthetic construct"
      /mol_type="unassigned DNA"
      /db_xref="taxon:32630"
      /note="Synthetic DNA"
ORIGIN
Query Match      94.4%; Score 17; DB 6; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 TCGTCGGTGCAGGGG 17
Db 3 TCGTCGGTGCAGGGG 19
RESULT 2
AX194440
LOCUS      AX194440      19 bp      DNA      linear      PAT 16-JUL-2002
DEFINITION Sequence 97 from Patent WO0211761.
ACCESSION  AX194440
VERSION     AX194440.1 GI:21899792
KEYWORDS   .
SOURCE      synthetic construct
            synthetic construct
            artificial sequences.
REFERENCE   1
AUTHORS     Mond, J.J., Prince, G. and Klimman, D.M.
TITLE       Vaccine against RSV.
JOURNAL     Patent: WO 0211761-A 97 14-FEB-2002;
            HENRY M. JACKSON FOUNDATION FOR THE ADVANCEMENT OF MILITARY
            MEDICINE (US)
FEATURES    source
            Location/Qualifiers
              1..19
                /organism="synthetic construct"
                /mol_type="unassigned DNA"
                /db_xref="taxon:32630"
                /note="Synthetic oligonucleotide"
ORIGIN
Query Match      94.4%; Score 17; DB 6; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 TCGTCGGTGCAGGGG 17
Db 3 TCGTCGGTGCAGGGG 19
RESULT 3
AX194440
LOCUS      AX194440      20 bp      DNA      linear      PAT 28-AUG-2001
DEFINITION Sequence 40 from Patent WO0151500.
ACCESSION  AX194440
VERSION     AX194440.1 GI:15385096
KEYWORDS   .
SOURCE      synthetic construct
            synthetic construct
            artificial sequences.
REFERENCE   1
AUTHORS     Kliman, D., Ishii, K. and Verthelyi, D.
TITLE       Oligodeoxynucleotide and its use to induce an immune response
JOURNAL     Patent: WO 0151500-A 40 19-JUL-2001;
            Secretary of the Department of Health and Human Services (US)
FEATURES    source
            Location/Qualifiers
              1..20
                /organism="synthetic construct"
                /mol_type="unassigned DNA"
                /db_xref="taxon:32630"
                /note="Synthetic DNA"
ORIGIN
Query Match      91.1%; Score 16.4; DB 6; Length 20;
Best Local Similarity 94.4%; Pred. No. 2.8e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 TCGTCGGTGCAGGGG 18
Db 3 TCGTCGGTGCAGGGG 20
RESULT 4
AX194481
LOCUS      AX194481      20 bp      DNA      linear      PAT 28-AUG-2001
DEFINITION Sequence 81 from Patent WO0151500.
ACCESSION  AX194481
VERSION     AX194481.1 GI:15385137
KEYWORDS   .
SOURCE      synthetic construct
            synthetic construct
            artificial sequences.
REFERENCE   1
AUTHORS     Kliman, D., Ishii, K. and Verthelyi, D.
TITLE       Oligodeoxynucleotide and its use to induce an immune response
JOURNAL     Patent: WO 0151500-A 81 19-JUL-2001;
            Secretary of the Department of Health and Human Services (US)
FEATURES    source
            Location/Qualifiers
              1..20
                /organism="synthetic construct"
                /mol_type="unassigned DNA"
                /db_xref="taxon:32630"
                /note="Synthetic DNA"
ORIGIN
Query Match      91.1%; Score 16.4; DB 6; Length 20;
Best Local Similarity 94.4%; Pred. No. 2.8e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 TCGTCGGTGCAGGGG 18
Db 3 TCGTCGGTGCAGGGG 20
RESULT 5
AX194482
LOCUS      AX194482      20 bp      DNA      linear      PAT 28-AUG-2001
DEFINITION Sequence 82 from Patent WO0151500.
ACCESSION  AX194482
VERSION     AX194482.1 GI:15385138
KEYWORDS   .
SOURCE      synthetic construct
            synthetic construct
            artificial sequences.
REFERENCE   1
AUTHORS     Kliman, D., Ishii, K. and Verthelyi, D.
TITLE       Oligodeoxynucleotide and its use to induce an immune response
JOURNAL     Patent: WO 0151500-A 82 19-JUL-2001;
            Secretary of the Department of Health and Human Services (US)
FEATURES    source
            Location/Qualifiers
              1..20
                /organism="synthetic construct"
                /mol_type="unassigned DNA"
                /db_xref="taxon:32630"
                /note="Synthetic DNA"
ORIGIN
Query Match      91.1%; Score 16.4; DB 6; Length 20;
Best Local Similarity 94.4%; Pred. No. 2.8e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 TCGTCGGTGCAGGGG 18
Db 3 TCGTCGGTGCAGGGG 20
```

```

RESULT 6
AX465390
LOCUS AX465390 20 bp DNA linear PAT 16-JUL-2002
DEFINITION Sequence 58 from Patent WO0211761.
ACCESSION AX465390
VERSION AX465390.1 GI:21899753
KEYWORDS
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE
1 Mond,J.J., Prince,G. and Klinman,D.M.
AUTHORS Vaccine against RSV
TITLE Patent: WO 0211761-A 58 14-FEB-2002;
JOURNAL HENRY M. JACKSON FOUNDATION FOR THE ADVANCEMENT OF MILITARY
MEDICINE (US)
FEATURES
source Location/Qualifiers
1..20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic oligonucleotide"
ORIGIN
Query Match 91.1%; Score 16.4; DB 6; Length 20;
Best Local Similarity 94.4%; Pred. No. 2.8e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 TCGTCGGTGCAGGGGG 18
Db 3 TCGTCGATGCAGGGGG 20
RESULT 7
AX465431
LOCUS AX465431 20 bp DNA linear PAT 16-JUL-2002
DEFINITION Sequence 99 from Patent WO0211761.
ACCESSION AX465431
VERSION AX465431.1 GI:21899794
KEYWORDS
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE
1 Mond,J.J., Prince,G. and Klinman,D.M.
AUTHORS Vaccine against RSV
TITLE Patent: WO 0211761-A 99 14-FEB-2002;
JOURNAL HENRY M. JACKSON FOUNDATION FOR THE ADVANCEMENT OF MILITARY
MEDICINE (US)
FEATURES
source Location/Qualifiers
1..20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic oligonucleotide"
ORIGIN
Query Match 91.1%; Score 16.4; DB 6; Length 20;
Best Local Similarity 94.4%; Pred. No. 2.8e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 TCGTCGGTGCAGGGGG 18
Db 3 TCGTCGATGCAGGGGG 20
RESULT 8
AX465432
LOCUS AX465432 20 bp DNA linear PAT 16-JUL-2002
DEFINITION Sequence 100 from Patent WO0211761.
ACCESSION AX465432
VERSION AX465432.1 GI:21899795
KEYWORDS

```

```

SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE
1 Mond,J.J., Prince,G. and Klinman,D.M.
AUTHORS Vaccine against RSV
TITLE Patent: WO 0211761-A 100 14-FEB-2002;
JOURNAL HENRY M. JACKSON FOUNDATION FOR THE ADVANCEMENT OF MILITARY
MEDICINE (US)
FEATURES
source Location/Qualifiers
1..20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic oligonucleotide"
ORIGIN
Query Match 91.1%; Score 16.4; DB 6; Length 20;
Best Local Similarity 94.4%; Pred. No. 2.8e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 TCGTCGGTGCAGGGGG 18
Db 3 TCGTCGATGCAGGGGG 20
RESULT 9
AE008951
LOCUS AE008951 10007 bp DNA linear BCT 20-DEC-2001
DEFINITION Agrobacterium tumefaciens str. C58 AT plasmid section 26 of 49 of
the complete sequence.
ACCESSION AE008951
VERSION AE008951.1 GI:17743725
KEYWORDS
SOURCE Agrobacterium tumefaciens str. C58 (U. Washington)
ORGANISM Agrobacterium tumefaciens str. C58 (U. Washington)
REFERENCE
1 Agrobacterium tumefaciens str. C58 AT plasmid section 26 of 49 of
the complete sequence.
AUTHORS
Wood,D.W., Setubal,J.C., Kaul,R., Monks,D., Chen,L., Wood,G.E.,
Chen,Y., Woo,L., Kitajima,J.P., Okura,V.K., Almeida Jr.,N.F.,
Zhou,Y., Bovee Sr.,D., Chapman,P., Clendenning,J., Deatherage,G.,
Gillet,W., Grant,C., Guenther,D., Kutyavin,T., Levy,R., Li,M.,
McLelland,E., Palmieri,A., Raymond,C., Rouse,G.,
Saenphimmachak,C., Wu,Z., Gordon,D., Eisen,J.A., Paulsen,I.,
Karp,P., Romero,P., Zhang,S., Yoo,H., Biddle,P., Jung,M.,
Krespan,W., Perry,M., Gordon-Kamm,B., Liao,L., Kim,S., Hendrick,C.,
Zhao,Z., Dolan,M., Tingey,S.V., Tomb,J., Gordon,M.P., Olson,M.V.
and Nester,E.W.
TITLE The genome of the natural genetic engineer Agrobacterium
tumefaciens C58
JOURNAL Science 294 (5550), 2317-2323 (2001)
MEDLINE 21608550
PUBMED 11743193
REFERENCE
2 (bases 1 to 10007)
AUTHORS
Wood,D.W., Setubal,J.C., Kaul,R., Monks,D., Chen,L., Wood,G.E.,
Chen,Y., Woo,L., Kitajima,J.P., Okura,V.K., Almeida Jr.,N.F.,
Zhou,Y., Bovee Sr.,D., Chapman,P., Clendenning,J., Deatherage,G.,
Gillet,W., Grant,C., Guenther,D., Kutyavin,T., Levy,R., Li,M.,
McLelland,E., Palmieri,A., Raymond,C., Rouse,G.,
Saenphimmachak,C., Wu,Z., Gordon,D., Eisen,J.A., Paulsen,I.,
Karp,P., Romero,P., Zhang,S., Yoo,H., Biddle,P., Jung,M.,
Krespan,W., Perry,M., Gordon-Kamm,B., Liao,L., Kim,S., Hendrick,C.,
Zhao,Z., Dolan,M., Tingey,S.V., Tomb,J., Gordon,M.P., Olson,M.V.
and Nester,E.W.
TITLE Direct Submission
JOURNAL Submitted (27-SEP-2001) Department of Microbiology, University of
Washington, 1959 NE Pacific Ave, Box 357242, Seattle, WA
98195-7242, USA
FEATURES
source Location/Qualifiers
1..10007
/organism="Agrobacterium tumefaciens str. C58 (U.
Washington)"

```

```

/mol_type="genomic DNA"
/strain="C58"
/db_xref="taxon:180835"
/plasmid="AT"
/complement (73..1860)
/gene="Atu5284"
/complement (73..1860)
/gene="Atu5284"
/translation="MNNARYKNGAQRHQSGDTSIWPASATVTKLWLNDAEFTMGH
TAGGWHDTKPPGLGDRYGVFLADTRVADPNASNRQQGPRGSLVNHDSFAWKFN
WGRGPWHEAVYALHGTFTPEGTFAAAAEKLEYLADVGITTELMPLATFAGSRGNG
YDVLQGFSPQDGTDELKATIDQARHGIMVLVDVYVHFGPAGNTLQAVAPAFK
KHETPGAPDENRAEVRFFLQAFYWLETTYRFDGLRIDAADHLAGGDCVDFLIEM
AREVETIRNRVHLVIEDARNAASPMTFADGAILVDQWMDDDHVIHVAFTTNEEG
GIYEDFASRPYENRSLATGVYCGEPSPSNFASCEPSGHLPHRFVNLHNDQ
AGNRLGERLALIPPLFGTLALILLCCQPTPLVPMGDHGSANPFFPFSDDPHNR
EQIRNLKQAESFQGLPEPDASQVMDENDQHTQLSTLKWTHAETTEGQRSDMA
ALLAKRGHWLPLCSHFBEKISLDCPEPCLADWHPKAGRLMRANLSENKCELPAY
KGEILHRNGSVGNTRYEGYAAQFAIVAGR"
/complement (1884..3476)
/gene="glgA"
/notes="synonym: Atu5285"
/complement (1884..3476)
/gene="glgA"
/notes="identified by sequence similarity; putative; ORF
located using Blastx/Glimmer"
/codon_start=1
/translation="MSPCTFRAPHHLKSLRRRQRRLAVTAEMFPFVKTTGLADAT
SALPQALERKADVRLTLPLVRKPLVAVNILEQVSVYVYVSDGHKLLI
LEAASLPDSGHPYGVGPFADNDLRPAVLKVAEIALGAIQGVVHVHWHHA
KLTCTVADTSPVASVLTNLNLPQGVPLERAGMLGPSHLCTVDCLEYDDMSFL
KGLGTSASVTSPYAREILTPMGCMGHVARRRGDLRGIVGVDHVDWNPATD
PYLANFTATATRSNLKALLQALGAPTCQGVGVSVRLTWKGDILLPHVPLI
IRKGLHIVGSGDALSQALAKRYPELVCAHIGYDERLAHMIQAGSDPIIQPSR
FPKQITQYALRYALGAPLIVSRGTGLAETIDANDAAIEAGVATGQFEPANEDLRA
ALERATISYNDRELFRLOQVQANFSDKSAQAQVMALESVLVNGNSTRETDAVADIR
TETFAKIRADRLAGTPGSPG"
/complement (3923..4336)
/gene="Atu5286"
/complement (3923..4336)
/gene="Atu5286"
/notes="putative; ORF located using Glimmer"
/codon_start=1
/translation="hypothetical protein"
/protein_id="AAL45975.1"
/db_xref="GI:17743728"
/translation="NRQPRRGVWSCLETIVCQRHGISBELASNPVRDQMSRATSQLL
LRSSRKRAISCLQPRSRMSRPSRSTRSADRSKPTSDLCRISNPKRQARLA
AFARYLTFDRGVDPKSLQGLPALYFRTKLRIG"
/complement (4411..5010)
/gene="Atu5287"
/complement (4411..5010)
/gene="Atu5287"
/notes="identified by sequence similarity; putative; ORF
located using Blastx/Glimmer"
/codon_start=1
/translation="conserved hypothetical protein"
/protein_id="AAL45976.1"
/db_xref="GI:17743729"
/translation="NRTVTGLFDYSDASAAVSALESAGVRSDDISIVSNADKREHGD
SNAABGATGAGIGAVVGAGGLITGLGLMAIPGVGPVVAAGLAAATAGAAAGAVAG
GATGIGIAGMTSSGVSEHDAHYAEGVRRGTLVTAKVDDALVSEABAILKRSNWDP
AARVAYEEQWTRFDDADPDYDAQIRQLERLVRAGL"
/complement (5026..5403)
/gene="Atu5288"
/complement (5026..5403)
/gene="Atu5288"
/notes="putative; ORF located using Glimmer"
/codon_start=1
/translation="hypothetical protein"
/protein_id="AAL45977.1"
/db_xref="GI:17743730"
/translation="MQRGYLGSVHEVNTGSPKWAIEAALFSAISISAPACTAP
TANNNDTPAVATPDTKNPTAPVVGANSFTEAQAQRIEKAGYSVDKOLKDDKGIWN
AAGMKDCAVSAIDYQGNVAK"
/complement (5566..6289)
/gene="Atu5289"
/complement (5566..6289)
/gene="Atu5289"
/notes="identified by sequence similarity; putative; ORF
located using Blastx/Glimmer"
/codon_start=1
/translation="transcriptional regulator, TetR family"
/protein_id="AAL45978.1"
/db_xref="GI:17743731"
/translation="MKSSEHGADGGLREKRETKRLTEKGLALPLBERGFONTTL
DEIASAGISRTFFYFKSKDEILLQSIGCEMLADAVRAPSSTPISEVRDAAL
GVKVIPTNDMIENDRLMKTSQVQARKQSVQCEGHIYALSERWPEPBRSTALRV
VAMLSVGAMRIAGDIFSQEGVPRPMDLLEAFGLSIQEVRSQDPRV"
/6367..7272
/gene="Atu5290"
/6367..7272
/gene="Atu5290"
/notes="identified by sequence similarity; putative; ORF
located using Blastx/Glimmer"
/codon_start=1
/translation="dehydrogenase"
/protein_id="AAL45979.1"
/db_xref="GI:17743732"
/translation="MTKERTANIQRGSAVVTGCGLETALALARAGCDVTIAG
RNPBKSDASVRIORAAPHVTVSFEKDLADLISIALPAQWMDRSLDLVNNAGI
MVPKREKDFGELQGTNYLGHFALTALHMLPKKGTDAVVTVSVSVAARAKINF
ADINSKRYHPMRAYSQSLCLMFALELDQSRAGAGVSSIAAHFQVSTDLHNA
PGRNSLOGLARTFLWFLPQVPAQALPQFSATSKEVKSQGYGPDRLGETRGHPQA
RIPPEALDRVAGKQLWEISQRMTEL"
/7411..8076
/gene="Atu5291"
/7411..8076
/gene="Atu5291"
/notes="identified by sequence similarity; putative; ORF
located using Blastx/Glimmer"
/codon_start=1
/translation="transcriptional regulator, TetR family"
/protein_id="AAL45980.1"
/db_xref="GI:17743733"
/translation="MTKERPFVLSMSSINTRKAILHIGIDQSVSLAGVTVQOLAN
ASALSKSLFAHFKSKEQLQIELISEAARIKTLTIPEKAMQDQGLSRLRAVVELWFG
WSRRAGLQGGCLAAALFELDDVDGVDHAAQLTVWRNLLTMLVGSVTAHLSAA
TDVAQPTWELNGIYNHVVSTRPFREKEADARATYAEALIAHRPESGSAVTAWKEC
TDC"
/8069..8431
/gene="Atu5292"
/8069..8431
/gene="Atu5292"
/notes="identified by sequence similarity; putative; ORF
located using Blastx/Glimmer"
/codon_start=1
/translation="conserved hypothetical protein"

```

[illegible]

```
gene 6340. 7272
CDS /gene="AGR_PAT_417"
6340. 7272
/gene="AGR_PAT_417"
/notes="hypotheical protein Rv2263 - Mycobacterium
tuberculosis (strain H37RV)"
/codon_start=1
/transl_table=11
/product="AGR_PAT_417p"
/protein_id="AAK90666.1"
/db_xref="GI:15162067"
/translation="MRKMKRPEMTKWTETANI PNQGRSAVVVTGGGLGLETALALAR
ACDVTIAGNPEKSDAVRIQRAAPHVTVSFKEKLDLADLTSIALFAQRMENDRESL
DLVNNAGIMVPPKQETVPELOFTGTYLGHFALTAHMLPKKGTDAVWTVSSV
ARAKGINFADINSKNVHPMAYSQSLACIMFALELDQSRRAAGWGVSSIAAPRGV
SRTDLHNAFGNSLQGLARTFLMELFQPVAGALPOLFSATSKVSGGYGPPRLG
ETRGHPQARIPEALDRVAGKQLMEISQRMGL"
7411. 8076
/gene="AGR_PAT_419"
7411. 8076
/gene="AGR_PAT_419"
/notes="(AL512667) putative tetr-family transcriptional
regulator"
/codon_start=1
/transl_table=11
/product="AGR_PAT_419p"
/protein_id="AAK90667.1"
/db_xref="GI:15162068"
/translation="MTKERPFVLLSMSSINTKAKILHIGIDLSVSLAGVTVGOLAN
ASALSKGGLCPAFHFKSKEOLOIELISSAARIAKLITVEPMKADQGLSLRAVVELMFG
KSRAGLQGLCPALAELOELDQVDEHRAQLTVRWENLLTMLVGSVTAHLSAA
TDVAFIHELNGIYLNHVSTRFFREKEDAKARATYAFALTAHHPFSGSAVTAWKEC
TDG"
8069. 8431
/gene="AGR_PAT_420"
8069. 8431
/gene="AGR_PAT_420"
/notes="hypotheical protein"
/codon_start=1
/transl_table=11
/product="AGR_PAT_420p"
/protein_id="AAK90668.1"
/db_xref="GI:15162069"
/translation="NDEGADADAESALVELOQLRELEMAETTLVLLGLAVPAK
HLPWPESKYLGPVHGIAFLTYMHTITQLAGGWRDRDARUPAAAFIPFAGFYNI
QWLRRTILMAINICDGH"
complement(9349. 9609)
/gene="AGR_PAT_421"
complement(9349. 9609)
/gene="AGR_PAT_421"
/notes="hypotheical protein"
/codon_start=1
/transl_table=11
/product="AGR_PAT_421p"
/protein_id="AAK90669.1"
/db_xref="GI:15162070"
/translation="MHGILKRPMEGRTRPLATVSKRDMARDIAEALGRWLDPER
SKSPARFLAVLQGSVQARDGATSELEEVITQALRIQTG"
complement(9552. 9971)
/gene="AGR_PAT_422"
complement(9552. 9971)
/gene="AGR_PAT_422"
/notes="(AL357432) putative transcriptional regulator"
/codon_start=1
/transl_table=11
/product="AGR_PAT_422p"
/protein_id="AAK90670.1"
/db_xref="GI:15162071"
/translation="MISVKSQSLVIAKMDQVRRRGSPRTFNREEAIDIAKRLPWRHG
YEGVSLNLTVAIGIAPPSLYAFAFGSKAQLYREALDRYGGIPGALLNDAASTLDEVV
ATILRQGDADVTDGGGRCMVSSGMLQCAEEHAPSL"
10021. 10929
/gene="AGR_PAT_424"
10021. 10929
/gene="AGR_PAT_424"
/notes="hypotheical protein Rv2263 - Mycobacterium
tuberculosis (strain H37RV)"
/codon_start=1
/transl_table=11
/product="AGR_PAT_424p"
/protein_id="AAK90672.1"
/db_xref="GI:15162073"
/translation="MISVKSQSLVIAKMDQVRRRGSPRTFNREEAIDIAKRLPWRHG
YEGVSLNLTVAIGIAPPSLYAFAFGSKAQLYREALDRYGGIPGALLNDAASTLDEVV
ATILRQGDADVTDGGGRCMVSSGMLQCAEEHAPSL"
10021. 10929
/gene="AGR_PAT_424"
10021. 10929
/gene="AGR_PAT_424"
/notes="hypotheical protein Rv2263 - Mycobacterium
tuberculosis (strain H37RV)"
/codon_start=1
/transl_table=11
/product="AGR_PAT_424p"
/protein_id="AAK90672.1"
/db_xref="GI:15162073"
/translation="MISVKSQSLVIAKMDQVRRRGSPRTFNREEAIDIAKRLPWRHG
YEGVSLNLTVAIGIAPPSLYAFAFGSKAQLYREALDRYGGIPGALLNDAASTLDEVV
ATILRQGDADVTDGGGRCMVSSGMLQCAEEHAPSL"
```

```
CDS 10021. 10929
/gene="AGR_PAT_424"
Query Match 91.1%; Score 16.4; DB 1; Length 11009;
Best Local Similarity 94.4%; Pred. No. 1.2e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 TGGCTCGGTGCGAGGGGG 18
Db 9276 TGGCTCGGTGCGAGGGGG 9293
RESULT 11
LMFLCHR32_22/c
WPCOMMENT
Sequence split into 28 fragments LOCUS LMFLCHR32 Accession AL499622
Fragment Name Begin End
LMFLCHR32_00 1 110000
LMFLCHR32_01 100001 210000
LMFLCHR32_02 200001 310000
LMFLCHR32_03 300001 410000
LMFLCHR32_04 400001 510000
LMFLCHR32_05 500001 610000
LMFLCHR32_06 600001 710000
LMFLCHR32_07 700001 810000
LMFLCHR32_08 800001 910000
LMFLCHR32_09 900001 1010000
LMFLCHR32_10 1000001 1110000
LMFLCHR32_11 1100001 1210000
LMFLCHR32_12 1200001 1310000
LMFLCHR32_13 1300001 1410000
LMFLCHR32_14 1400001 1510000
LMFLCHR32_15 1500001 1610000
LMFLCHR32_16 1600001 1710000
LMFLCHR32_17 1700001 1810000
LMFLCHR32_18 1800001 1910000
LMFLCHR32_19 1900001 2010000
LMFLCHR32_20 2000001 2110000
LMFLCHR32_21 2100001 2210000
LMFLCHR32_22 2200001 2310000
LMFLCHR32_23 2300001 2410000
LMFLCHR32_24 2400001 2510000
LMFLCHR32_25 2500001 2610000
LMFLCHR32_26 2600001 2710000
LMFLCHR32_27 2700001 2727709
Continuation (23 of 28) of LMFLCHR32 from base 2200001 (AL499622 Leishmania major chro
Query Match 91.1%; Score 16.4; DB 2; Length 110000;
Best Local Similarity 94.4%; Pred. No. 9.2e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 TGGCTCGGTGCGAGGGGG 18
Db 23220 TGGCTCGGTGCGAGGGGG 23203
RESULT 12
LMFLCHR34_06
WPCOMMENT
Sequence split into 18 fragments LOCUS LMFLCHR34 Accession AL499623
Fragment Name Begin End
LMFLCHR34_00 1 110000
LMFLCHR34_01 100001 210000
LMFLCHR34_02 200001 310000
LMFLCHR34_03 300001 410000
LMFLCHR34_04 400001 510000
LMFLCHR34_05 500001 610000
LMFLCHR34_06 600001 710000
LMFLCHR34_07 700001 810000
LMFLCHR34_08 800001 910000
LMFLCHR34_09 900001 1010000
LMFLCHR34_10 1000001 1110000
```

LMFLCHR34_11 1100001 1210000
 LMFLCHR34_12 1200001 1310000
 LMFLCHR34_13 1300001 1410000
 LMFLCHR34_14 1400001 1510000
 LMFLCHR34_15 1500001 1610000
 LMFLCHR34_16 1600001 1710000
 LMFLCHR34_17 1700001 1720777

Continuation (7 of 18) of LMFLCHR34 from base 600001 (AL499523 Leishmania major chromosome)

Query Match 91.1%; Score 16.4; DB 2; Length 110000;
 Best Local Similarity 94.4%; Pred. No. 9.2e+02;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TGGCTCGTGCAGGGGG 18
 Db 66619 TGGCTCTGTCAGGGGG 66636

RESULT 13
 AC018659/c

LOCUS AC018659 178145 bp DNA linear PRI 18-MAR-2003
 DEFINITION Homo sapiens 12 BAC RP11-528M18 (Roswell Park Cancer Institute Human BAC Library) complete sequence.
 ACCESSION AC018659
 VERSION AC018659.35 GI:14277213
 KEYWORDS HTG
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE
 AUTHORS Rukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 1 (bases 1 to 178145)
 Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-Osman, P.R., Allen, C., Alsbrooks, S.L., Amarantunge, H.C., Are, J.R., Banks, T., Barbaria, J., Benton, J., Binage, K., Blankenburg, K., Bonnin, D., Bouck, J., Bowie, S., Brieva, M., Brown, R., Brown, M., Bryant, N.P., Buha, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C., Carron, T.F., Carter, M., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Z., Chiu, D., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox, C., Coyle, M.D., Dathorne, S.A., David, R., Davila, M.L., Davis, C., Davy-Carroll, L., Dederich, D.A., Delaney, K.R., Delgado, O., Dunn, A.L., Ding, Y., Dinh, H.H., Douthwaite, K.J., Draper, H., Dugan-Rocha, S., Durbin, K.J., Earnhart, C., Edgar, D., Edwards, C.C., Elnaj, C., Emerling, S., Escotto, M., Falls, T., Ferraguto, D., Flagg, N., Ford, J., Foster, P., Frantz, P., Gabisi, A., Gao, J., Garcia, A., Garner, R., Garza, N., Gill, R., Gorrell, J.H., Guevara, W., Gunaratne, P., Hale, S., Hamilton, K., Han, J., Harris, C., Harris, K., Hart, M., Havlak, P., Hawes, A., Hernandez, J., Hernandez, O., Hodgson, A., Hognes, M., Holloway, C., Hollins, B., Homs, F., Howard, S., Huber, J., Hulyk, S., Hume, J., Ioshikhes, I., Jackson, L.B., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Kovar, C., Kratovic, J., Kureshi, A., Landry, N., Leal, B., Lee, E., Lewis, L.C., Lewis, L., Li, J., Li, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, W., Louie, H., Lozano, R., Lu, X., Lucier, A., Lucier, R., Luna, R., Ma, J., Maheshwari, M., Mapa, P., Marandel, I., Martin, R., Martindale, A., Martinez, E., Massey, E., Mawhinney, B., McLeod, M.P., Meador, M., Mei, G., Merscher, S., Metzger, M., Miller, A., Miner, G., Mirer, Z., Mitchell, T., Mohabbat, K., Montgomery, K.T., Morgan, M., Morris, S., Moser, M., Neal, D., Nelson, D., Newton, J., Newton, N., Nguyen, A., Nguyen, N., Nguyen, N., Nickerson, E., Nwokweto, S., Oquh, M., Okwono, G., Oragunye, N., Oviedo, R., Pace, A., Payton, B., Peery, J., Perez, L., Peters, L., Pickens, R., Primus, E., Pu, L.L., Quiles, M., Ren, F., Rives, M., Rojas, A., Rojibokan, I., Rolfe, M., Ruiz, S., Savary, G., Scherer, S., Scott, G., Shen, H., Shim, C., Shoostari, N., Sisson, I., Sodergren, E., Sonake, T., Sparks, A., Stanley, H., Stone, H., Sutton, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, K., Tang, H., Tansey, J., Taylor, C., Taylor, T., Telford, B., Thomas, N., Thomas, S., Usmani, K., Vasquez, L., Vera, V., Villalon, D., Vinson, R., Wall, R., Wang, S., Ward-Moore, S., Warren, R., Washington, C., Washington, S., Williams, G., Williamson, A., Wlecyk, R., Wooden, S., Worley, K., Wu, C., Wu, Y., Wu, Y.F., Zhou, J., Zorrilla, S., Zuchelapati, R., Weinstein, G. and Gibbs, R.
 Direct Submission

TITLE

JOURNAL
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 JOURNAL
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT

Unpublished
 2 (bases 1 to 178145)
 Worley, K.C.
 Direct Submission
 Submitted (16-DEC-1999) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
 3 (bases 1 to 178145)
 Worley, K.C.
 Direct Submission
 Submitted (01-JUN-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
 4 (bases 1 to 178145)
 Worley, K.C.
 Direct Submission
 Submitted (05-JUN-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
 5 (bases 1 to 178145)
 Worley, K.C.
 Direct Submission
 Submitted (31-MAY-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
 6 (bases 1 to 178145)
 Worley, K.C.
 Direct Submission
 Submitted (18-MAR-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
 On Jun 1, 2001 this sequence version replaced gi:14269664.
 INFORMATION: <http://www.hgsc.bcm.tmc.edu/> or email gc-help@bcm.tmc.edu

CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are only sequenced and submitted once, so the sequence for the remainder of the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the Features listing.

ANNOTATION OF FEATURES:

STSS are identified using ePCR (Genome Res. 7:541-550) searches of a local database that includes entries from dbSTS, GDB, and local mapping efforts.

Repeats are identified using RepeatMasker (A. Smit and P. Green, unpublished.) for Human and Mouse sequences.

Genes and Region of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.

SEQUENCING READ COVERAGE: Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the annotation as Low Coverage.

QUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality standards - estimated error rate less than 1 per 10,000 bases. Reports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found at URL: <http://gc.bcm.tmc.edu:8088/quality.info/genbank.annotation.html>.

QUALSTAT-REPORT:

Location/Qualifiers
 1..178145
 /organism="Homo sapiens"

FEATURES
 source


```

/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="12"
/clone="RP11-528M18"
1..5920
/rpt_family="L1PA5"
1..2089
/notes="overlaps bases 81513..83601 of clone AC007424"
2640..2741
/standard_name="152792"
complement(5931..6187)
/rpt_family="MLT2CB"
complement(6208..6289)
/rpt_family="L2"
6933..7081
/rpt_family="CT-rich"
8001..8036
/rpt_family="AT-rich"
8243..8568
/standard_name="135532"
complement(9345..9478)
/rpt_family="AluYo"
complement(9534..9689)
/rpt_family="AluYo"
complement(9744..10002)
/rpt_family="AluY"
10495..10529
/rpt_family="A-rich"
10871..11106
/rpt_family="MIR"
11247..11375
/rpt_family="MIR"
complement(11452..11536)
/rpt_family="L1MBC"
11538..11772
/rpt_family="CT-rich"
complement(11829..14890)
/rpt_family="L1MBC"
complement(14986..15129)
/rpt_family="MIR"
complement(17517..17807)
/rpt_family="AluSx"
complement(17811..18136)
/rpt_family="AluSx"
complement(18163..21485)
/rpt_family="L1PA6"
complement(21486..21793)
/rpt_family="AluY"
complement(21794..24659)
/rpt_family="L1PA6"
25057..25402
/rpt_family="THE1B"
25438..25507
/rpt_family="TATG)n"
25802..25961
/rpt_family="MER103"
26757..27003
/rpt_family="L1MBC"
complement(27004..27312)
/rpt_family="AluSx"
27304
/notes="C/T"
/function="polymorphic site"
27313..27340
/rpt_family="L1MBC"
27341..27636
/rpt_family="AluSg"
27637..28212
/rpt_family="L1MBC"
28322..28626
/rpt_family="L2"
28990..29026

```

Query Match 91.1%; Score 16.4; DB 9; Length 178145;
Best Local Similarity 94.4%; Pred. No. 8.6e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

/rpt_family="(CAA)n"

QY 1 TCGCTCGGTGCGGGGGG 18
Db 94986 TCGTCTCGGTGCGGGGGG 94969

RESULT 14
SC0939110 283100 bp DNA linear BCT 11-FEB-2003
LOCUS Streptomyces coelicolor A3(2) complete genome; segment 7/29
DEFINITION AL039110 AL035591 AL079332 AL096743 AL096811 AL096839 AL096844
ACCESSION AL096849 AL096848 AL132844 AL445403 AL513407 AL591322 AL645862
VERSION AL0939110.1 GI:24413753
KEYWORDS Streptomyces coelicolor A3(2)
SOURCE Streptomyces coelicolor A3(2)
ORGANISM Streptomyces coelicolor A3(2)
Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
Streptomycineae; Streptomycetaceae; Streptomyces.

REFERENCE 1 Bentley, S.D., Chater, K.F., Cerdeno-Tarraga, A.M., Challis, G.L.,
Thomson, N.R., James, K.D., Harris, D.E., Quail, M.A., Kieser, H.,
Harper, D., Bateman, A., Brown, S., Chandra, G., Chen, C.W., Collins, M.,
Cronin, A., Fraser, A., Goble, A., Hidalgo, J., Hornsby, T., Howarth, S.,
Huang, C.H., Kieser, T., Larke, L., Murphree, L., Oliver, K., O'Neill, S.,
Rabinowitsch, E., Rajandream, M.A., Rutherford, K., Rutter, S.,
Seeger, K., Saunders, D., Sharp, S., Squares, R., Squares, S.,
Taylor, K., Warren, T., Wietzorrek, A., Woodward, J., Barrall, B.G.,
Parkhill, J. and Hopwood, D.A.
Complete genome sequence of the model actinomycete Streptomyces
coelicolor A3(2)
NATURE 417 (6885), 141-147 (2002)

JOURNAL Nature 417 (6885), 141-147 (2002)
MEDLINE 21996410
PubMed 12009553

REFERENCE 2 (bases 1 to 283100)
Bentley, S.D.
Direct Submission
Submitted (09-MAY-2002) Submitted on behalf of the Streptomyces
Sequencing team, Sanger Institute, Wellcome Trust Genome Campus,
Hinxton, Cambridge CB10 1SA E-mail: sdb@sanger.ac.uk

On or before Oct 26, 2002 this sequence version replaced
GI:20520819, GI:20520879, GI:20520880, GI:20520919, GI:20520821,
GI:20520887, GI:20520888, GI:20520889, GI:20520884, GI:20520704,
GI:20520915, GI:20520918.

FEATURES Location/Qualifiers
1..283100
/organism="Streptomyces coelicolor A3(2)"
/mol_type="genomic DNA"
/strain="A3(2)"
/db_xref="taxon:100226"
59..520
/gene="SCO1698"
/notes="synonym: SCI30A.19"
59..520
/gene="SCO1698"
/notes="SCO1698"
/notes="SCO1698, unknown, len: 153 aa; similar to many of
undefined function e.g. TR:P96807 (EMBL:Z92770)
hypothetical protein from Mycobacterium tuberculosis (151
aa) fasta scores; opt: 639, z-score: 785.9, E(): 0, (60.8%
identity in 148 aa overlap) and SW:MODN RHIVY modulation
protein from Rhizobium leguminosarum (161 aa) fasta
scores; opt: 388, z-score: 482.2, E(): 1.6e-19, (44.8%
identity in 145 aa overlap)"
/codon_start=1
/transl_table=11
/product="conserved hypothetical protein"
/protein_id="CA846796.1"
/db_xref="GI:5441772"
/db_xref="GOA:Q9S254"

gene
CDS

Search completed: July 2, 2004, 10:08:13
Job time : 636.732 secs

DBb 153387 TCGGCGGTGCAGGGGG 153404

RESULT 15

BC008984	1166 bp	mRNA	linear	PRI 12-JUL-2001
LOCUS				
DEFINITION	Homo sapiens, hypothetical protein FLJ23476, clone MGC:16780			
ACCESSION	IMAGE:438853, mRNA, complete cds.			
VERSION	BC008984			
KEYWORDS	BC008984.1 GI:14290439			
SOURCE	MGC.			
ORGANISM	Homo sapiens (human)			
REFERENCE	Homo sapiens			
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
TITLE	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
JOURNAL	1 (bases 1 to 1166)			
	Strausberg,R.			
	Direct Submission			
	Submitted (30-MAY-2001) National Institutes of Health, Mammalian			
	Gene Collection (MGC), Cancer Genomics Office, National Cancer			
	Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,			
	USA			
REMARK	NIH-MGC Project URL: http://mgc.nci.nih.gov			
COMMENT	Contact: MGC help desk			
	Email: cgabs-remail.nih.gov			
	Tissue Procurement: Lou Staudt			
	cDNA Library Preparation: Life Technologies, Inc.			
	cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILML)			
	DNA Sequencing by: Baylor College of Medicine Human Genome			
	Sequencing Center			
	Center code: BCM-HGSC			
	Web site: http://www.hgsc.bcm.tmc.edu/cdna/			
	Contact: vila@nshcm.tmc.edu			
	Villalón, D.K., Luna, R.A., Hale, S.M., Rulyk, S., Lu, X., Garcia,			
	A.M., Holloway, M., Telford, B, Hodgson, A., Bouck, J., Yu, W.,			
	Muzny, D.M., Gibbs, R.A.			

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Series: IRAK file: 12 Row: 0 Column: 18
 This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA qi: 10440198.

FEATURES	SOURCE
1. High Accuracy: The model achieves a high accuracy rate, indicating its effectiveness in predicting the target variable.	Model Performance Metrics
2. Robustness: The model demonstrates robustness against various input variations and noise, ensuring reliable predictions.	Model Performance Metrics
3. Interpretability: The model's predictions are interpretable, allowing users to understand the underlying factors influencing the outcome.	Model Performance Metrics
4. Scalability: The model is scalable, capable of handling large volumes of data and complex tasks efficiently.	Model Performance Metrics
5. Real-time Processing: The model is designed for real-time processing, enabling immediate decision-making based on incoming data.	Model Performance Metrics
6. Integration with Existing Systems: The model seamlessly integrates with existing systems, facilitating a smooth transition and adoption.	Model Performance Metrics
7. Customizable Parameters: The model offers customizable parameters, allowing users to tailor the model to their specific requirements.	Model Performance Metrics
8. Comprehensive Documentation: The model is accompanied by comprehensive documentation, providing detailed information on its usage and capabilities.	Model Performance Metrics
9. Regular Updates: The model is regularly updated with the latest data and insights, ensuring its relevance and accuracy over time.	Model Performance Metrics
10. Support and Maintenance: The model is supported by a dedicated team, ensuring timely assistance and maintenance for any issues.	Model Performance Metrics

```

1. 11166
/organism="Homo sapiens"
/mol_type="mRNA"
/db xref="LocustID:79693"
/db xref="taxon:9606"
/clone="MGC:16780 IMAGE:4338853"
/tissue_type="lymph, lymphoma"
/clone_id="NH1 MGC_85"
/lab_host="DH10B"
/notes="Vector: pCMV-SPORT6"
197..880
/codon_start=1
/product="hypothetical protein F1
/protein_id="AAH09884.1"
/db xref="GI:14290440"
/translation="MERSELEINLPFTPLVAV
GCAESTTAVNEEPOPLQLSLVDGSGQGD
GCAESTTAVNEEPOPLQLSLVDGSGQGD

```

CD5

```

497:..080
/codon_start=1
/product="hypothetical protein FLJ23476"
/protein_id="AH08984.1"
/db_xref="GI:14290440"
/translation="MERSELEKDLNPFTPLVGRIPPHAN
NLGSQASLVNVEQNPQLSLVSLVGLGIDGOSPECRU
GCALESITLQOKYGLIPHSYLVN"

```

ORIGIN

```
Query Match      88.9%; Score 16; DB 9; Length 1166;
Best Local Similarity 100.0%; Pred. No. 2.6e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

2 GCGTCGGTGACGGGG 17

db 52 GCGTCGGTGCA GGGG 67


```
; EARLIER FILING DATE: 1999-04-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1443
; TYPE: DNA
; ORGANISM: Bacillus amyloliquefaciens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1443)
US-09-537-168-1

Query Match      82.2%; Score 14.8; DB 4; Length 1443;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TGCATCGACGACGGGGG 18
    |||||
Db 876 TGCATCGACGACGGGGG 893

RESULT 3
US-08-814-052-5
; Sequence 5, Application US/08814052
; Patent No. 6015783
; GENERAL INFORMATION:
; APPLICANT: von der Osten, Claus
; APPLICANT: Cherry, Joel R.
; APPLICANT: Bjornvad, Mads E.
; APPLICANT: Vind, Jesper
; TITLE OF INVENTION: PROCESS FOR REMOVAL OR BLEACHING OF SOILING
; TITLE OF INVENTION: OR STAINS FROM CELLULOSIC FABRIC
; NUMBER OF SEQUENCES: 55
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 60157830 No. 6015783disk of No. 6015783th America, Inc.
; STREET: 405 Lexington Avenue, Suite 6400
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; FILING DATE: 06-MAR-1997
; CLASSIFICATION: 510
; ATTORNEY/AGENT INFORMATION:
; NAME: Lambiris, Elias J
; REGISTRATION NUMBER: 33,728
; REFERENCE/DOCKET NUMBER: 4684.204-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; TELEX:
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1683 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-814-052-5

Query Match      82.2%; Score 14.8; DB 3; Length 1683;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TGCATCGACGACGGGGG 18
    |||||
Db 876 TGCATCGACGACGGGGG 893

RESULT 5
US-08-146-422-33
; Sequence 33, Application US/08146422
; Patent No. 5543576
; GENERAL INFORMATION:
; APPLICANT: VAN COIJEN, ALBERT J. J.
; APPLICANT: RIETVELD, KEIJN
; APPLICANT: HOEKEMA, ANDREAS
; APPLICANT: PEN, JAN
; APPLICANT: SIJMONS, PETER C.
; APPLICANT: VERWOERD, TEUNIS C.
; APPLICANT: QUAX, WILHEMUS J.
; TITLE OF INVENTION: PRODUCTION OF ENZYMES IN SEEDS AND THEIR
; TITLE OF INVENTION: USE
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 60177510 No. 6017751disk of No. 6017751th America, Inc.
; STREET: 405 Lexington Avenue, Suite 6400
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; FILING DATE: 06-MAR-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Lambiris, Elias J
; REGISTRATION NUMBER: 33,728
; REFERENCE/DOCKET NUMBER: 4690.204-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; TELEX:
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1683 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-812-829-5

Query Match      82.2%; Score 14.8; DB 3; Length 1683;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TGCATCGACGACGGGGG 18
    |||||
Db 969 TGCATCGACGACGGGGG 986

RESULT 5
US-08-146-422-33
; Sequence 33, Application US/08146422
; Patent No. 5543576
; GENERAL INFORMATION:
; APPLICANT: VAN COIJEN, ALBERT J. J.
; APPLICANT: RIETVELD, KEIJN
; APPLICANT: HOEKEMA, ANDREAS
; APPLICANT: PEN, JAN
; APPLICANT: SIJMONS, PETER C.
; APPLICANT: VERWOERD, TEUNIS C.
; APPLICANT: QUAX, WILHEMUS J.
; TITLE OF INVENTION: PRODUCTION OF ENZYMES IN SEEDS AND THEIR
; TITLE OF INVENTION: USE
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
```

```

; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM: disk
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/146,422
; FILING DATE: 02-NOV-1993
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: KENNEDY, BILL
; REGISTRATION NUMBER: 33,407
; REFERENCE/DOCKET NUMBER: 44615-20011.23
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1777 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-146-422-33

Query Match      82.2%; Score 14.8; DB 1; Length 1777;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 TGCATCGACGACGGGGGG 18
      |||||
Db      978 TGCATCGACGACGGGG 995

RESULT 6
US-08-253-575-1
; Sequence 1, Application US/0823575
; Patent No. 5705375
; GENERAL INFORMATION:
; APPLICANT: VAN COYEN, ALBERT J.J.
; APPLICANT: RIETVELD, KRJUN
; APPLICANT: QUAX, WILHELMUS J.
; APPLICANT: VAN DEN ELZEN, PETRUS J.M.
; APPLICANT: PEN, JAN
; APPLICANT: HOEKEMA, ANDREAS
; APPLICANT: SIJMONS, PETER C.
; TITLE OF INVENTION: TRANSGENIC PLANTS HAVING A MODIFIED
; TITLE OF INVENTION: CARBOHYDRATE CONTENT
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM: disk
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/253,575
; FILING DATE:
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/849,422

```

```

; FILING DATE: 12-JUN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: MURASHIGE, KATE H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 24615-20033.00
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 813-5600
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1777 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-253-575-1

Query Match      82.2%; Score 14.8; DB 1; Length 1777;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 TGCATCGACGACGGGGGG 18
      |||||
Db      978 TGCATCGACGACGGGG 995

RESULT 7
US-08-626-554-16
; Sequence 16, Application US/08626554
; Patent No. 5714474
; GENERAL INFORMATION:
; APPLICANT: VAN COIJEN, ALBERT J.J.
; APPLICANT: RIETVELD, KRJUN
; APPLICANT: HOEKEMA, ANDREAS
; APPLICANT: PEN, JAN
; APPLICANT: SIJMONS, PETER C.
; APPLICANT: VERWOERD, TRUNIS C.
; APPLICANT: QUAX, WILHELMUS J.
; TITLE OF INVENTION: PRODUCTION OF ENZYMES IN SEEDS AND THEIR
; TITLE OF INVENTION: USE
; NUMBER OF SEQUENCES: 32
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 2000 PENNSYLVANIA AVENUE NW
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20006-1888
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/626,554
; FILING DATE: 02-APR-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: MURASHIGE, KATE H.
; REGISTRATION NUMBER: 29,959
; REFERENCE/DOCKET NUMBER: 26192-20011.10
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 887-1500
; TELEFAX: (202) 887-0763
; TELEX: 90-4030 MESNFOERSWSH
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1777 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-626-554-16

```

```
Query Match      82.2%; Score 14.8; DB 1; Length 1777;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TGCATCGACGACGGGGG 18
    |||||
Db 978 TGCATCGACACAGGGAGG 995

RESULT 8
US-08-814-052-7
; Sequence 7, Application US/08814052
; Patent No. 6015783
; GENERAL INFORMATION:
; APPLICANT: von der Osten, Claus
; APPLICANT: Cherry, Joel R.
; APPLICANT: Bjornvad, Mads E.
; APPLICANT: Vind, Jesper
; APPLICANT: Rasmussen, Michael Dolberg
; TITLE OF INVENTION: PROCESS FOR REMOVAL OR BLEACHING OF SOILING
; OR STAINS FROM CELLULOSIC FABRIC
; NUMBER OF SEQUENCES: 55
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6015783 No. 6015783disk of No. 6015783th America, Inc.
; STREET: 405 Lexington Avenue, Suite 6400
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/814,052
; FILING DATE: 06-MAR-1997
; CLASSIFICATION: 510
; ATTORNEY/AGENT INFORMATION:
; NAME: Lambiris, Elias J
; REGISTRATION NUMBER: 33,728
; REFERENCE/DOCKET NUMBER: 4684.204-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; TELEX:
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1893 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-814-052-7

Query Match      82.2%; Score 14.8; DB 3; Length 1893;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TGCATCGACGACGGGGG 18
    |||||
Db 1323 TGCATCGACACAGGGAGG 1340

RESULT 10
US-09-264-097-1
; Sequence 1, Application US/09264097
; Patent No. 6287826
; GENERAL INFORMATION:
; APPLICANT: No. 6287826man, Barrie Edmund
; APPLICANT: Hendriksen, Hanne Vang
; TITLE OF INVENTION: Enzymatic Preparation of Glucose Syrup
; FROM STARCH
; FILE REFERENCE: 5278.200-US
; CURRENT APPLICATION NUMBER: US/09/264,097
; CURRENT FILING DATE: 1999-03-08
; EARLIER APPLICATION NUMBER: PA 0321/98
; EARLIER FILING DATE: 1998-03-09
; EARLIER APPLICATION NUMBER: 60/079,209
; EARLIER FILING DATE: 1998-03-24
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 1912
; TYPE: DNA
; ORGANISM: Bacillus licheniformis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (421)...(1872)
; NAME/KEY: mat peptide
; LOCATION: (421)...(1869)
US-09-264-097-1
```

Query Match 82.2%; Score 14.8; DB 3; Length 1918;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TGCATCGACGACGGGGG 18
|||||
DB 1302 TGCATCGACGACGGGAGG 1319

RESULT 11

US-08-720-899-1
; Sequence 1, Application US/08720899
; Patent No. 5753460
; GENERAL INFORMATION:
; APPLICANT: Bisgaard-Frantzen, Henrik
; APPLICANT: Borchert, Torben Vedel
; APPLICANT: Svendsen, Allan
; APPLICANT: Thellersen, Marianne
; APPLICANT: Van der Zee, Pia
; TITLE OF INVENTION: AMYLASE VARIANTS
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5753460 No. 5753460disk of No. 5753460th America, Inc.
; STREET: 405 Lexington Avenue, 64th Floor
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08720,899
; FILING DATE: 10-OCT-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/343,804
; FILING DATE: 22-NOV-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Lowney Dr., Karen A.
; REGISTRATION NUMBER: 31,274
; REFERENCE/DOCKET NUMBER: 4054.214-US
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1920 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 334..1872
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 334..420
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 421..1869
US-08-720-899-1

Query Match 82.2%; Score 14.8; DB 1; Length 1920;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TGCATCGACGACGGGGG 18
|||||
DB 1302 TGCATCGACGACGGGAGG 1319

RESULT 12

US-08-459-610-1
; Sequence 1, Application US/08459610
; Patent No. 5801043
; GENERAL INFORMATION:
; APPLICANT: Bisgaard-Frantzen, Henrik
; APPLICANT: Borchert, Torben Vedel
; APPLICANT: Svendsen, Allan
; APPLICANT: Thellersen, Marianne
; APPLICANT: Van der Zee, Pia
; TITLE OF INVENTION: AMYLASE VARIANTS
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 5801043 No. 5801043disk of No. 5801043th America, Inc.
; STREET: 405 Lexington Avenue, 64th Floor
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10174-6401
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/459,610
; FILING DATE: 02-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/343,804
; FILING DATE: 22-NOV-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Lowney Dr., Karen A.
; REGISTRATION NUMBER: 31,274
; REFERENCE/DOCKET NUMBER: 4054.214-US
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1920 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 334..1872
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 334..420
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 421..1869
US-08-459-610-1

Query Match 82.2%; Score 14.8; DB 1; Length 1920;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TGCATCGACGACGGGGG 18
|||||
DB 1302 TGCATCGACGACGGGAGG 1319

RESULT 13

US-08-343-804-1
; Sequence 1, Application US/08343804
; Patent No. 5830837
; GENERAL INFORMATION:
; APPLICANT: Bisgaard-Frantzen, Henrik
; APPLICANT: Borchert, Torben Vedel
; APPLICANT: Svendsen, Allan

APPLICANT: Thellersen, Marianne
TITLE OF INVENTION: AMYLASE VARIANTS
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSER: No. 58308370 No. 5830837disk of No. 5830837th America, Inc.
STREET: 405 Lexington Avenue, 64th Floor
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10174-6401
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/343,804
FILING DATE: 22-NOV-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Lowney Dr., Karen A.
REGISTRATION NUMBER: 31,274
REFERENCE/DOCKET NUMBER: 4054.214-US
TELEPHONE: 212-867-0123
TELEFAX: 212-867-9655
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1920 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: CDS
LOCATION: 334..1872
FEATURE:
NAME/KEY: sig_peptide
LOCATION: 334..420
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 421..1869
US-08-343-804-1

Query Match 82.2%; Score 14.8; DB 2; Length 1920;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TGCATCGACGACGAGGGG 18
Db 1302 TGCATCGACGACGAGGG 1319

RESULT 14
US-08-687-399-1
Sequence 1, Application US/08687399
Patent No. 5928381
GENERAL INFORMATION:
APPLICANT: Toft, Annette H.
APPLICANT: Marcher, Dorte
APPLICANT: Pedersen, Ranne H.
APPLICANT: Nilsson, Thomas E.
TITLE OF INVENTION: A Combined Desizing and Bleaching
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSER: No. 59283810 No. 5928381disk of No. 5928381th America, Inc.
STREET: 405 Lexington Avenue, 64th Floor
CITY: New York
STATE: New York
COUNTRY: United States of America
ZIP: 10174-6401
COMPUTER READABLE FORM:

APPLICANT: Thellersen, Marianne
TITLE OF INVENTION: AMYLASE VARIANTS
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSER: No. 58308370 No. 5830837disk of No. 5830837th America, Inc.
STREET: 405 Lexington Avenue, 64th Floor
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10174-6401
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/687,399
FILING DATE:
CLASSIFICATION: 008
ATTORNEY/AGENT INFORMATION:
NAME: Lambiris, Elias J.
REGISTRATION NUMBER: 33,728
REFERENCE/DOCKET NUMBER: 4127.204-US
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1920 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 334..1869
FEATURE:
NAME/KEY: sig_peptide
LOCATION: 334..420
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 421..1869
US-08-687-399-1

Query Match 82.2%; Score 14.8; DB 2; Length 1920;
Best Local Similarity 88.9%; Pred. No. 1.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TGCATCGACGACGAGGGG 18
Db 1302 TGCATCGACGACGAGGG 1319

RESULT 15
US-08-600-908A-1
Sequence 1, Application US/08600908A
Patent No. 5989169
GENERAL INFORMATION:
APPLICANT: Svendsen, Allan
APPLICANT: Bisg rd-Frantzen, Henrik
APPLICANT: Borchert, Torben Vedel
TITLE OF INVENTION: '-Amylase Mutants
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSER: No. 59891690 No. 5989169disk of No. 5989169th America, Inc.
STREET: 405 Lexington Avenue, 64th Floor
CITY: New York
STATE: New York
COUNTRY: United States of America
ZIP: 10174-6401
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/600,908A
FILING DATE: 13-FEB-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Green, Reza
REGISTRATION NUMBER: 38,475
REFERENCE/DOCKET NUMBER: 4394.204-US
TELECOMMUNICATION INFORMATION:

```

;
; TELEPHONE: 212-867-0123
; TELEFAX: 212-878-9655
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1920 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 334..1869
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 334..420
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 421..1869
;
US-08-600-908A-1

Query Match      82.2%; Score 14.8; DB 2; Length 1920;
Best Local Similarity 88.9%; Pred.No. 1.1e+02;
Matches 16; Conservatives 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1 TGCATCGACGACGAGGGGG 18
        |||||
Db      1302 TGCATCGACGACGAGGG 1319

Search completed: July 2, 2004, 13:37:53
Job time : 29.2073 secs
```

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 2, 2004, 06:05:50 ; Search time 134.89 Seconds

(without alignments)
566.887 Million cell updates/sec

Title: US-10-068-160-19

Perfect score: 18
Sequence: 1 tgcacgacgcagggggg 18

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

```
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
```

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_29Jan04:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match	Length	DB	ID	Description
1	18	100.0	20	4	AA09650	Aa09650	Immunorea
2	18	100.0	20	6	ABL35616	Immunorea	Immunorea
3	18	100.0	20	6	ABL35572	Immunosti	Immunosti
4	18	100.0	20	6	ABL35583	Immunosti	Immunosti
5	18	100.0	20	7	ACC48314	Cpg oligo	Cpg oligo
6	18	100.0	20	7	ACC48304	Cpg oligo	Cpg oligo
7	18	100.0	20	8	ACC83119	D class C	D class C
8	18	100.0	20	9	ADD01057	Cpg D oli	Cpg D oli
9	18	100.0	28	6	ABL35605	Immunosti	Immunosti
10	18	100.0	28	6	ABL35593	Immunosti	Immunosti
11	17	94.4	19	4	AA080668	Immunogen	Immunogen
12	17	94.4	19	4	AA09638	Immunorea	Immunorea
13	17	94.4	19	6	ABK46516	Immunosti	Immunosti
14	16.4	91.1	18	6	ABL35587	Immunosti	Immunosti
15	16.4	91.1	18	6	ABL35577	Immunosti	Immunosti
16	16.4	91.1	18	6	ABL35625	Immunosti	Immunosti
17	16.4	91.1	18	9	ADD01052	Cpg D oli	Cpg D oli
18	16.4	91.1	20	4	AA080619	Immunogen	Immunogen
19	16.4	91.1	20	4	AA080621	Immunogen	Immunogen
20	16.4	91.1	20	4	AA080652	Immunogen	Immunogen
21	16.4	91.1	20	4	AA080614	Immunogen	Immunogen
22	16.4	91.1	20	4	AA080612	Immunogen	Immunogen
23	16.4	91.1	20	4	AA080617	Immunogen	Immunogen

ALIGNMENTS

RESULT 1

AAS09650

ID AAS09650 standard; DNA; 20 BP.

XX

AC AAS09650;

XX

DT	26-SEP-2001	(first entry)	Immunoreactive CpG sequence-containing oligonucleotide #100.
XX			
XX			
DE			CpG sequence; immune response; non-B cell activation; interferon gamma;
KW			IFN-gamma; humoral; antibody production; interleukin-6 production;
KW			therapeutic; allergy; asthma; cancer; autoimmune disorder; infection;
KW			bio-warfare; vaccine; antisense therapy; eczema; allergic rhinitis;
KW			coryza; hay fever; urticaria; hives; food allergy; atopic condition;
KW			hepatitis; human immunodeficiency virus; HIV; malaria; Francisella;
KW			lupus erythematosus; rheumatoid arthritis; multiple sclerosis;
KW			schistosomiasis; tuberculosis; acquired immunodeficiency syndrome; AIDS
KW			Leishmania; Ebola; Anthrax; Listeria; ss.

CC ODN are useful for inducing an immune response, preferably a cell-mediated immune response, involving non-B cell activation, interferon gamma (IFN-gamma) production or a humoral immune response involving B cell activation, antibody and interleukin-6 production in a host, for treating, preventing or ameliorating an allergic reaction, e.g. asthma, cancer, e.g. solid tumour cancer, a disease associated with the immune system, e.g. autoimmune disorder or an immune system deficiency, infection or a symptom resulting from exposure to bio-warfare agent in a human. The induction of immune response improves the efficacy of a vaccine and is used in antisense therapy. The ODN are useful for treating, preventing or ameliorating allergic reactions, including eczema, allergic rhinitis or coryza, hay fever, bronchial asthma, urticaria (hives), food allergies and other atopic conditions, for improving the efficacy of vaccines against hepatitis A, B and C, human immunodeficiency virus (HIV) and malaria, for treating immune system deficiencies, e.g. lupus erythematosus and autoimmune diseases such as rheumatoid arthritis and multiple sclerosis, infections including Francisella, schistosomiasis, tuberculosis, acquired immunodeficiency syndrome (AIDS), Leishmania and symptoms resulting from exposure of bio-warfare agent, including Ebola, Anthrax and Listeria

SQ Sequence 20 BP; 3 A; 4 C; 11 G; 2 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGCATCGACGCGGGGG 18
Db 3 TGCATCGACGCGGGGG 20

RESULT 2

ABL35616
ID ABL35616 standard; DNA; 20 BP.

AC ABL35616;

DT 04-APR-2002 (first entry)

DE Immunostimulatory oligonucleotide SEQ ID NO: 542.

KW DNA/RNA hybrid; phosphorothioate backbone; immunostimulatory; vaccine; infection; allergy; cancer; hypersensitivity; bio-warfare;
KW immunostimulant; antiallergic; cytostatic; antimicrobial; anti-HIV;
KW immunosuppressive; protozoacide; virucide; hepatotropic; gene therapy; antiinflammatory; antibacterial; ss.

OS Synthetic.

FT Key Location/Qualifiers
FT misc_RNA 1..20

FT /tag= a
FT /note= "optionally thymidine is replaced by uracil to form RNA or DNA/RNA hybrids. Thymidine is linked to at least one other base through a ribose sugar"

PN WO200193902-A2.

PD 13-DEC-2001.

PF 07-JUN-2001; 2001WO-US018276.

PR 07-JUN-2000; 2000US-0209797P.

PA (BIOS-) BIOSYNEXUS INC.

PI Mond JJ, Flora M, Klinman DM;

DR WPI; 2002-130570/17.

PT New immunostimulatory compositions comprising RNA/DNA hybrid oligonucleotides, useful for enhancing an immune response or inducing

PT cytokines, particularly for treating diseases, e.g. cancer, allergy or HIV infection.
PT Example 11; Page 62; 68pp; English.
PS The present invention relates to an immunostimulatory composition, which comprises at least one oligonucleotide comprising both an RNA region and a DNA region. The composition is useful for enhancing an immune response or inducing cytokines. It can be used as a vaccine adjuvant and in treating diseases, including pathogenic infection, (non-)malignant tumours (e.g. cancers of the brain, lung, ovary, breast, prostate or colon or carcinomas and sarcomas), autoimmune diseases or allergies (e.g. allergic rhinitis, hay fever or food allergies), Lyme disease, hepatitis, HIV or malaria. The composition is also useful for treating, preventing or ameliorating the symptoms resulting from exposure to a bio-warfare agent, e.g. Ebola, Anthrax or Listeria. The present sequence is an immunostimulatory oligonucleotide described in the exemplification of the invention

SQ Sequence 20 BP; 3 A; 4 C; 11 G; 2 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGCATCGACGCGGGGG 18
Db 3 TGCATCGACGCGGGGG 20

RESULT 3

ABL35572
ID ABL35572 standard; DNA; 20 BP.

AC ABL35572;

DT 04-APR-2002 (first entry)

DE Immunostimulatory oligonucleotide SEQ ID NO: 498.

KW DNA/RNA hybrid; phosphorothioate backbone; immunostimulatory; vaccine; infection; allergy; cancer; hypersensitivity; bio-warfare;
KW immunostimulant; antiallergic; cytostatic; antimicrobial; anti-HIV;
KW immunosuppressive; protozoacide; virucide; hepatotropic; gene therapy; antiinflammatory; antibacterial; ss.

OS Synthetic.

FT Key Location/Qualifiers
FT misc_RNA 1..20

FT /tag= a
FT /note= "optionally thymidine is replaced by uracil to form RNA or DNA/RNA hybrids. Thymidine is linked to at least one other base through a ribose sugar"

PN WO200193902-A2.

PD 13-DEC-2001.

PF 07-JUN-2001; 2001WO-US018276.

PR 07-JUN-2000; 2000US-0209797P.

PA (BIOS-) BIOSYNEXUS INC.

PI Mond JJ, Flora M, Klinman DM;

DR WPI; 2002-130570/17.

PT New immunostimulatory compositions comprising RNA/DNA hybrid oligonucleotides, useful for enhancing an immune response or inducing cytokines, particularly for treating diseases, e.g. cancer, allergy or HIV infection.

XX PS Example 11; Page 61; 69pp; English.

XX CC The present invention relates to an immunostimulatory composition, which

CC comprises at least one oligonucleotide comprising both an RNA region and

CC a DNA region. The composition is useful for enhancing an immune response

CC or inducing cytokines. It can be used as a vaccine adjuvant and in

CC treating diseases, including pathogenic infection, (non-)malignant

CC tumours (e.g. cancers of the brain, lung, ovary, breast, prostate or

CC colon, or carcinomas and sarcomas), autoimmune diseases or allergies

CC (e.g. allergic rhinitis, hay fever or food allergies), Lyme disease,

CC hepatitis, HIV or malaria. The composition is also useful for treating,

CC preventing or ameliorating the symptoms resulting from exposure to a bio-

CC warfare agent, e.g. Ebola, Anthrax or listeria. The present sequence is

CC an immunostimulatory oligonucleotide described in the exemplification of

CC the invention

XX SQ Sequence 20 BP; 3 A; 4 C; 11 G; 2 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 6; Length 20;

Best Local Similarity 100.0%; Pred. No. 11;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGCATCGACGCGAGGGGG 18

Db 3 TGCATCGACGCGAGGGGG 20

RESULT 4

ABL35583

ID ABL35583 standard; DNA; 20 BP.

XX AC ABL35583;

XX DT 04-APR-2002 (first entry)

XX DE Immunostimulatory oligonucleotide SEQ ID NO: 509.

XX KW DNA/RNA hybrid; phosphorothioate backbone; immunostimulatory; vaccine;

XX KW infection; allergy; cancer; hypersensitivity; bio-warfare;

XX KW immunostimulant; antiallergic; cytostatic; antimicrobial; anti-HIV;

XX KW immunosuppressive; protooncogene; virucide; hepatotropic; gene therapy;

XX KW antiinflammatory; antibacterial; ss.

XX OS Synthetic.

XX EH Key

XX FT Location/Qualifiers

XX FT misc_RNA

XX FT 1..20

XX FT /tag= a

XX FT /note= "optionally thymidine is replaced by uracil to

XX FT form RNA or DNA/RNA hybrids. Thymidine is linked to at

XX FT least one other base through a ribose sugar"

XX PN WO200193902-A2.

XX PD 13-DEC-2001.

XX PF 07-JUN-2001; 2001WO-US018276.

XX PR 07-JUN-2000; 2000US-0209797P.

XX PA (BIOS-) BIOSYNEXUS INC.

XX PI Mond JJ, Flora M, Klinman DM;

XX DR WPI; 2002-130570/17.

XX PT New immunostimulatory compositions comprising RNA/DNA hybrid

PT oligonucleotides, useful for enhancing an immune response or inducing

PT cytokines, particularly for treating diseases, e.g. cancer, allergy or

PT HIV infection.

XX PS Example 11; Page 61; 68pp; English.

XX CC The present invention relates to an immunostimulatory composition, which

CC comprises at least one oligonucleotide comprising both an RNA region and

CC a DNA region. The composition is useful for enhancing an immune response

CC or inducing cytokines. It can be used as a vaccine adjuvant and in

CC treating diseases, including pathogenic infection, (non-)malignant

CC tumours (e.g. cancers of the brain, lung, ovary, breast, prostate or

CC colon, or carcinomas and sarcomas), autoimmune diseases or allergies

CC (e.g. allergic rhinitis, hay fever or food allergies), Lyme disease,

CC hepatitis, HIV or malaria. The composition is also useful for treating,

CC preventing or ameliorating the symptoms resulting from exposure to a bio-

CC warfare agent, e.g. Ebola, Anthrax or listeria. The present sequence is

CC an immunostimulatory oligonucleotide described in the exemplification of

CC the invention

XX SQ Sequence 20 BP; 3 A; 4 C; 11 G; 2 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 6; Length 20;

Best Local Similarity 100.0%; Pred. No. 11;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGCATCGACGCGAGGGGG 18

Db 3 TGCATCGACGCGAGGGGG 20

RESULT 5

ACC48314

ID ACC48314 standard; DNA; 20 BP.

XX AC ACC48314;

XX DT 11-AUG-2003 (first entry)

XX DE CpG oligodeoxynucleotide DV30.

XX KW CpG oligodeoxynucleotide; dendritic cell; tumour; immunotherapy; vaccine;

XX KW cytostatic; immunostimulant; gene therapy; ss.

XX OS Synthetic.

XX PN WO2003020894-A2.

XX PD 13-MAR-2003.

XX PF 13-AUG-2002; 2002WO-US025732.

XX PR 14-AUG-2001; 2001US-0312190P.

XX PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX PI Klinman DM, Gursel M, Verthelyi D;

XX DR WPI; 2003-300874/29.

XX PT Generating mature dendritic cells for tumor immunotherapy or as vaccines

PT for activating the immune system to treat diseases such as cancer,

PT comprises contacting a dendritic cell precursor with a D type

PT oligodeoxynucleotide.

XX PS Disclosure; Fig 8; 69pp; English.

XX CC The present sequence is that of CpG oligodeoxynucleotide DV30 of the

CC invention. A claimed method for generating dendritic cells involves

CC contacting a dendritic cell precursor, especially a monocyte, with a D

CC type oligodeoxynucleotide (see ACC48294) containing a central

CC unmethylated CpG motif. The method is useful for generating mature

CC dendritic cells and enhancing T cell responses, thus enhancing antigen

CC presentation. Mature dendritic cells are useful for tumour immunotherapy,

CC for augmenting an immune response to an infectious agent or to a vaccine,

CC and as vaccines to prevent future infection or to activate the immune

CC system to treat diseases such as cancer. Mature dendritic cells may also

CC be used to produce activated T lymphocytes

XX SQ Sequence 20 BP; 3 A; 4 C; 11 G; 2 T; 0 U; 0 Other;
 Query Match 100.0%; Score 18; DB 7; Length 20;
 Best Local Similarity 100.0%; Pred. No. 11;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGCATCGACGAGGGGG 18
 |||||
 Db 3 TGCATCGACGAGGGGG 20
 |||||

RESULT 7
 ACC83119
 ID ACC83119 standard; DNA; 20 BP.
 XX AC ACC83119;
 XX DT 27-AUG-2003 (first entry)
 XX DE D class CpG ODN sequence useful for encapsulating in SSCL, DV30.
 XX KW Sterically stabilised cationic liposome; SSCL; ODN; oligodeoxynucleotide;
 KW tuberculosis; cytokine; leishmaniasis; AIDS-associated Kaposi's tumour;
 KW thymoid; cancer; allergy; eczema; allergic rhinitis; coryza; hay fever;
 KW schistosomiasis; interferon gamma; lupus erythematosus; antimicrobial;
 KW asthma; urticaria; autoimmune disease; diabetes; rheumatoid arthritis;
 KW CpG motif; interleukin-13; cytostatic; tularemia; malaria; psoriasis;
 KW multiple sclerosis; infection; tumour; ss.
 XX CS Unidentified.
 XX WO2003040308-A2.
 XX PN 15-MAY-2003.
 XX PD 29-JUL-2002; 2002WO-US024235.
 XX PF 27-JUL-2001; 2001US-0308283P.
 XX PR 25-JUL-2002; 2002US-00206407.
 XX PA {USSH } US DEPT HEALTH & HUMAN SERVICES.
 XX PI Klinman DM, Gursel I, Ishii KJ, Kawakami K, Joshi BH, Puri RK;
 XX WPI; 2003-482260/45.
 XX CC Cationic liposome composition for delivering oligodeoxynucleotides
 CC including a CpG motif in clinical applications, comprises a cationic
 CC lipid, a co-lipid, stabilizing agent and an encapsulated oligonucleotide.
 XX PS Disclosure; Fig 10C; 110pp; English.
 XX CC The invention relates to sterically stabilised cationic liposomes (SSCL)
 CC which comprises a cationic lipid, a co-lipid, stabilising agent and
 CC encapsulating a K type oligodeoxynucleotide (ODN) including a CpG motif.
 CC The invention is useful in pharmaceutical composition for impairing
 CC growth of a solid tumour cell (e.g. human tumour cell) bearing an
 CC interleukin-13 receptor in a subject; for stimulating an immune response,
 CC which is expression of a cytokine (e.g. interferon gamma), particularly
 CC immunotherapeutic response against tumours or stimulating an in vivo or
 CC an in vitro immune cell, and for inducing an immune response against an
 CC infectious agent e.g. virus, bacteria and fungus. It is also useful for
 CC delivering oligodeoxynucleotides including a CpG motif in clinical
 CC applications; for treating infectious diseases (e.g. tularemia, malaria,
 CC francisella, schistosomiasis, tuberculosis and leishmaniasis), cancer
 CC (e.g. solid tumours, AIDS-associated Kaposi's tumour, thymoid, cancer
 CC etc), allergy (e.g. eczema, allergic rhinitis or coryza, hay fever,
 CC bronchial or allergic asthma, urticaria, food allergies), autoimmune
 CC diseases (e.g. diabetes, rheumatoid arthritis, lupus erythematosus and
 CC multiple sclerosis) and psoriasis. The present sequence is a D class CpG
 CC ODN potentially useful for encapsulating in SSCL
 XX SQ Sequence 20 BP; 3 A; 4 C; 11 G; 2 T; 0 U; 0 Other;
 Query Match 100.0%; Score 18; DB 8; Length 20;
 Best Local Similarity 100.0%; Pred. No. 11;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX SQ Sequence 20 BP; 3 A; 4 C; 11 G; 2 T; 0 U; 0 Other;
 Query Match 100.0%; Score 18; DB 7; Length 20;
 Best Local Similarity 100.0%; Pred. No. 11;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGCATCGACGAGGGGG 18
 |||||
 Db 3 TGCATCGACGAGGGGG 20
 |||||

RESULT 6
 ACC48304
 ID ACC48304 standard; DNA; 20 BP.
 XX AC ACC48304;
 XX DT 11-AUG-2003 (first entry)
 XX DE CpG oligodeoxynucleotide used for dendritic cell maturation.
 XX KW CpG oligodeoxynucleotide; dendritic cell; tumour; immunotherapy; vaccine;
 KW cytostatic; immunostimulant; gene therapy; ss.
 XX CS Synthetic.
 XX FH Key Location/Qualifiers
 FT misc_difference 1 /*tag= a
 FT /note= "N is any base (especially G) or no base"
 FT misc_difference 2 /*tag= b
 FT /note= "N is any base (especially G) or no base"
 XX PN WO2003020884-A2.
 XX PD 13-MAR-2003.
 XX PF 13-AUG-2002; 2002WO-US025732.
 XX PR 14-AUG-2001; 2001US-0312190P.
 XX PA {USSH } US DEPT HEALTH & HUMAN SERVICES.
 XX PI Klinman DM, Gursel M, Verthelyi D;
 XX WPI; 2003-300874/29.
 XX CC Generating mature dendritic cells for tumor immunotherapy or as vaccines
 CC for activating the immune system to treat diseases such as cancer,
 CC comprises contacting a dendritic cell precursor with a D type
 CC oligodeoxynucleotide.
 XX PS Disclosure; Page 26; 69pp; English.
 XX CC The present sequence is that of a D type CpG oligodeoxynucleotide that is
 CC an example of claimed D type oligodeoxynucleotides (see ACC48294) of the
 CC invention. Mature dendritic cells are obtained by contacting a dendritic
 CC cell precursor, such as a monocyte, with such an oligodeoxynucleotide.
 CC The method is useful for generating mature dendritic cells and enhancing
 CC T cell responses, thus enhancing antigen presentation. Mature dendritic
 CC cells are useful for tumour immunotherapy, for augmenting an immune
 CC response to an infectious agent or to a vaccine, and as vaccines to
 CC prevent future infection or to activate the immune system to treat
 CC diseases such as cancer. Mature dendritic cells may also be used to
 CC produce activated T lymphocytes
 XX SQ Sequence 20 BP; 3 A; 4 C; 9 G; 2 T; 0 U; 2 Other;
 Query Match 100.0%; Score 18; DB 7; Length 20;
 Best Local Similarity 100.0%; Pred. No. 11;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGCATCGACGCGGGGG 18
 |||||
 Db 3 TGCATCGACGCGGGGG 20

RESULT 8

ADD01057
 ID ADD01057 standard; DNA; 20 BP.
 XX
 AC ADD01057;
 XX
 DT 01-JAN-2004 (first entry)
 XX
 DE Cpg D oligonucleotide SEQ ID NO:21.

XX vascular endothelial growth factor; VEGF; Cpg oligonucleotide;
 KW neovascularisation; angiogenesis; vulnerary; vasotropic;
 KW antiarteriosclerotic; gene therapy; skin graft; male pattern baldness;
 XX atherosclerosis; ischaemia; ss.
 XX
 OS Synthetic.

XX WO2003054161-A2.

XX 03-JUL-2003.

XX 19-DEC-2002; 2002WO-US040955.

XX 20-DEC-2001; 2001US-0343457P.

XX (UYTE-) UNIV TENNESSEE RES CORP.
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX Klinman DM, Zheng M, Rouse BT;
 PI
 XX WPI; 2003-559138/52.

XX Inducing the production of vascular endothelial growth factor by a cell,
 PT useful for inducing angiogenesis, comprises contacting the cell with a
 PT Cpg oligodeoxynucleotide.

XX Example 7; SEQ ID NO 21; 37pp; English.

XX The present invention describes a method for inducing the production of
 CC vascular endothelial growth factor (VEGF) by a cell comprising contacting
 CC the cell with a Cpg oligonucleotide and therefore inducing the production
 CC of VEGF by the cell. Also described: (1) inducing neovascularisation in a
 CC tissue, comprising introducing a Cpg oligonucleotide into an area of the
 CC tissue where the formation of new blood vessels is desired, and so
 CC inducing neovascularisation in the area of the tissue; (2) promoting
 CC angiogenesis in an area of the subject where angiogenesis is desired,
 CC comprising introducing a Cpg oligonucleotide to the area, and so
 CC promoting angiogenesis in the subject; and (3) screening for an agent
 CC that inhibits neovascularisation, comprising administering a Cpg
 CC oligonucleotide to a non-human mammal and administering the agent to the
 CC mammal, where inhibition of angiogenesis in the animal indicates that the
 CC agent is effective in inhibiting neovascularisation. The Cpg
 CC oligonucleotides have vulnerary, vasotropic and antiarteriosclerotic
 CC activities, and can be used in gene therapy. The method and the Cpg
 CC oligonucleotides can be used in inducing angiogenesis or
 CC neovascularisation, such as in subjects with a skin graft, subjects who
 CC exhibit male pattern baldness, or subjects who have a wound or who have
 CC atherosclerosis or ischaemia. The method may also be used in screening
 CC for agents that inhibit neovascularisation. The present sequence
 CC represents a Cpg oligonucleotide which is used in the exemplification of
 CC the present invention.

XX SQ Sequence 20 BP; 3 A; 4 C; 11 G; 2 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 9; Length 20;
 Best Local Similarity 100.0%; Pred. No. 11;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGCATCGACGCGGGGG 18
 |||||
 Db 3 TGCATCGACGCGGGGG 20

RESULT 9

ABL35605
 ID ABL35605 standard; DNA; 28 BP.
 XX
 AC ABL35605;
 XX
 DT 04-APR-2002 (first entry)
 XX
 DE Immunostimulatory oligonucleotide SEQ ID NO: 531.

XX DNA/RNA hybrid; phosphorothioate backbone; immunostimulatory; vaccine;
 KW infection; allergy; cancer; hypersensitivity; bio-warfare;
 KW immunostimulant; antiallergic; cytostatic; antimicrobial; anti-HIV;
 KW immunosuppressive; protozoicide; virucide; hepatotropic; gene therapy;
 KW antiinflammatory; antibacterial; ss.

XX Synthetic.

XX Key Location/Qualifiers
 FH misc_RNA 1..28

FT /*tag= a
 FT /note= "optionally thymidine is replaced by uracil to
 FT form RNA or DNA/RNA hybrids. Thymidine is linked to at
 FT least one other base through a ribose sugar"

XX WO200193902-A2.

XX 13-DEC-2001.

XX 07-JUN-2001; 2001WO-US018276.

XX 07-JUN-2000; 2000US-0209797P.

XX (BIOS-) BIOSYNEXUS INC.

XX Mond JJ, Flora M, Klinman DM;

XX WPI; 2002-130570/17.

XX New immunostimulatory compositions comprising RNA/DNA hybrid
 PT oligonucleotides, useful for enhancing an immune response or inducing
 PT cytokines, particularly for treating diseases, e.g. cancer, allergy or
 PT HIV infection.

XX Example 11; Page 61; 68pp; English.

XX The present invention relates to an immunostimulatory composition, which
 CC comprises at least one oligonucleotide comprising both an RNA region and
 CC a DNA region. The composition is useful for enhancing an immune response
 CC or inducing cytokines. It can be used as a vaccine adjuvant and in
 CC treating diseases, including pathogenic infection, (non-)malignant
 CC tumours (e.g. cancers of the brain, lung, ovary, breast, prostate or
 CC colon, or carcinomas and sarcomas), autoimmune diseases or allergies
 CC (e.g. allergic rhinitis, hay fever or food allergies), Lyme disease,
 CC hepatitis, HIV or malaria. The composition is also useful for treating,
 CC preventing or ameliorating the symptoms resulting from exposure to a bio-
 CC warfare agent, e.g. Ebola, Anthrax or Listeria. The present sequence is
 CC an immunostimulatory oligonucleotide described in the exemplification of
 CC the invention

XX SQ Sequence 28 BP; 5 A; 6 C; 12 G; 5 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 6; Length 28;
 Best Local Similarity 100.0%; Pred. No. 11;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGCATCGACGCGGGGG 18
 |||||

Db 11 TGCATCGACGAGGGGG 28

RESULT 10

ABL35593

ID ABL35593 standard; DNA; 28 BP.

XX

XX

AC ABL35593;

DT 04-APR-2002 (first entry)

XX

DE Immunostimulatory oligonucleotide SEQ ID NO: 519.

XX

KW DNA/RNA hybrid; phosphorothioate backbone; immunostimulatory; vaccine;

KW infection; allergy; cancer; hypersensitivity; bio-warfare;

KW immunostimulant; antiallergic; cytostatic; antimicrobial; anti-HIV;

KW immunosuppressive; protozoacide; virucide; hepatotropic; gene therapy;

KW antiinflammatory; antibacterial; ss.

XX

OS Synthetic.

XX

Key Location/Qualifiers

FT misc_RNA 1..28

FT /tag= a

FT /note= "optionally thymidine is replaced by uracil to

FT form RNA or DNA/RNA hybrids. Thymidine is linked to at

FT least one other base through a ribose sugar"

XX

XX WO200193902-A2.

XX

XX 13-DEC-2001.

XX

XX 07-JUN-2001; 2001WO-US018276.

XX

XX 07-JUN-2000; 2000US-0209797P.

XX

XX (BIOS-) BIOSYNEXUS INC.

XX

XX Mond JJ, Flora M, Klinman DM;

XX

XX WPI; 2002-130570/17.

XX

XX New immunostimulatory compositions comprising RNA/DNA hybrid

PT oligonucleotides, useful for enhancing an immune response or inducing

PT cytokines, particularly for treating diseases, e.g. cancer, allergy or

PT HIV infection.

XX

PS Example 11; Page 61; 68pp; English.

XX

CC The present invention relates to an immunostimulatory composition, which

CC comprises at least one oligonucleotide comprising both an RNA region and

CC a DNA region. The composition is useful for enhancing an immune response

CC or inducing cytokines. It can be used as a vaccine adjuvant and in

CC treating diseases, including pathogenic infection, (non-)malignant

CC tumours (e.g. cancers of the brain, lung, ovary, breast, prostate or

CC colon, or carcinomas and sarcomas), autoimmune diseases or allergies

CC (e.g. allergic rhinitis, hay fever or food allergies), Lyme disease,

CC hepatitis, HIV or malaria. The composition is also useful for treating,

CC preventing or ameliorating the symptoms resulting from exposure to a bio-

CC warfare agent, e.g. Ebola, anthrax or Listeria. The present sequence is

CC an immunostimulatory oligonucleotide described in the exemplification of

CC the invention

XX

XX Sequence 28 BP; 11 A; 4 C; 11 G; 2 T; 0 U; 0 Other;

XX

Query Match 100.0%; Score 18; DB 6; Length 28;

Best Local Similarity 100.0%; Pred. No. 11;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGCATCGACGAGGGGG 18

|||||

Db 3 TGCATCGACGAGGGGG 20

RESULT 11

AAC80668

ID AAC80668 standard; DNA; 19 BP.

XX

AC AAC80668;

XX

DT 14-FEB-2001 (first entry)

XX

DE Immunogenic CpG oligodeoxynucleotide, SEQ ID NO:88.

XX

KW CpG oligodeoxynucleotide; unmethylated; antigen-presenting cell;

KW immunogenic; cytokine release; natural killer cell; NK cell activation;

KW cell-mediated immune response; T-cell response; humoral response;

KW B-cell response; antibody production; immune response induction; vaccine;

KW allergy; asthma; infection; bacterial; viral; fungal; protozoal;

KW parasitic; tuberculosis; AIDS; autoimmune disease; lupus erythematosus;

KW rheumatoid arthritis; multiple sclerosis; solid tumour; cancer;

KW immune deficiency; biological warfare agent; cytostatic; antiarthritic;

KW antimicrobial; antiallergic; protozoacide; tuberculostatic;

KW antiasthmatic; dermatological; phosphorothioate; ss.

XX

OS Synthetic.

XX

PN WO2000061151-A2.

XX

PD 19-OCT-2000.

XX

XX 12-APR-2000; 2000WO-US009839.

XX

XX 12-APR-1999; 99US-0128898P.

XX

XX (KLIN/) KLINMAN D.

PA (ISHI/) ISHII K.

PA (VERT/) VERTHELYI D.

XX

PI Klinman D, Ishii K, Verthelyi D;

XX

XX WPI; 2001-006880/01.

XX

XX Novel oligonucleotides useful for the prevention and treatment of

PT allergies, cancer, and autoimmune disorders and for ameliorating symptoms

PT resulting from exposure to a bio-warfare agent.

XX

PS Claim 4; Page 37; 46pp; English.

XX

CC The invention relates to novel immunogenic CpG oligodeoxynucleotides

CC (AAC80681-C80723). The oligonucleotides are at least 10 bases long and

CC comprise one of the generic sequences 5'-NNNT-CpG-WNNN-3' or 5'-RY-CpG-RY

CC -3'. The central CpG motif is unmethylated, and the oligonucleotides

CC optionally have phosphorothioate linkages which make them more resistant

CC to degradation. The invention also relates to an oligonucleotide delivery

CC complex comprising an oligonucleotide of the invention and a targeting

CC agent, and a pharmaceutical composition comprising the oligonucleotide

CC delivery complex. The oligonucleotides are able to induce either a cell-

CC mediated (T-cell) response or a humoral (B-cell, antibody) response, with

CC oligonucleotides of the sequence 5'-RY-CpG-RY-3' being able to induce a

CC cell-mediated response, and those of the sequence 5'-NNNT-CpG-WNNN-3'

CC being able to induce a humoral response. It is thought that after

CC administration, the oligonucleotide acts on antigen-presenting cells

CC (e.g., macrophages and dendritic cells), which then release cytokines,

CC leading to activation of natural killer (NK) cells. A cell-mediated or

CC humoral response can then occur by activation of T- or B-cells. The

CC induction of an immune response is useful for treating, preventing or

CC ameliorating an allergic reaction (preferably asthma), or an infection,

CC where an immunogenic CpG oligonucleotide is administered either alone or

CC in combination with an anti-allergenic agent or anti-infectious agent.

CC The allergic conditions which may be treated include eczema, allergic

CC rhinitis, hayfever, urticaria, food allergies and other atopic

CC conditions, and the infections which may be treated include viral,

CC bacterial, fungal and protozoal infections such as tuberculosis, AIDS,

CC leishmania and schistosomiasis. Immune response induction may also be

CC used in the treatment of an autoimmune disorder (e.g., lupus

erythematous, rheumatoid arthritis and multiple sclerosis), a disease associated with immune system deficiency, and symptoms resulting from exposure to an agent of biological warfare. An immunogenic CpG oligonucleotide, either alone or in combination with an anti-cancer agent, is useful for treating solid tumour cancer. The induction of an immune response is used in antisense therapy and to improve the efficacy of a vaccine. The oligonucleotide is preferably administered to lymphocytes ex vivo, producing activated lymphocytes which are then administered to the host. The present sequence represents an immunogenic CpG oligodeoxynucleotide of the invention

Sequence 19 BP; 3 A; 4 C; 10 G; 2 T; 0 U; 0 Other;

Query Match 94.4%; Score 17; DB 4; Length 19;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGCATCGACGCGGGG 17
Db 3 TGCATCGACGCGGGG 19

RESULT 12

AAS09638

ID AAS09638 standard; DNA; 19 BP.

AC AAS09638;

26-SEP-2001 (first entry)

Immunoreactive CpG sequence-containing oligonucleotide #88.

CpG sequence; immune response; non-B cell activation; interferon gamma; IFN-gamma; humoral; antibody production; interleukin-6 production; therapeutic; allergy; asthma; cancer; autoimmune disorder; infection; bio-warfare; vaccine; antisense therapy; eczema; allergic rhinitis; coryza; hay fever; urticaria; hives; food allergy; atopic condition; hepatitis; human immunodeficiency virus; HIV; malaria; Francisella; lupus erythematosus; rheumatoid arthritis; multiple sclerosis; schistosomiasis; tuberculosis; acquired immunodeficiency syndrome; AIDS; Leishmania; Ebola; Anthrax; Listeria; ss.

Synthetic.

WO200151500-A1.

19-JUL-2001.

12-JAN-2001; 2001WO-US001122.

14-JAN-2000; 2000US-0176115P.

(USSH) US DEPT HEALTH & HUMAN SERVICES.

Klinman D, Ishii K, Verthelyi D;

WPI; 2001-442129/47.

Oligodeoxynucleotides for inducing an immune response to treat and prevent an allergic reaction, cancer, an autoimmune disorder and symptoms resulting from exposure to bio-warfare agents, comprise multiple CpG sequences.

Claim 5; Page 41; 48pp; English.

AAS09551-AAS09662 represent oligodeoxynucleotides (ODN) of at least 10 nucleotides comprising multiple CpG sequences, where one of the CpG sequences is different from another of the multiple CpG sequences. The ODN are useful for inducing an immune response, preferably a cell-mediated immune response, involving non-B cell activation, interferon gamma (IFN-gamma) production or a humoral immune response involving B cell activation, antibody and interleukin-6 production in a host, for treating, preventing or ameliorating an allergic reaction, e.g. asthma,

cancer, e.g. solid tumour cancer, a disease associated with the immune system e.g. autoimmune disorder or an immune system deficiency, infection or a symptom resulting from exposure to bio-warfare agent in a human. The induction of immune response improves the efficacy of a vaccine and is used in antisense therapy. The ODN are useful for treating, preventing or ameliorating allergic reactions, including eczema, allergic rhinitis or coryza, hay fever, bronchial asthma, urticaria (hives), food allergies and other atopic conditions for improving the efficacy of vaccines against hepatitis A, B and C, human immunodeficiency virus (HIV) and malaria, for treating immune system deficiencies, e.g. lupus erythematosus and autoimmune diseases such as rheumatoid arthritis and multiple sclerosis, infections including Francisella, schistosomiasis, tuberculosis, acquired immunodeficiency syndrome (AIDS), Leishmania and symptoms resulting from exposure of bio-warfare agent, including Ebola, Anthrax and Listeria

Sequence 19 BP; 3 A; 4 C; 10 G; 2 T; 0 U; 0 Other;

Query Match 94.4%; Score 17; DB 4; Length 19;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGCATCGACGCGGGG 17
Db 3 TGCATCGACGCGGGG 19

RESULT 13

ABK46516

ID ABK46516 standard; DNA; 19 BP.

AC ABK46516;

05-JUN-2002 (first entry)

Immunostimulatory unmethylated CpG oligodeoxynucleotide #106.

unmethylated CpG; oligodeoxynucleotide; ODN; virucide; vaccine; Paramyxoviridae; F protein; respiratory syncytial virus; RSV; viral bronchiolitis; pneumonia; infectious pulmonary disease; bronchopulmonary dysplasia; congenital heart condition; ss.

Synthetic.

WO200211761-A2.

14-FEB-2002.

09-AUG-2001; 2001WO-US041633.

10-AUG-2000; 2000US-0224011P.

01-SEP-2000; 2000US-0229307P.

(JACK-) JACKSON FOUND ADVANCEMENT MILITARY MED.

Mond JJ, Prince G, Klinman DM;

WPI; 2002-227118/28.

Vaccine for immunizing patient against respiratory syncytial virus, has epitopes of Paramyxoviridae F protein, and cytosine followed by guanine linked by phosphate bond-oligodeoxynucleotides.

Claim 4; Page 9; 30pp; English.

The invention describes a vaccine comprising one or more epitopes of a Paramyxoviridae F protein, and one or more CpG (cytosine followed by guanine linked by phosphate bond)-oligodeoxynucleotides (ODNs). The vaccine is useful for vaccinating a patient especially against viruses of the Paramyxoviridae family e.g. respiratory syncytial virus (RSV), the primary cause of viral bronchiolitis and pneumonia in infants and children, and infectious pulmonary disease in infants. RSV has been particularly implicated in death of infants that are premature, have

CC bronchopulmonary dysplasia, or congenital heart conditions. This sequence
CC represents an oligonucleotide that can be used in the creation of
CC the vaccine

XX
SQ Sequence 19 BP; 3 A; 4 C; 10 G; 2 T; 0 U; 0 Other;
Query Match 94.4%; Score 17; DB 6; Length 19;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGCATCGACGAGGGGG 17
|||||
Db 3 TGCATCGACGAGGGGG 19

RESULT 14

ABL35587
ID ABL35587 standard; DNA; 18 BP.

XX
AC ABL35587;

XX
DT 04-APR-2002 (first entry)

XX
DE Immunostimulatory oligonucleotide SEQ ID NO: 513.

XX
KW DNA/RNA hybrid; phosphorothioate backbone; immunostimulatory; vaccine;
KW infection; allergy; cancer; hypersensitivity; bio-warfare;
KW immunostimulant; antiallergic; cytostatic; antimicrobial; anti-HIV;
KW immunosuppressive; protozoacide; virucide; hepatotropic; gene therapy;
KW antiinflammatory; antibacterial; ss.

XX
OS Synthetic.

XX
FH Key Location/Qualifiers

FT misc_RNA

FT 1..18

FT /*tag= a

FT /note= "optionally thymidine is replaced by uracil to

FT form RNA or DNA/RNA hybrids. Thymidine is linked to at

FT least one other base through a ribose sugar"

XX
PN WO200193902-A2.

XX
PD 13-DEC-2001.

XX
PF 07-JUN-2001; 2001WO-US018276.

XX
PR 07-JUN-2000; 2000US-0209797P.

XX
PA (BIOS-) BIOSYNEXUS INC.

XX
PI Mond JJ, Flora M, Kliman DM;

XX
PS WPI; 2002-130570/17.

XX
DR New immunostimulatory compositions comprising RNA/DNA hybrid

XX
PT oligonucleotides, useful for enhancing an immune response or inducing

XX
PT cytokines, particularly for treating diseases, e.g. cancer, allergy or

XX
PT HIV infection.

XX
PS Example 11; Page 61; 68pp; English.

XX
CC The present invention relates to an immunostimulatory composition, which

XX
CC comprises at least one oligonucleotide comprising both an RNA region and

XX
CC a DNA region. The composition is useful for enhancing an immune response

XX
CC or inducing cytokines. It can be used as a vaccine adjuvant and in

XX
CC treating diseases, including pathogenic infection, (non-)malignant

XX
CC tumours (e.g. cancers of the brain, lung, ovary, breast, prostate or

XX
CC colon, or carcinomas and sarcomas), autoimmune diseases or allergies

XX
CC (e.g. allergic rhinitis, hay fever or food allergies), Lyme disease,

XX
CC hepatitis, HIV or malaria. The composition is also useful for treating,

XX
CC preventing or ameliorating the symptoms resulting from exposure to a bio-

XX
CC warfare agent, e.g. Ebola, Anthrax or Listeria. The present sequence is

XX
CC an immunostimulatory oligonucleotide described in the exemplification of

CC the invention

XX
SQ Sequence 18 BP; 3 A; 3 C; 9 G; 3 T; 0 U; 0 Other;

Query Match 91.1%; Score 16.4; DB 6; Length 18;
Best Local Similarity 94.4%; Pred. No. 76;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TGCATCGACGAGGGGG 18

|||||
Db 1 TGCATCGACGAGGGGG 18

RESULT 15

ABL35577

ID ABL35577 standard; DNA; 18 BP.

XX
AC ABL35577;

XX
DT 04-APR-2002 (first entry)

XX
DE Immunostimulatory oligonucleotide SEQ ID NO: 503.

XX
KW DNA/RNA hybrid; phosphorothioate backbone; immunostimulatory; vaccine;
KW infection; allergy; cancer; hypersensitivity; bio-warfare;
KW immunostimulant; antiallergic; cytostatic; antimicrobial; anti-HIV;
KW immunosuppressive; protozoacide; virucide; hepatotropic; gene therapy;
KW antiinflammatory; antibacterial; ss.

XX
OS Synthetic.

XX
FH Key Location/Qualifiers

FT misc_RNA

FT 1..18

FT /*tag= a

FT /note= "optionally thymidine is replaced by uracil to

FT form RNA or DNA/RNA hybrids. Thymidine is linked to at

FT least one other base through a ribose sugar"

XX
PN WO200193902-A2.

XX
PD 13-DEC-2001.

XX
PF 07-JUN-2001; 2001WO-US018276.

XX
PR 07-JUN-2000; 2000US-0209797P.

XX
PA (BIOS-) BIOSYNEXUS INC.

XX
PI Mond JJ, Flora M, Kliman DM;

XX
PS WPI; 2002-130570/17.

XX
DR New immunostimulatory compositions comprising RNA/DNA hybrid

XX
PT oligonucleotides, useful for enhancing an immune response or inducing

XX
PT cytokines, particularly for treating diseases, e.g. cancer, allergy or

XX
PT HIV infection.

XX
PS Example 11; Page 61; 68pp; English.

XX
CC The present invention relates to an immunostimulatory composition, which

XX
CC comprises at least one oligonucleotide comprising both an RNA region and

XX
CC a DNA region. The composition is useful for enhancing an immune response

XX
CC or inducing cytokines. It can be used as a vaccine adjuvant and in

XX
CC treating diseases, including pathogenic infection, (non-)malignant

XX
CC tumours (e.g. cancers of the brain, lung, ovary, breast, prostate or

XX
CC colon, or carcinomas and sarcomas), autoimmune diseases or allergies

XX
CC (e.g. allergic rhinitis, hay fever or food allergies), Lyme disease,

XX
CC hepatitis, HIV or malaria. The composition is also useful for treating,

XX
CC preventing or ameliorating the symptoms resulting from exposure to a bio-

XX
CC warfare agent, e.g. Ebola, Anthrax or Listeria. The present sequence is

XX
CC an immunostimulatory oligonucleotide described in the exemplification of

XX
CC the invention

SQ Sequence 18 BP; 3 A; 3 C; 9 G; 3 T; 0 U; 0 Other;
Query Match 91.13; Score 16.4; DB 6; Length 18;
Best Local Similarity 94.43; Pred. NO. 76;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 TGCATCGACGCGGGGG 18
Db 1 TGCATCGATCGAGGGGG 18
Search completed: July 2, 2004, 08:31:38
Job time : 134.89 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 2, 2004, 07:36:05 ; Search time 633.732 Seconds
(without alignments)
1231.080 Million cell updates/sec

Title: US-10-068-160-18
Perfect score: 18
Sequence: 1 tgcgcgcatgcaggg9999 18
Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues
Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 20000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl.*
1: gb.ba.*
2: gb.htg.*
3: gb.in.*
4: gb.om.*
5: gb.ov.*
6: gb.pat.*
7: gb.ph.*
8: gb.pl.*
9: gb.pr.*
10: gb.ro.*
11: gb.sts.*
12: gb.sy.*
13: gb.un.*
14: gb.vi.*
15: gb.ba.*
16: em.fun.*
17: em.hum.*
18: em.in.*
19: em.mu.*
20: em.om.*
21: em.ot.*
22: em.ov.*
23: em.pat.*
24: em.ph.*
25: em.pl.*
26: em.ro.*
27: em.sts.*
28: em.un.*
29: em.vi.*
30: em.htg.hum.*
31: em.htg.inv.*
32: em.htg.other.*
33: em.htg.mus.*
34: em.htg.pln.*
35: em.htg.tod.*
36: em.htg.mam.*
37: em.htg.vrt.*
38: em.sy.*
39: em.htgo.hum.*
40: em.htgo.mus.*
41: em.htgo.other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	17	94.4	19	6	AX194476	AX194476 Sequence
2	17	94.4	19	6	AX465426	AX465426 Sequence
3	16.4	91.1	20	6	AX194440	AX194440 Sequence
4	16.4	91.1	20	6	AX194481	AX194481 Sequence
5	16.4	91.1	20	6	AX194482	AX194482 Sequence
6	16.4	91.1	20	6	AX194501	AX194501 Sequence
7	16.4	91.1	20	6	AX352203	AX352203 Sequence
8	16.4	91.1	20	6	AX352214	AX352214 Sequence
9	16.4	91.1	20	6	AX352247	AX352247 Sequence
10	16.4	91.1	20	6	AX465390	AX465390 Sequence
11	16.4	91.1	20	6	AX465431	AX465431 Sequence
12	16.4	91.1	20	6	AX465432	AX465432 Sequence
13	16.4	91.1	28	6	AX352224	AX352224 Sequence
14	16.4	91.1	28	6	AX352236	AX352236 Sequence
15	16.4	91.1	13936	1	AB012163	AB012163 Xanthomon
16	16.4	91.1	77283	2	AC131504	AC131504 Lytechinu
17	16.4	91.1	189981	2	AC137048	AC137048 Rattus no
18	16.4	91.1	209366	2	AC128918	AC128918 Rattus no
19	16.4	91.1	213593	2	AC131402	AC131402 Rattus no
20	16.4	91.1	249762	2	AC111422	AC111422 Rattus no
21	16	88.9	31252	3	LMFL6293	LMFL6293 Leishmani
22	16	88.9	221641	3	LMFL6293	LMFL6293 Leishmani
23	16	88.9	298050	1	BX321861	BX321861 Nitrosomo
24	15.4	85.6	19	6	AX194422	AX194422 Sequence
25	15.4	85.6	19	6	AX194483	AX194483 Sequence
26	15.4	85.6	19	6	AX465372	AX465372 Sequence
27	15.4	85.6	19	6	AX465433	AX465433 Sequence
28	15.4	85.6	450	8	HVU234869	HVU234869 Hordeum v
29	15.4	85.6	675	6	AX283967	AX283967 Sequence
30	15.4	85.6	1093	5	HEM412873	HEM412873 Hypostomu
31	15.4	85.6	1690	5	BC061414	BC061414 Silurana
32	15.4	85.6	3639	8	AKL10229	AKL10229 Oryza sat
33	15.4	85.6	6633	1	AB015669	AB015669 Ralstonia
34	15.4	85.6	12929	10	RNO276628	RNO276628 Rattus no
35	15.4	85.6	13187	10	RNO276629	RNO276629 Rattus no
36	15.4	85.6	29593	1	AY255829	AY255829 Erwinia s
37	15.4	85.6	35904	1	AV123045	AV123045 Erwinia p
38	15.4	85.6	80800	8	AP004090	AP004090 Oryza sat
39	15.4	85.6	92745	8	AP006104	AP006104 Lotus cor
40	15.4	85.6	150597	2	AP005005	AP005005 Oryza sat
41	15.4	85.6	151369	8	AP001080	AP001080 Oryza sat
42	15.4	85.6	160847	8	AC120307	AC120307 Oryza sat
43	15.4	85.6	181794	2	AC145186	AC145186 Bos tauru
44	15.4	85.6	199027	2	AC137061	AC137061 Bos tauru
45	15.4	85.6	218460	2	AC097608	AC097608 Rattus no

ALIGNMENTS

RESULT 1	AX194476	Sequence 76 from Patent WO0151500.	19 bp	DNA	linear	PAT 28-AUG-2001
LOCUS	AX194476	Sequence 76 from Patent WO0151500.	19 bp	DNA	linear	PAT 28-AUG-2001
DEFINITION	AX194476	Sequence 76 from Patent WO0151500.	19 bp	DNA	linear	PAT 28-AUG-2001
ACCESSION	AX194476	Sequence 76 from Patent WO0151500.	19 bp	DNA	linear	PAT 28-AUG-2001
VERSION	AX194476.1	GI:15385132	19 bp	DNA	linear	PAT 28-AUG-2001
KEYWORDS	AX194476.1	GI:15385132	19 bp	DNA	linear	PAT 28-AUG-2001
SOURCE	AX194476.1	GI:15385132	19 bp	DNA	linear	PAT 28-AUG-2001
ORGANISM	AX194476.1	GI:15385132	19 bp	DNA	linear	PAT 28-AUG-2001
REFERENCE	AX194476.1	GI:15385132	19 bp	DNA	linear	PAT 28-AUG-2001
AUTHORS	AX194476.1	GI:15385132	19 bp	DNA	linear	PAT 28-AUG-2001
TITLE	AX194476.1	GI:15385132	19 bp	DNA	linear	PAT 28-AUG-2001
JOURNAL	AX194476.1	GI:15385132	19 bp	DNA	linear	PAT 28-AUG-2001

Klinman, D., Ishii, K. and Verthelyi, D.
Oligodeoxynucleotide and its use to induce an immune response
Patent: WO 0151500-A 76 19-JUL-2001;
Secretary of the Department of Health and Human Services (US)

Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gs.c.riken.go.jp,
uri:http://genome.gsc.riken.go.jp/
Sasaki,N., Izawa,M., Watahiki,M., Ozawa,K., Tanaka,T., Yoneda,Y.,
Matsuyama,S., Carninci,P., Muramatsu,M., Okazaki,Y. and
Hayashizaki,Y.
Transcriptional sequencing: A method for DNA sequencing using RNA
polymerase. Proc. Natl. Acad. Sci. U.S.A. 95 (7) 3455-3460 (1998)
Itoh,M., Kitsuai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J.,
Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M.,
Okazaki,Y. and Hayashizaki,Y.
Automated filtration-based high-throughput plasmid preparation
system. Genome Res. 9 (5), 463-470 (1999)
Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
19-44 (1999)
Please visit our web site (<http://genome.rtc.riken.go.jp>) for
further details.

FEATURES	SOURCE
-----------------	---------------

```

details:
location/Qualifiers
1. .240
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="4933425J05"
/sex="male"
/tissue_type="testis"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="RIKEN full-length enriched, adult male testis
(DH10B)"
/notes="Site 1: Sali; Site 2: BamHI; cDNA library was
prepared and sequenced in Mouse Genome Encyclopedia
Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in
RIKEN. Division of Experimental Animal Research in Riken
contributed to prepare mouse tissues. 1st strand cDNA was
primed with a primer [5'
GAGAGAGAGAGATTCACAGATCTTTTTTTTTTTTNN 3'], cDNA was
prepared by using tetralose thermo-activated reverse
transcriptase and subsequently enriched for full-length by
the cap-trapper. Second strand cDNA was prepared with the
primer adapter of sequence [5'
GAGAGAGAGATTCGAGTTAATTAATTAATTCCTCCCCCCCC 3']. cDNA
was cloned into the XhoI and BamHI sites. Vector: a
modified pBluescript KS(+) after bulk excision from Lambda
phage. Cloning sites 5' end: Sali, 3' end: BamHI "
```

ORIGIN

```

Query Match      91.1%; Score 16.4; DB 9; Length 240;
Best Local Similarity 94.4%;
Pred. No. 4e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

y      1  TGCATCGACGCGAGGGGG 18
      |||||
b      85  TGCATCGAGCGAGGGGG 102

```

RESULT 2	AV268287	257 bp	linear	EST 05-NOV-1999
LOCUS	AV268287			
DEFINITION	RIKEN full-length enriched, adult male testis (DH10B) Mus musculus cDNA clone 490534F16.3', mRNA sequence.			
ACCESSION	AV268287			
VERSION	AV268287.1	GI:6256324		
KEYWORDS	EST.			
SOURCE	Mus musculus (house mouse)			
ORGANISM	Mus musculus			
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			

ORIGIN

Query Match 91.1%; Score 16.4; DB 9; Length 257;
Best Local Similarity 94.4%; Pred.No. 4.1e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

REFERENCE
AUTHORS

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 257)
Konno,H., Aizawa,K., Akahira,S., Akiyama,J., Carninci,P., Endo,T.,
Fukuda,S., Fukunishi,Y., Hara,A., Hayatsu,N., Hirozane,T., Hori,g.
Ishii,Y., Ishikawa,T., Itoh,M., Izawa,M., Kadota,K., Kagawa,I.,
Kai,C., Kawai,J., Kikuchi,N., Kojima,Y., Koya,S., Kusakabe,M.,
Matsuyama,T., Miki,R., Mizuno,Y., Nakamura,M., Oda,H., Okazaki,Y.,
Owa,C., Ozawa,Y., Saito,H., Sano,M., Sato,K., Shibata,K.,
Shibata,Y., Shigemoto,Y., Shiraki,T., Sogabe,Y., Sugahara,Y.,
Suzuki,H., Suzuki,H., Takahashi,P., Taten,M., Tomingha,N.,
Tsunoda,Y., Watahiki,A., Watanabe,S., Yamamura,T., Yasunishi,A.,
Yokota,T., Yoshiki,A., Yoshino,M., Muramatsu,M. and Hayashiaki,Y.
Riken Mouse ESTs (Konno,H., et al. 1999)

TITLE	JOURNAL	COMMENT
1. The Role of the State in Economic Development	Journal of Economic Surveys	See page 100
2. The Impact of Globalization on the Environment	Environmental Economics and Organization	See page 100
3. The Effect of Trade Liberalization on Income Distribution	Journal of Development Economics	See page 100
4. The Role of the State in the Provision of Social Services	Journal of Public Economics	See page 100
5. The Impact of Financial Globalization on the Real Economy	Journal of International Money and Finance	See page 100
6. The Effect of Trade Liberalization on the Environment	Journal of Environmental Economics and Organization	See page 100
7. The Role of the State in the Provision of Health Services	Journal of Health Economics	See page 100
8. The Impact of Globalization on the Labor Market	Journal of Labor Economics	See page 100
9. The Effect of Trade Liberalization on the Labor Market	Journal of International Trade and Development	See page 100
10. The Role of the State in the Provision of Education Services	Journal of Public Economics	See page 100

Contact: Yoshihide Hayashizaki
 Laboratory for Genome Exploration Research
 Sciences Center (GSC), Yokohama Institute
 The Institute of Physical and Chemical Research (RIKEN)
 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
 Tel: 81-45-503-9222
 Fax: 81-45-503-9216
 Email: genome-res@gscc.riken.go.jp,
 URL: <http://genome.gsc.riken.go.jp/>
 Sasaki N., Izawa M., Watabiki M., Ozawa K., Tanaka T., Yoneda Y.,
 Matsura S., Carninci P., Muramatsu M., Okazaki Y. and
 Hayashizaki Y.
 Transcriptional sequencing: A method for DNA sequencing using RNA
 polymerase. *Proc. Natl. Acad. Sci. U.S.A.* 95 (7), 3455-3460 (1998)
 Itoh M., Kitsuana T., Akiyama G., Shibata K., Izawa M., Kawai J.,
 Tomaru Y., Carninci P., Shibata Y., Ozawa Y., Muramatsu M.,
 Okazaki Y. and Hayashizaki Y.
 Automated filtration-based high-throughput plasmid preparation
 system. *Genome Res.* 9 (5), 463-470 (1999)
 Carninci P. and Hayashizaki Y.
 High-efficiency full-length cDNA cloning. *Methods Enzymol.* 303,
 19-44 (1999)
 Please visit our web site (<http://genome.rtc.riken.go.jp/>) for
 further details.

FEATURES
SOURCE

```

1. --257
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clones="4930534F16"
/sex="male"
/tissue_type="testis"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="RIKEN full-length enriched, adult male testis
(DH10B)"
/notes="Site 1: SalI; Site 2: BamHI; cDNA library was
prepared and sequenced in Mouse Genome Encyclopedia
Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in
RIKEN, Division of Experimental Animal Research in Riken
contributed to prepare mouse tissues. 1st strand cDNA was
primed with a primer [5'.
GAGAGGAGGAGGATCCAGAGCTCTTTTCTTTTCTTTT 3']. cDNA was
prepared by using trehalose thermo-activated reverse
transcriptase and subsequently enriched for full-length by
cap-trapper. Second strand cDNA was prepared with the
primer adapter of sequence [5'.
GAGAGGAGGATCTCCAGTAAATTAATTCCTCCCCCCCC 3']. cDNA
was cloned into the XhoI and BamHI sites. Vector: a
modified pBluescript KS(+) after bulk excision from Lambda.
EUC111C1 was sites 3' end. BamHI "
```

QY 1 TGCATCGACGAGGGGG 18
 Db 97 TGCATCGAGGAGGGGG 114

RESULT 3
 AV269637
 LOCUS
 DEFINITION
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

AV269637 303 bp mRNA linear EST 05-NOV-1999
 AV269637 RIKEN full-length enriched, adult male testis (DH10B) Mus
 musculus cDNA clone 4930544G09 3', mRNA sequence.

AV269637 1 GI:6257674
 EST.
 Mus musculus (house mouse)
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 303)
 Konno, H., Aizawa, K., Akahira, S., Akiyama, J., Carninci, P., Endo, T.,
 Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N., Hirozane, F., Hori, F.,
 Ishii, Y., Ishikawa, T., Itoh, M., Izawa, M., Kadota, K., Kagawa, I.,
 Kai, C., Kawai, J., Kikuchi, N., Kojima, Y., Koya, S., Kusakabe, M.,
 Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y.,
 Owa, C., Ozawa, Y., Saito, H., Sano, M., Sato, K., Shibata, K.,
 Shibata, Y., Shigemoto, Y., Shiraki, T., Sogabe, Y., Sugahara, Y.,
 Suzuki, H., Suzuki, H., Takahashi, P., Tateno, M., Tomimaga, N.,
 Tsunoda, Y., Watahiki, A., Watanabe, S., Yamamura, T., Yasunishi, A.,
 Yokota, T., Yoshiki, A., Yoshino, M., Muramatsu, M. and Hayashizaki, Y.
 RIKEN Mouse ESTs (Konno, H., et al. 1999)
 Unpublished (1999)
 Contact: Yoshihide Hayashizaki
 Laboratory for Genome Exploration Research Group, RIKEN Genomic
 Sciences Center (GSC), Yokohama Institute
 The Institute of Physical and Chemical Research (RIKEN)
 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
 Tel: 81-45-503-9222
 Fax: 81-45-503-9216
 Email: genome-res@res.riken.go.jp/
 URL: http://genome.gsc.riken.go.jp/
 Sasaki, N., Izawa, M., Watahiki, Y., Ozawa, K., Tanaka, T., Yoneda, Y.,
 Matsura, S., Carninci, P., Muramatsu, M., Okazaki, Y. and
 Hayashizaki, Y.
 Transcriptional sequencing: A method for DNA sequencing using RNA
 polymerase. Proc. Natl. Acad. Sci. U.S.A. 95 (7), 3455-3460 (1998)
 Itoh, M., Kitsumi, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J.,
 Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M.,
 Okazaki, Y. and Hayashizaki, Y.
 Automated filtration-based high-throughput plasmid preparation
 system. Genome Res. 9 (5), 463-470 (1999)
 Carninci, P. and Hayashizaki, Y.
 High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
 19-44 (1999)
 Please visit our web site (http://genome.rtc.riken.go.jp) for
 further details.

FEATURES
 source
 Location/Qualifiers
 1..303
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="4930544G09"
 /sex="male"
 /tissue_type="testis"
 /dev_stage="adult"
 /lab_host="DH10B"
 /clone_lib="RIKEN full-length enriched, adult male testis
 (DH10B)"
 /note="Site 1: SalI; Site 2: BamHI; cDNA library was
 prepared and sequenced in Mouse Genome Encyclopedia
 Project of Genome Exploration Research Group in Riken
 Genomic Sciences Center and Genome Science Laboratory in
 RIKEN. Division of Experimental Animal Research in Riken
 contributed to prepare mouse tissues. 1st strand cDNA was

ORIGIN
 Query Match 91.1%; Score 16.4; DB 9; Length 303;
 Best Local Similarity 94.4%; Pred. No. 4.2e+03;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 TGCATCGACGAGGGGG 18
 Db 143 TGCATCGAGGAGGGGG 160

RESULT 4
 AQ831712/c
 LOCUS
 DEFINITION
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM

AQ831712 410 bp DNA linear GSS 27-AUG-1999
 HS_2087_A1_C07_T7C CIT Approved Human Genomic Sperm Library D Homo
 sapiens genomic clone Plate=2087 Col=13 Row=E, genomic survey
 sequence.
 AQ831712
 AQ831712.1 GI:5797774
 GSS.
 Homo sapiens (human)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 410)
 Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T.,
 Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and
 Hood, L.
 Sequence-tagged connectors: A sequence approach to mapping and
 scanning the human genome
 Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
 99380589
 10449764
 Contact: Mahairas GG, Wallace JC, Hood L
 High Throughput Sequencing Center
 University of Washington
 401 Queen Anne Avenue North, Seattle, WA 98109, USA
 Tel: (206) 616-3618
 Fax: (206) 616-3887
 Email: jwallace@u.washington.edu
 Clones may be purchased from Research Genetics (info@resgen.com).
 BAC end Web Server: http://www.htsc.washington.edu
 Plate: 2087 row: E column: 13
 Seq primer: T7
 Class: BAC ends
 High quality sequence stop: 410.
 Location/Qualifiers
 1..410
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 /clone="Plate=2087 Col=13 Row=E"
 /sex="male"
 /clone_lib="CIT Approved Human Genomic Sperm Library D"
 /note="Organ: sperm; Vector: pBelOAG11; BAC Clones in
 E-Coli DH10B"

ORIGIN
 Query Match 91.1%; Score 16.4; DB 28; Length 410;
 Best Local Similarity 94.4%; Pred. No. 4.5e+03;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 TGCATCGAGGAGGGGG 18

Db 21 TGCATCGACTCAGGGGG 4
|||||

RESULT 5
BG853689
LOCUS
DEFINITION 693 bp mRNA linear EST 29-MAY-2001
1024037H01.y1 C. reinhardtii CC-1690, normalized, Lambda Zap II
Chlamydomonas reinhardtii cDNA, mRNA sequence.
BG853689
Chlamydomonas reinhardtii
EST.
BG853689.1 GI:14234873
Chlamydomonas reinhardtii
Chlamydomonas reinhardtii
Chlamydomonas reinhardtii
Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
Chlamydomonadales; Chlamydomonas.
1 (bases 1 to 693)
Grossman, A., Davies, J., Federspiel, N., Harris, E., Lefebvre, P.,
McDermott, J. P., Silflow, C., Stern, D. and Surzycki, R.
Analyses of the Chlamydomonas reinhardtii Genome: A Model,
Unicellular System for Analyzing Gene Function and Regulation in
Vascular Plants; Project phase 2
Unpublished (2000)
Contact: Charles Hauser
DCMB Box 91000
Duke University
Durham, NC 27708-1000
Tel: 919 613 8159
Fax: 919 613 8177
Email: chauser@duke.edu.
Location/Qualifiers
1..693
/organism="Chlamydomonas reinhardtii"
/mol_type="mRNA"
/strain="CC-1690 wild type at+ 21gr"
/db_xref="taxon:3055"
/clone_lib="C. reinhardtii CC-1690, normalized, Lambda Zap
II"
/note="Vector: pBluescript II SK-; Site 1: EcoRI; Site 2:
XhoI; This library, constructed by John Davies and Jeffrey
McDermott, combines cDNAs from CC-1690 cells grown to
mid-log phase in TAP (acetate-containing) medium in the
light, TAP medium in the dark, HS (minimal) medium in
ambient levels of CO2 and HS medium bubbled with 5% CO2.
PolyA mRNA was purified from each sample, pooled and cDNA
synthesized. The cDNA was directionally cloned into lambda
Zap II (Stratagene) in the EcoRI (5') and XhoI (3') sites.
pBluescript II SK- plasmids were excised from the lambda
Zap clones by superinfection with ExAssist (Stratagene)
phage. The library was normalized using method 4 described
in Bonaldo et al (1996) Genome Research 6: 791-806."

ORIGIN
Query Match 91.1%; Score 16.4; DB 12; Length 693;
Best Local Similarity 94.4%; Pred. No. 5.1e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 TGCATCGACGCGAGGGGG 18
|||||
Db 317 TGCATCGACACAGGGGG 334
|||||

RESULT 6
CG225411
LOCUS
DEFINITION 878 bp DNA linear GSS 22-AUG-2003
OG2AN65PH ZM 0.7.1.5 KB Zea mays genomic clone ZMMBMA0744K10,
genomic survey sequence.
CG225411
VERSION
CG225411.1 GI:34125299
GSS.
Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliopsida; Poales; Poaceae; PACCAD
clade; Panicoidae; Andropogoneae; Zea.
1 (bases 1 to 878)
Resnick, A., Fraser, C.M., Quackenbush, J., Van Aken, S., Utterback, T.,
Bennetzen, J.
Maize Genomics Consortium
Unpublished (2003)
Other_GSSs: PUFX02ITFC
Contact: Cathy Whitelaw
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@cigr.org
Seq primer: TR
Class: sheared ends.
Location/Qualifiers
1..888
/organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
/db_xref="taxon:4577"
/clones="ZMMBTA0756C17"

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@cigr.org
Seq primer: TR
Class: sheared ends.
Location/Qualifiers
1..888
/organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
/db_xref="taxon:4577"
/clones="ZMMBTA0756C17"

ORIGIN
Query Match 91.1%; Score 16.4; DB 29; Length 878;
Best Local Similarity 94.4%; Pred. No. 5.4e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 TGCATCGACGCGAGGGGG 18
|||||
Db 643 TCCATCGACGCGAGGGGG 660
|||||

RESULT 7
CG458305/c
LOCUS
DEFINITION 888 bp DNA linear GSS 17-SEP-2003
PUFX02ITDC ZM 0.6.1.0 KB Zea mays genomic clone ZMMBTA0756C17,
genomic survey sequence.
CG458305
VERSION
CG458305.1 GI:34843305
GSS.
Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliopsida; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoidae; Andropogoneae; Zea.
1 (bases 1 to 888)
Resnick, A., Fraser, C.M., Quackenbush, J., Van Aken, S., Utterback, T.,
Bennetzen, J.
Maize Genomics Consortium
Unpublished (2003)
Other_GSSs: PUFX02ITFC
Contact: Cathy Whitelaw
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@cigr.org
Seq primer: TR
Class: sheared ends.
Location/Qualifiers
1..888
/organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
/db_xref="taxon:4577"
/clones="ZMMBTA0756C17"

/clone lib="ZM 0.6 1.0 KB"
/note="Vector: PCR4-TOPO; Site 1: EcoRI; 0.6-1.0 kb high
Cor selected genomic DNA library"

ORIGIN

Query Match 91.1%; Score 16.4; DB 29; Length 888;
Best Local Similarity 94.4%; Pred. No. 5.4e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TGCATCGACGCGGGGG 18
| | | | | | | | | | | | | | | | | | | | | |
Db 314 TCCATCGACGCGGGGG 297

RESULT 8
CG225423/C

LOCUS CG225423 960 bp DNA linear GSS 22-AUG-2003
DEFINITION CG2AN65TV ZM 0.7 1.5 KB Zea mays genomic clone ZMMBMA0744K10,
genomic survey sequence.

ACCESSION CG225423
VERSION CG225423.1 GI:34125311
KEYWORDS GSS.

SOURCE
ORGANISM

Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.

REFERENCE

AUTHORS Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,
Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T.,
Citek, R.W., Nunberg, A., Robbins, D. and Lakey, N.
Consortium for Maize Genomics
Unpublished (2002)
Other GSSs: CG2AN65TH

TITLE
JOURNAL
COMMENT

Contact: Cathy Whitelaw
TIGR

9712 Medical Center Drive, Rockville, MD 20850, USA

Tel: 301-838-5843

Fax: 301-838-0208

Email: whitelaw@tigr.org

Seq primer: TP

Class: sheared ends.

Location/Qualifiers

1..960
/organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
/db_xref="taxon:4577"
/clone="ZMMBMA0744K10"
/clone lib="ZM 0.7 1.5 KB"
/note="Vector: pBC5K; Site 1: HincII; 0.7-1.5 kb
methylation filtered genomic DNA library"

ORIGIN

Query Match 91.1%; Score 16.4; DB 29; Length 960;
Best Local Similarity 94.4%; Pred. No. 5.5e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TGCATCGACGCGGGGG 18
| | | | | | | | | | | | | | | | | | | | | |
Db 947 TCCATCGACGCGGGGG 930

RESULT 9

LOCUS CC655225 980 bp DNA linear GSS 19-JUN-2003
DEFINITION CGU070TV ZM 0.7 1.5 KB Zea mays genomic clone ZMMBMA0469K19,
genomic survey sequence.

ACCESSION CC655225
VERSION CC655225.1 GI:32058344
KEYWORDS GSS.

SOURCE
ORGANISM

Zea mays
Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.

REFERENCE
AUTHORS

Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,
Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T.,
Citek, R.W., Nunberg, A., Robbins, D. and Lakey, N.
Consortium for Maize Genomics
Unpublished (2002)

TITLE
JOURNAL
COMMENT

Other GSSs: CGU070TH
Contact: Cathy Whitelaw
TIGR

9712 Medical Center Drive, Rockville, MD 20850, USA

Tel: 301-838-5843

Fax: 301-838-0208

Email: whitelaw@tigr.org

Seq primer: TP

Class: sheared ends.

Location/Qualifiers

1..980
/organism="Zea mays"
/mol_type="genomic DNA"
/strain="B73"
/db_xref="taxon:4577"
/clone="ZMMBMA0469K19"
/clone lib="ZM 0.7 1.5 KB"
/note="Vector: pBC5K; Site 1: HincII; 0.7-1.5 kb
methylation filtered genomic DNA library"

ORIGIN

Query Match 91.1%; Score 16.4; DB 29; Length 980;
Best Local Similarity 94.4%; Pred. No. 5.5e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TGCATCGACGCGGGGG 18
| | | | | | | | | | | | | | | | | | | | | |
Db 268 TCCATCGACGCGGGGG 285

RESULT 10
AV253772

LOCUS AV253772 246 bp mRNA linear EST 04-NOV-1999
DEFINITION AV253772 RIKEN full-length enriched adult male testis (DH10B) Mus
musculus cDNA clone 4921504P03 3', mRNA sequence.

ACCESSION AV253772.1 GI:6241231
VERSION AV253772.1
KEYWORDS EST.
SOURCE Mus musculus (house mouse)

ORGANISM

Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 246)

REFERENCE
AUTHORS

Konno, H., Aizawa, K., Akahira, S., Akiyama, J., Carninci, P., Endo, T.,
Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N., Hirozane, T., Hori, F.,
Ishii, Y., Ishikawa, T., Itoh, M., Izawa, M., Kadota, K., Kagawa, I.,
Kai, C., Kawai, J., Kikuchi, N., Kojima, Y., Koya, S., Kusakabe, M.,
Mateuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y.,
Owa, C., Ozawa, Y., Saito, H., Sano, M., Sato, K., Shibata, K.,
Shibata, Y., Shigemoto, Y., Shiraki, T., Sogabe, Y., Suganara, Y.,
Suzuki, H., Suzuki, H., Takahashi, F., Tateo, M., Tomimaga, N.,
Tsunoda, Y., Watahiki, A., Watanabe, S., Yamamura, T., Yasunishi, A.,
Yokota, T., Yoshiki, A., Yoshino, M., Muramatsu, M. and Hayashizaki, Y.
RIKEN Mouse ESTs (Konno, H., et al. 1999)
Unpublished (1999)

TITLE
JOURNAL
COMMENT

Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan

Tel: 81-45-503-9222

Fax: 81-45-503-9216

Email: genome-res@gsc.riken.go.jp

URL: http://genome.gsc.riken.go.jp/

units. For more information on RescueMu, go to the web site 'www.zmdd.state.edu' and follow the links for 'RescueMu.' Grid AA was grown at UC San Diego in 2002. DNA was extracted from leaf strips, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin."

RESULT 14
BI507147/c

Query Match 85.6%; Score 15.4; DB 29; Length 468;
Best Local Similarity 94.1%; Pred. No. 1.3e+04;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

2 GCATCGACGCAGGGGG 18
17 GCATCGACGCATGGGG 33

RESULT 14
BI507147/c

CGT14924 458 bp DNA linear GSS 20-OCT-2003
1119039B04.y1 1119 - RescueMu Grid AA Zea mays genomic, genomic
survey sequence.

Zea mays Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 468)

1 bases

AUTHORS	Walbot, V.
TITLE	Maize genomic sequences found using engineered RescueMu transposon
JOURNAL	Unpublished (2001)
COMMENT	Contact: Walbot V

CONTACT: MARLOU A.
Department of Biological Sciences

Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221

Fax: 650 743 8821
 Email: walbot@stanford.edu
 Possible ligation site so sequence was trimmed. Post-ligation
 sequence submitted separately.
 Plate: 1119039 row: 42
 Class: transposon-tagged.

FEATURES

```

1. 468
2. 469
3. 470
4. 471
5. 472
6. 473
7. 474
8. 475
9. 476
10. 477
11. 478
12. 479
13. 480
14. 481
15. 482
16. 483
17. 484
18. 485
19. 486
20. 487
21. 488
22. 489
23. 490
24. 491
25. 492
26. 493
27. 494
28. 495
29. 496
30. 497
31. 498
32. 499
33. 500
34. 501
35. 502
36. 503
37. 504
38. 505
39. 506
40. 507
41. 508
42. 509
43. 510
44. 511
45. 512
46. 513
47. 514
48. 515
49. 516
50. 517
51. 518
52. 519
53. 520
54. 521
55. 522
56. 523
57. 524
58. 525
59. 526
60. 527
61. 528
62. 529
63. 530
64. 531
65. 532
66. 533
67. 534
68. 535
69. 536
70. 537
71. 538
72. 539
73. 540
74. 541
75. 542
76. 543
77. 544
78. 545
79. 546
80. 547
81. 548
82. 549
83. 550
84. 551
85. 552
86. 553
87. 554
88. 555
89. 556
90. 557
91. 558
92. 559
93. 560
94. 561
95. 562
96. 563
97. 564
98. 565
99. 566
100. 567
101. 568
102. 569
103. 570
104. 571
105. 572
106. 573
107. 574
108. 575
109. 576
110. 577
111. 578
112. 579
113. 580
114. 581
115. 582
116. 583
117. 584
118. 585
119. 586
120. 587
121. 588
122. 589
123. 590
124. 591
125. 592
126. 593
127. 594
128. 595
129. 596
130. 597
131. 598
132. 599
133. 600
134. 601
135. 602
136. 603
137. 604
138. 605
139. 606
140. 607
141. 608
142. 609
143. 610
144. 611
145. 612
146. 613
147. 614
148. 615
149. 616
150. 617
151. 618
152. 619
153. 620
154. 621
155. 622
156. 623
157. 624
158. 625
159. 626
160. 627
161. 628
162. 629
163. 630
164. 631
165. 632
166. 633
167. 634
168. 635
169. 636
170. 637
171. 638
172. 639
173. 640
174. 641
175. 642
176. 643
177. 644
178. 645
179. 646
180. 647
181. 648
182. 649
183. 650
184. 651
185. 652
186. 653
187. 654
188. 655
189. 656
190. 657
191. 658
192. 659
193. 660
194. 661
195. 662
196. 663
197. 664
198. 665
199. 666
200. 667
201. 668
202. 669
203. 670
204. 671
205. 672
206. 673
207. 674
208. 675
209. 676
210. 677
211. 678
212. 679
213. 680
214. 681
215. 682
216. 683
217. 684
218. 685
219. 686
220. 687
221. 688
222. 689
223. 690
224. 691
225. 692
226. 693
227. 694
228. 695
229. 696
230. 697
231. 698
232. 699
233. 700
234. 701
235. 702
236. 703
237. 704
238. 705
239. 706
240. 707
241. 708
242. 709
243. 710
244. 711
245. 712
246. 713
247. 714
248. 715
249. 716
250. 717
251. 718
252. 719
253. 720
254. 721
255. 722
256. 723
257. 724
258. 725
259. 726
260. 727
261. 728
262. 729
263. 730
264. 731
265. 732
266. 733
267. 734
268. 735
269. 736
270. 737
271. 738
272. 739
273. 740
274. 741
275. 742
276. 743
277. 744
278. 745
279. 746
280. 747
281. 748
282. 749
283. 750
284. 751
285. 752
286. 753
287. 754
288. 755
289. 756
290. 757
291. 758
292. 759
293. 760
294. 761
295. 762
296. 763
297. 764
298. 765
299. 766
300. 767
301. 768
302. 769
303. 770
304. 771
305. 772
306. 773
307. 774
308. 775
309. 776
310. 777
311. 778
312. 779
313. 780
314. 781
315. 782
316. 783
317. 784
318. 785
319. 786
320. 787
321. 788
322. 789
323. 790
324. 791
325. 792
326. 793
327. 794
328. 795
329. 796
330. 797
331. 798
332. 799
333. 800
334. 801
335. 802
336. 803
337. 804
338. 805
339. 806
340. 807
341. 808
342. 809
343. 810
344. 811
345. 812
346. 813
347. 814
348. 815
349. 816
350. 817
351. 818
352. 819
353. 820
354. 821
355. 822
356. 823
357. 824
358. 825
359. 826
360. 827
361. 828
362. 829
363. 830
364. 831
365. 832
366. 833
367. 834
368. 835
369. 836
370. 837
371. 838
372. 839
373. 840
374. 841
375. 842
376. 843
377. 844
378. 845
379. 846
380. 847
381. 848
382. 849
383. 850
384. 851
385. 852
386. 853
387. 854
388. 855
389. 856
390. 857
391. 858
392. 859
393. 860
394. 861
395. 862
396. 863
397. 864
398. 865
399. 866
400. 867
401. 868
402. 869
403. 870
404. 871
405. 872
406. 873
407. 874
408. 875
409. 876
410. 877
411. 878
412. 879
413. 880
414. 881
415. 882
416. 883
417. 884
418. 885
419. 886
420. 887
421. 888
422. 889
423. 890
424. 891
425. 892
426. 893
427. 894
428. 895
429. 896
430. 897
431. 898
432. 899
433. 900
434. 901
435. 902
436. 903
437. 904
438. 905
439. 906
440. 907
441. 908
442. 909
443. 910
444. 911
445. 912
446. 913
447. 914
448. 915
449. 916
450. 917
451. 918
452. 919
453. 920
454. 921
455. 922
456. 923
457. 924
458. 925
459. 926
460. 927
461. 928
462. 929
463. 930
464. 931
465. 932
466. 933
467. 93
```

FEATURES	SOURCE
----------	--------

```

/organism="Apis mellifera"
/mol_type="mRNA"
/strain="mixed strains of European bees, predominantly
A.m. ligustica"
/db_xref="taxon:7460"
/clone="BB170025B20H07"

```

```

/tissue_type="brain"
/dev_stage="adult worker honey bee"
/lab_host="DHI0B"
/clone_lib="Bee Brain Normalized/Subtracted Library, BB17"
/note="Organ: brain; Vector: pTT3-Pac; Site_1: EcoR1;
Site_2: NotI. This BB17 cDNA library was generated by

```


OK nucleic - nucleic search, using sw model
Run on: July 2, 2004, 07:36:05 ; Search time 633.732 Seconds
(without alignments)
1231.080 Million cell updates/sec

Title: US-10-068-160-19
Perfect score: 18
Sequence: 1 tgcacgcagcagggggg 18

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl.*
1: gb_ba.*
2: gb_hg.*
3: gb_in.*
4: gb_om.*
5: gb_ov.*
6: gb_pat.*
7: gb_ph.*
8: gb_pl.*
9: gb_pt.*
10: gb_ro.*
11: gb_sts.*
12: gb_sy.*
13: gb_un.*
14: gb_vi.*
15: em_ba.*
16: em_fun.*
17: em_hum.*
18: em_in.*
19: em_mu.*
20: em_om.*
21: em_or.*
22: em_ov.*
23: em_pat.*
24: em_ph.*
25: em_pl.*
26: em_ro.*
27: em_sts.*
28: em_un.*
29: em_vi.*
30: em_htg_hum.*
31: em_htg_inv.*
32: em_htg_other.*
33: em_htg_mus.*
34: em_htg_pln.*
35: em_htg_rod.*
36: em_htg_man.*
37: em_htg_vrt.*
38: em_sy.*
39: em_htgo_hum.*
40: em_htgo_mus.*
41: em_htgo_other.*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	18	100.0	20	6	AX194500 Sequence
2	18	100.0	20	6	AX352202 Sequence
3	18	100.0	20	6	AX352213 Sequence
4	18	100.0	20	6	AX352246 Sequence
5	18	100.0	28	6	AX352223 Sequence
6	18	100.0	28	6	AX352235 Sequence
7	17	94.4	19	6	AX194488 Sequence
8	17	94.4	19	6	AX465438 Sequence
9	16.4	91.1	18	6	AX352207 Sequence
10	16.4	91.1	18	6	AX352217 Sequence
11	16.4	91.1	18	6	AX352255 Sequence
12	16.4	91.1	20	6	AX194432 Sequence
13	16.4	91.1	20	6	AX194434 Sequence
14	16.4	91.1	20	6	AX194437 Sequence
15	16.4	91.1	20	6	AX194438 Sequence
16	16.4	91.1	20	6	AX194439 Sequence
17	16.4	91.1	20	6	AX194441 Sequence
18	16.4	91.1	20	6	AX194443 Sequence
19	16.4	91.1	20	6	AX194472 Sequence
20	16.4	91.1	20	6	AX352198 Sequence
21	16.4	91.1	20	6	AX352206 Sequence
22	16.4	91.1	20	6	AX352209 Sequence
23	16.4	91.1	20	6	AX352216 Sequence
24	16.4	91.1	20	6	AX352242 Sequence
25	16.4	91.1	20	6	AX352250 Sequence
26	16.4	91.1	20	6	AX352254 Sequence
27	16.4	91.1	20	6	AX465382 Sequence
28	16.4	91.1	20	6	AX465384 Sequence
29	16.4	91.1	20	6	AX465387 Sequence
30	16.4	91.1	20	6	AX465388 Sequence
31	16.4	91.1	20	6	AX465389 Sequence
32	16.4	91.1	20	6	AX465391 Sequence
33	16.4	91.1	20	6	AX465393 Sequence
34	16.4	91.1	20	6	AX465422 Sequence
35	16.4	91.1	20	6	AX816067 Sequence
36	16.4	91.1	22	6	AX352204 Sequence
37	16.4	91.1	22	6	AX352248 Sequence
38	16.4	91.1	26	6	AX352228 Sequence
39	16.4	91.1	26	6	AX352240 Sequence
40	16.4	91.1	28	6	AX352219 Sequence
41	16.4	91.1	28	6	AX352227 Sequence
42	16.4	91.1	28	6	AX352231 Sequence
43	16.4	91.1	28	6	AX352239 Sequence
44	16.4	91.1	29	6	AX352237 Sequence
45	16.4	91.1	30	6	AX352225 Sequence

ALIGNMENTS

RESULT 1
AX194500
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL

AX194500
Sequence 100 from Patent WO0151500.
AX194500
AX194500.1 GI:15385156

synthetic construct
synthetic construct
artificial sequences.

1
Kliman,D., Ishii,K. and Verthelyi,D.
Oligodeoxynucleotide and its use to induce an immune response
Patent: WO 0151500-A 100 19-JUL-2001;
Secretary of the Department of Health and Human Services (US)

Pred. No. is the number of results predicted by chance to have a

```
FEATURES
  source      Location/Qualifiers
  1..20
  /organism="synthetic construct"
  /mol_type="unassigned DNA"
  /db_xref="taxon:32630"
  /note="Synthetic DNA"

ORIGIN

Query Match      100.0%; Score 18; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TGCATCGACGACGAGGGGG 18
        |||||
Db       3 TGCATCGACGACGAGGGGG 20

RESULT 2
AX352202
LOCUS      AX352202      20 bp      DNA      linear      PAT 06-FEB-2002
DEFINITION Sequence 498 from Patent WO0193902.
ACCESSION  AX352202
VERSION     AX352202.1 GI:18617495
KEYWORDS   .
SOURCE      synthetic construct
            synthetic construct
            artificial sequences.
ORGANISM
REFERENCE   1
AUTHORS     Mond, J.J., Flora, M. and Klinman, D.M.
TITLE       Immunostimulatory rna/dna hybrid molecules
JOURNAL     Patent: WO 0193902-A 498 13-DEC-2001;
            Biosynexus Incorporated (US)
FEATURES    source
            1..20
            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"
            /note="Synthetic HDR"

ORIGIN

Query Match      100.0%; Score 18; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TGCATCGACGACGAGGGGG 18
        |||||
Db       3 TGCATCGACGACGAGGGGG 20

RESULT 3
AX352213
LOCUS      AX352213      20 bp      DNA      linear      PAT 06-FEB-2002
DEFINITION Sequence 509 from Patent WO0193902.
ACCESSION  AX352213
VERSION     AX352213.1 GI:18617496
KEYWORDS   .
SOURCE      synthetic construct
            synthetic construct
            artificial sequences.
ORGANISM
REFERENCE   1
AUTHORS     Mond, J.J., Flora, M. and Klinman, D.M.
TITLE       Immunostimulatory rna/dna hybrid molecules
JOURNAL     Patent: WO 0193902-A 509 13-DEC-2001;
            Biosynexus Incorporated (US)
FEATURES    source
            1..20
            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"
            /note="Synthetic HDR"

ORIGIN

Query Match      100.0%; Score 18; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TGCATCGACGACGAGGGGG 18
        |||||
Db       3 TGCATCGACGACGAGGGGG 20

RESULT 4
AX352246
LOCUS      AX352246      20 bp      DNA      linear      PAT 06-FEB-2002
DEFINITION Sequence 542 from Patent WO0193902.
ACCESSION  AX352246
VERSION     AX352246.1 GI:18617529
KEYWORDS   .
SOURCE      synthetic construct
            synthetic construct
            artificial sequences.
ORGANISM
REFERENCE   1
AUTHORS     Mond, J.J., Flora, M. and Klinman, D.M.
TITLE       Immunostimulatory rna/dna hybrid molecules
JOURNAL     Patent: WO 0193902-A 542 13-DEC-2001;
            Biosynexus Incorporated (US)
FEATURES    source
            1..20
            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"
            /note="Synthetic HDR"

ORIGIN

Query Match      100.0%; Score 18; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TGCATCGACGACGAGGGGG 18
        |||||
Db       3 TGCATCGACGACGAGGGGG 20

RESULT 5
AX352223
LOCUS      AX352223      28 bp      DNA      linear      PAT 06-FEB-2002
DEFINITION Sequence 519 from Patent WO0193902.
ACCESSION  AX352223
VERSION     AX352223.1 GI:18617506
KEYWORDS   .
SOURCE      synthetic construct
            synthetic construct
            artificial sequences.
ORGANISM
REFERENCE   1
AUTHORS     Mond, J.J., Flora, M. and Klinman, D.M.
TITLE       Immunostimulatory rna/dna hybrid molecules
JOURNAL     Patent: WO 0193902-A 519 13-DEC-2001;
            Biosynexus Incorporated (US)
FEATURES    source
            1..28
            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"
            /note="Synthetic HDR"

ORIGIN

Query Match      100.0%; Score 18; DB 6; Length 28;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TGCATCGACGACGAGGGGG 18
        |||||
Db       3 TGCATCGACGACGAGGGGG 20

RESULT 6
```

```
AX352235
LOCUS AX352235 28 bp DNA linear PAT 06-FEB-2002
DEFINITION Sequence S31 from Patent WO0193902.
ACCESSION AX352235
VERSION AX352235.1 GI:18617518
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM synthetic construct
          artificial sequences.
REFERENCE
AUTHORS Mond, J.J., Flora, M. and Klinman, D.M.
TITLE Immunostimulatory rna/dna hybrid molecules
JOURNAL Patent: WO 0193902-A 531 13-DEC-2001;
          Biosynexus Incorporated (US)
FEATURES
source
1. .28
   /organism="synthetic construct"
   /mol_type="unassigned DNA"
   /db_xref="taxon:32630"
   /note="Synthetic HDR"
ORIGIN
Query Match 100.0%; Score 18; DB 6; Length 28;
Best Local Similarity 100.0%; Pred. No. 2.9e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGCATCGACGCGGGGG 18
   |||||
Db 11 TGCATCGACGCGGGGG 28
   |||||

RESULT 7
AX194488
LOCUS AX194488 19 bp DNA linear PAT 28-AUG-2001
DEFINITION Sequence 88 from Patent WO0151500.
ACCESSION AX194488
VERSION AX194488.1 GI:15385144
KEYWORDS synthetic construct
SOURCE synthetic construct
          artificial sequences.
REFERENCE
AUTHORS Klinman, D., Ishii, K. and Verthelyi, D.
TITLE Oligodeoxynucleotide and its use to induce an immune response
JOURNAL Patent: WO 0151500-A 88 19-JUL-2001;
          Secretary of the Department of Health and Human Services (US)
FEATURES
source
1. .19
   /organism="synthetic construct"
   /mol_type="unassigned DNA"
   /db_xref="taxon:32630"
   /note="Synthetic DNA"
ORIGIN
Query Match 94.4%; Score 17; DB 6; Length 19;
Best Local Similarity 100.0%; Pred. No. 9.6e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGCATCGACGCGGGGG 17
   |||||
Db 3 TGCATCGACGCGGGGG 19
   |||||

RESULT 8
AX465438
LOCUS AX465438 19 bp DNA linear PAT 16-JUL-2002
DEFINITION Sequence 106 from Patent WO0211761.
ACCESSION AX465438
VERSION AX465438.1 GI:21899801
KEYWORDS synthetic construct
SOURCE synthetic construct
          artificial sequences.
REFERENCE
AUTHORS Mond, J.J., Flora, M. and Klinman, D.M.
TITLE Immunostimulatory rna/dna hybrid molecules
JOURNAL Patent: WO 0193902-A 513 13-DEC-2001;
          Biosynexus Incorporated (US)
FEATURES
source
1. .18
   /organism="synthetic construct"
   /mol_type="unassigned DNA"
   /db_xref="taxon:32630"
   /note="Synthetic HDR"
ORIGIN
Query Match 91.1%; Score 16.4; DB 6; Length 18;
Best Local Similarity 94.4%; Pred. No. 2e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TGCATCGACGCGGGGG 18
   |||||
Db 1 TGCATCGATCGCGGGGG 18
   |||||

RESULT 10
AX352217
LOCUS AX352217 18 bp DNA linear PAT 06-FEB-2002
DEFINITION Sequence 513 from Patent WO0193902.
ACCESSION AX352217
VERSION AX352217.1 GI:18617500
KEYWORDS synthetic construct
SOURCE synthetic construct
          artificial sequences.
ORGANISM synthetic construct
          artificial sequences.
REFERENCE
AUTHORS Mond, J.J., Flora, M. and Klinman, D.M.
TITLE Immunostimulatory rna/dna hybrid molecules
JOURNAL Patent: WO 0193902-A 513 13-DEC-2001;
          Biosynexus Incorporated (US)
FEATURES
source
1. .18
   /organism="synthetic construct"
   /mol_type="unassigned DNA"
   /db_xref="taxon:32630"
   /note="Synthetic HDR"
ORIGIN
Query Match 94.4%; Score 16.4; DB 6; Length 18;
Best Local Similarity 94.4%; Pred. No. 2e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TGCATCGACGCGGGGG 18
   |||||
Db 1 TGCATCGATCGCGGGGG 18
   |||||
```

```
REFERENCE
AUTHORS Mond, J.J., Prince, G. and Klinman, D.M.
JOURNAL Vaccine against RSV
          Patent: WO 0211761-A 106 14-FEB-2002;
          HENRY M. JACKSON FOUNDATION FOR THE ADVANCEMENT OF MILITARY
          MEDICINE (US)
FEATURES
source
1. .19
   /organism="synthetic construct"
   /mol_type="unassigned DNA"
   /db_xref="taxon:32630"
   /note="Synthetic oligonucleotide"
ORIGIN
Query Match 94.4%; Score 17; DB 6; Length 19;
Best Local Similarity 100.0%; Pred. No. 9.6e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGCATCGACGCGGGGG 17
   |||||
Db 3 TGCATCGACGCGGGGG 19
   |||||

RESULT 9
AX352207
LOCUS AX352207 18 bp DNA linear PAT 06-FEB-2002
DEFINITION Sequence 503 from Patent WO0193902.
ACCESSION AX352207
VERSION AX352207.1 GI:18617490
KEYWORDS synthetic construct
SOURCE synthetic construct
          artificial sequences.
REFERENCE
AUTHORS Mond, J.J., Flora, M. and Klinman, D.M.
JOURNAL Immunostimulatory rna/dna hybrid molecules
          Patent: WO 0193902-A 503 13-DEC-2001;
          Biosynexus Incorporated (US)
FEATURES
source
1. .18
   /organism="synthetic construct"
   /mol_type="unassigned DNA"
   /db_xref="taxon:32630"
   /note="Synthetic HDR"
ORIGIN
Query Match 91.1%; Score 16.4; DB 6; Length 18;
Best Local Similarity 94.4%; Pred. No. 2e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TGCATCGACGCGGGGG 18
   |||||
Db 1 TGCATCGATCGCGGGGG 18
   |||||

RESULT 10
AX352217
LOCUS AX352217 18 bp DNA linear PAT 06-FEB-2002
DEFINITION Sequence 513 from Patent WO0193902.
ACCESSION AX352217
VERSION AX352217.1 GI:18617500
KEYWORDS synthetic construct
SOURCE synthetic construct
          artificial sequences.
ORGANISM synthetic construct
          artificial sequences.
REFERENCE
AUTHORS Mond, J.J., Flora, M. and Klinman, D.M.
JOURNAL Immunostimulatory rna/dna hybrid molecules
          Patent: WO 0193902-A 513 13-DEC-2001;
          Biosynexus Incorporated (US)
FEATURES
source
1. .18
   /organism="synthetic construct"
   /mol_type="unassigned DNA"
   /db_xref="taxon:32630"
   /note="Synthetic HDR"
ORIGIN
Query Match 91.1%; Score 16.4; DB 6; Length 18;
Best Local Similarity 94.4%; Pred. No. 2e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TGCATCGACGCGGGGG 18
   |||||
Db 1 TGCATCGATCGCGGGGG 18
   |||||
```

/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic HDR"

ORIGIN

Query Match 91.1%; Score 16.4; DB 6; Length 18;
Best Local Similarity 94.4%; Pred. No. 2e+03; 1; Indels 0; Gaps 0;
Matches 17; Conservative 0; Mismatches 0;

QY 1 TGCATCGACGACGAGGGGG 18
|||||
Db 1 TGCATCGATGCAGGGGG 18

RESULT 11

AX352255
LOCUS AX352255 18 bp DNA linear PAT 06-FEB-2002
DEFINITION Sequence 551 from Patent WO0193902.
ACCESSION AX352255
VERSION AX352255.1 GI:18617538

QY 1 TGCATCGACGACGAGGGGG 18
|||||
Db 1 TGCATCGATGCAGGGGG 18

SOURCE
ORGANISM
KEYWORDS
synthetic construct
synthetic construct
artificial sequences.

REFERENCE

1 Mord, J.J., Floxa, M. and Klimman, D.M.
AUTHORS
TITLE Immunostimulatory rna/dna hybrid molecules
JOURNAL Patent: WO 0193902-A 551 13-DEC-2001;
Biosynexus Incorporated (US)

FEATURES

source
1..18
Location/Qualifiers
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic HDR"

ORIGIN

Query Match 91.1%; Score 16.4; DB 6; Length 18;
Best Local Similarity 94.4%; Pred. No. 2e+03; 1; Indels 0; Gaps 0;
Matches 17; Conservative 0; Mismatches 0;

QY 1 TGCATCGACGACGAGGGGG 18
|||||
Db 1 TGCATCGATGCAGGGGG 18

RESULT 12

AX194432
LOCUS AX194432 20 bp DNA linear PAT 28-AUG-2001
DEFINITION Sequence 32 from Patent WO0151500.
ACCESSION AX194432
VERSION AX194432.1 GI:15385088

QY 1 TGCATCGACGACGAGGGGG 18
|||||
Db 1 TGCATCGATGCAGGGGG 18

SOURCE
ORGANISM
KEYWORDS
synthetic construct
synthetic construct
artificial sequences.

REFERENCE

1 Klimman, D., Ishii, K. and Verthelyi, D.
AUTHORS
TITLE Oligodeoxynucleotide and its use to induce an immune response
JOURNAL Patent: WO 0151500-A 32 19-JUL-2001;
Secretary of the Department of Health and Human Services (US)

FEATURES

source
1..20
Location/Qualifiers
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic HDR"

ORIGIN

Query Match 91.1%; Score 16.4; DB 6; Length 20;
Best Local Similarity 94.4%; Pred. No. 1.9e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TGCATCGACGACGAGGGGG 18
|||||
Db 3 TGCATCGATGCAGGGGG 20

RESULT 13

AX194434
LOCUS AX194434 20 bp DNA linear PAT 28-AUG-2001
DEFINITION Sequence 34 from Patent WO0151500.
ACCESSION AX194434
VERSION AX194434.1 GI:15385090

QY 1 TGCATCGACGACGAGGGGG 18
|||||
Db 3 TGCATCGATGCAGGGGG 20

SOURCE
ORGANISM
KEYWORDS
synthetic construct
synthetic construct
artificial sequences.

REFERENCE

1 Klimman, D., Ishii, K. and Verthelyi, D.
AUTHORS
TITLE Oligodeoxynucleotide and its use to induce an immune response
JOURNAL Patent: WO 0151500-A 34 19-JUL-2001;
Secretary of the Department of Health and Human Services (US)

FEATURES

source
1..20
Location/Qualifiers
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic DNA"

ORIGIN

Query Match 91.1%; Score 16.4; DB 6; Length 20;
Best Local Similarity 94.4%; Pred. No. 1.9e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TGCATCGACGACGAGGGGG 18
|||||
Db 3 TGCATCGATGCAGGGGG 20

RESULT 14

AX194437
LOCUS AX194437 20 bp DNA linear PAT 28-AUG-2001
DEFINITION Sequence 37 from Patent WO0151500.
ACCESSION AX194437
VERSION AX194437.1 GI:15385093

QY 1 TGCATCGACGACGAGGGGG 18
|||||
Db 3 TGCATCGATGCAGGGGG 20

SOURCE
ORGANISM
KEYWORDS
synthetic construct
synthetic construct
artificial sequences.

REFERENCE

1 Klimman, D., Ishii, K. and Verthelyi, D.
AUTHORS
TITLE Oligodeoxynucleotide and its use to induce an immune response
JOURNAL Patent: WO 0151500-A 37 19-JUL-2001;
Secretary of the Department of Health and Human Services (US)

FEATURES

source
1..20
Location/Qualifiers
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic DNA"

ORIGIN

Query Match 91.1%; Score 16.4; DB 6; Length 20;
Best Local Similarity 94.4%; Pred. No. 1.9e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TGCATCGACGACGAGGGGG 18
|||||
Db 3 TGCATCGATGCAGGGGG 20

RESULT 15

AX194438
LOCUS AX194438 20 bp DNA linear PAT 28-AUG-2001
DEFINITION Sequence 38 from Patent WO0151500.

```

ACCESSION AX194438
VERSION AX194438.1 GI:15385094
KEYWORDS
SOURCE Synthetic construct
ORGANISM Synthetic construct
          artificial sequences.
REFERENCE 1
AUTHORS Klinman,D., Ishii,K. and Verthelyi,D.
TITLE Oligodeoxynucleotide and its use to induce an immune response
JOURNAL Patent: WO 0151500-A 38 19-JUL-2001;
        Secretary of the Department of Health and Human Services (US)
FEATURES
    source
        1..20
            /organism="Synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"
            /note="Synthetic DNA"
ORIGIN

Query Match          91.1%; Score 16.4; DS 6; Length 20;
Best Local Similarity 94.4%; Pred. No. 1.9e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TGCATCGACGCGGGGG 18
    ||||| ||||| |||||
Db 3 TGCATCGATCGCGGGGG 20

Search completed: July 2, 2004, 10:08:10
Job time : 633.732 secs

```


GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 2, 2004, 07:38:45 ; Search time 1348.02 seconds
(without alignments)
398.746 Million cell updates/sec

Title: US-10-068-160-19

Perfect score: 18

Sequence: 1 tgcacgcagcagggggg 18

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: em_estba:*

2: em_esthum:*

3: em_estin:*

4: em_estmu:*

5: em_estov:*

6: em_estpl:*

7: em_estro:*

8: em_htc:*

9: gb_est1:*

10: gb_est2:*

11: gb_htc:*

12: gb_est3:*

13: gb_est4:*

14: gb_est5:*

15: em_estfun:*

16: em_estom:*

17: em_gss_hum:*

18: em_gss_inv:*

19: em_gss_pln:*

20: em_gss_vrt:*

21: em_gss_fun:*

22: em_gss_mam:*

23: em_gss_mus:*

24: em_gss_pro:*

25: em_gss_rod:*

26: em_gss_phg:*

27: em_gss_vrl:*

28: gb_gss1:*

29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	16.4	91.1	240	9	AV281636
2	16.4	91.1	257	9	AV268287
3	16.4	91.1	303	9	AV269637
4	16.4	91.1	410	28	AQ831712

5	16.4	91.1	593	12	EG853689
6	16.4	91.1	878	29	CG225411
7	16.4	91.1	888	29	CG458305
8	16.4	91.1	960	29	CG225423
9	16.4	91.1	980	29	CG655225
10	15.4	85.6	246	9	AV253772
11	15.4	85.6	355	13	BX566321
12	15.4	85.6	435	14	N91570
13	15.4	85.6	468	23	CG714924
14	15.4	85.6	473	12	BI507147
15	15.4	85.6	504	9	AI812904
16	15.4	85.6	523	28	AZ573909
17	15.4	85.6	524	28	AZ569840
18	15.4	85.6	554	14	CD216827
19	15.4	85.6	570	28	AZ568729
20	15.4	85.6	572	13	BX783110
21	15.4	85.6	572	13	BZ931640
22	15.4	85.6	574	14	CB186390
23	15.4	85.6	622	29	CE347538
24	15.4	85.6	709	14	CB031270
25	15.4	85.6	713	14	CB025221
26	15.4	85.6	807	13	CA101677
27	15.4	85.6	944	29	CNS02PE3
28	15.4	85.6	957	29	CG460886
29	15.4	85.6	971	29	CNS02WQO
30	15.4	85.6	1003	13	BQ708058
31	15.4	85.6	1011	29	CG460924
32	15.4	85.6	1207	12	BG722803
33	15.4	85.6	1522	10	AW729951
34	15	83.3	452	29	CG726899
35	15	83.3	480	29	CG721957
36	15	83.3	530	14	CB368184
37	15	83.3	572	12	BM175141
38	15	83.3	614	14	CD886393
39	15	83.3	687	14	CB026323
40	15	83.3	1147	9	AV715321
41	14.8	82.2	202	9	AV268789
42	14.8	82.2	228	10	BB016918
43	14.8	82.2	232	9	AV255944
44	14.8	82.2	245	9	AV256921
45	14.8	82.2	245	10	AW325275

ALIGNMENTS

RESULT 1
AV281636
LOCUS
DEFINITION
AV281636 RIKEN full-length enriched, adult male testis (DH10B) Mus musculus CDNA clone 4933425J05 3', mRNA sequence.
AV281636.1 GI:6269673
EST.
ACCSSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Mus musculus (house mouse)
REFERENCE
AUTHORS

AV281636 RIKEN full-length enriched, adult male testis (DH10B) Mus musculus CDNA clone 4933425J05 3', mRNA sequence.
AV281636.1 GI:6269673
EST.
ACCSSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Mus musculus (house mouse)
REFERENCE
AUTHORS
Konno, H., Aizawa, K., Akahira, S., Akiyama, J., Carninci, P., Endo, T., Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N., Hirozane, T., Hori, T., Ishii, Y., Ishikawa, T., Itoh, M., Izawa, M., Kadota, K., Kagawa, I., Kai, C., Kawai, J., Kikuchi, N., Kojima, Y., Koya, S., Kusakabe, M., Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y., Owa, C., Ozawa, Y., Saico, H., Sano, M., Sato, K., Shibata, K., Shibata, Y., Shigemoto, Y., Shiraki, T., Sogabe, Y., Sugahara, Y., Tsunoda, Y., Watahiki, A., Watanabe, S., Yamamura, T., Yasunishi, A., Yokota, T., Yoshiki, A., Yoshino, M., Muramatsu, M. and Hayashizaki, Y. RIKEN Mouse ESTs (Konno, H., et al. 1999)
Unpublished (1999)
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic

```

FEATURES
  source
    Location/Qualifiers
      1..19
        /organism="synthetic construct"
        /mol_type="unassigned DNA"
        /db_xref="taxon:32630"
        /note="Synthetic DNA"
ORIGIN
  Query Match
  Best Local Similarity 94.4%; Score 17; DB 6; Length 19;
  Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
  QY 1 TGC GCGGATG CAGGGGG 17
  Db 3 TGC GCGGATG CAGGGGG 19
RESULT 2
  LOCUS
  DEFINITION Sequence 94 from Patent WO0211761.
  ACCESSION AX465426
  VERSION AX465426.1 GI:21899789
  KEYWORDS
  SOURCE
  ORGANISM
    synthetic construct
    artificial sequences.
  REFERENCE
  1
  AUTHORS Mond J.J., Prince G. and Klinman, D.M.
  TITLE Vaccine against RSV
  JOURNAL HENRY M. JACKSON FOUNDATION FOR THE ADVANCEMENT OF MILITARY
  MEDICINE (US)
  Location/Qualifiers
    1..19
      /organism="synthetic construct"
      /mol_type="unassigned DNA"
      /db_xref="taxon:32630"
      /note="Synthetic oligonucleotide"
FEATURES
  source
    Location/Qualifiers
      1..19
        /organism="synthetic construct"
        /mol_type="unassigned DNA"
        /db_xref="taxon:32630"
        /note="Synthetic oligonucleotide"
ORIGIN
  Query Match
  Best Local Similarity 94.4%; Score 17; DB 6; Length 19;
  Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
  QY 1 TGC GCGGATG CAGGGGG 17
  Db 3 TGC GCGGATG CAGGGGG 19
RESULT 3
  LOCUS
  DEFINITION Sequence 40 from Patent WO0151500.
  ACCESSION AX194440
  VERSION AX194440.1 GI:15385096
  KEYWORDS
  SOURCE
  ORGANISM
    synthetic construct
    artificial sequences.
  REFERENCE
  1
  AUTHORS Klinman, D., Ishii, K. and Verthelyi, D.
  TITLE Oligodeoxynucleotide and its use to induce an immune response
  JOURNAL Patent: WO 0151500-A 40 19-JUL-2001;
  SECRETARY Secretary of the Department of Health and Human Services (US)
  Location/Qualifiers
    1..20
      /organism="synthetic construct"
      /mol_type="unassigned DNA"
      /db_xref="taxon:32630"
      /note="Synthetic DNA"
FEATURES
  source
    Location/Qualifiers
      1..20
        /organism="synthetic construct"
        /mol_type="unassigned DNA"
        /db_xref="taxon:32630"
        /note="Synthetic DNA"
ORIGIN
  Query Match
  Best Local Similarity 94.4%; Score 17; DB 6; Length 19;
  Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
  QY 1 TGC GCGGATG CAGGGGG 17
  Db 3 TGC GCGGATG CAGGGGG 19
RESULT 4
  LOCUS
  DEFINITION Sequence 81 from Patent WO0151500.
  ACCESSION AX194481
  VERSION AX194481.1 GI:15385137
  KEYWORDS
  SOURCE
  ORGANISM
    synthetic construct
    artificial sequences.
  REFERENCE
  1
  AUTHORS Klinman, D., Ishii, K. and Verthelyi, D.
  TITLE Oligodeoxynucleotide and its use to induce an immune response
  JOURNAL Patent: WO 0151500-A 81 19-JUL-2001;
  SECRETARY Secretary of the Department of Health and Human Services (US)
  Location/Qualifiers
    1..20
      /organism="synthetic construct"
      /mol_type="unassigned DNA"
      /db_xref="taxon:32630"
      /note="Synthetic DNA"
FEATURES
  source
    Location/Qualifiers
      1..20
        /organism="synthetic construct"
        /mol_type="unassigned DNA"
        /db_xref="taxon:32630"
        /note="Synthetic DNA"
ORIGIN
  Query Match
  Best Local Similarity 94.4%; Score 16.4; DB 6; Length 20;
  Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
  QY 1 TGC GCGGATG CAGGGGG 18
  Db 3 TGC GCGGATG CAGGGGG 20
RESULT 5
  LOCUS
  DEFINITION Sequence 82 from Patent WO0151500.
  ACCESSION AX194482
  VERSION AX194482.1 GI:15385138
  KEYWORDS
  SOURCE
  ORGANISM
    synthetic construct
    artificial sequences.
  REFERENCE
  1
  AUTHORS Klinman, D., Ishii, K. and Verthelyi, D.
  TITLE Oligodeoxynucleotide and its use to induce an immune response
  JOURNAL Patent: WO 0151500-A 82 19-JUL-2001;
  SECRETARY Secretary of the Department of Health and Human Services (US)
  Location/Qualifiers
    1..20
      /organism="synthetic construct"
      /mol_type="unassigned DNA"
      /db_xref="taxon:32630"
      /note="Synthetic DNA"
FEATURES
  source
    Location/Qualifiers
      1..20
        /organism="synthetic construct"
        /mol_type="unassigned DNA"
        /db_xref="taxon:32630"
        /note="Synthetic DNA"
ORIGIN
  Query Match
  Best Local Similarity 94.4%; Score 16.4; DB 6; Length 20;
  Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
  QY 1 TGC GCGGATG CAGGGGG 18
  Db 3 TGC GCGGATG CAGGGGG 20

```

```
RESULT 6
AX194501
LOCUS AX194501 20 bp DNA linear PAT 28-AUG-2001
DEFINITION Sequence 101 from Patent WO0151500.
ACCESSION AX194501
VERSION AX194501.1 GI:15385157
KEYWORDS
SOURCE
ORGANISM
synthetic construct
synthetic construct
artificial sequences.
REFERENCE
1
AUTHORS Kliman,D., Ishii,K. and Verthelyi,D.
TITLE Oligodeoxynucleotide and its use to induce an immune response
JOURNAL Patent: WO 0151500-A 101 19-JUL-2001;
Secretary of the Department of Health and Human Services (US)
FEATURES
LOCATION/Qualifiers
1..20
/mol_type="synthetic construct"
/db_xref="taxon:32630"
/note="Synthetic DNA"
ORIGIN
Query Match 91.1%; Score 16.4; DB 6; Length 20;
Best Local Similarity 94.4%; Pred. No. 2.2e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 TGCAGCGATGCGAGGGGG 18
||| ||||| ||||| |||||
Db 3 TGCAGCGATGCGAGGGGG 20
RESULT 7
AX352203
LOCUS AX352203 20 bp DNA linear PAT 06-FEB-2002
DEFINITION Sequence 499 from Patent WO0193902.
ACCESSION AX352203
VERSION AX352203.1 GI:18617486
KEYWORDS
SOURCE
ORGANISM
synthetic construct
synthetic construct
artificial sequences.
REFERENCE
1
AUTHORS Mond,J.J., Flora,M. and Klinman,D.M.
TITLE Immunostimulatory rna/dna hybrid molecules
JOURNAL Patent: WO 0193902-A 499 13-DEC-2001;
Biosynexus Incorporated (US)
FEATURES
LOCATION/Qualifiers
1..20
/mol_type="synthetic construct"
/db_xref="taxon:32630"
/note="Synthetic HDR"
ORIGIN
Query Match 91.1%; Score 16.4; DB 6; Length 20;
Best Local Similarity 94.4%; Pred. No. 2.2e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 TGCAGCGATGCGAGGGGG 18
||| ||||| ||||| |||||
Db 3 TGCAGCGATGCGAGGGGG 20
RESULT 8
AX352214
LOCUS AX352214 20 bp DNA linear PAT 06-FEB-2002
DEFINITION Sequence 510 from Patent WO0193902.
ACCESSION AX352214
VERSION AX352214.1 GI:18617497
KEYWORDS
SOURCE
ORGANISM
synthetic construct
synthetic construct
artificial sequences.
REFERENCE
1
AUTHORS Mond,J.J., Prince,G. and Klinman,D.M.
TITLE Vaccine against RSV
JOURNAL Patent: WO 0211761-A 58 14-FEB-2002;
HENRY M. JACKSON FOUNDATION FOR THE ADVANCEMENT OF MILITARY
MEDICINE (US)
FEATURES
LOCATION/Qualifiers
1..20
/mol_type="synthetic construct"
/db_xref="taxon:32630"
/note="Synthetic HDR"
ORIGIN
Query Match 91.1%; Score 16.4; DB 6; Length 20;
Best Local Similarity 94.4%; Pred. No. 2.2e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 TGCAGCGATGCGAGGGGG 18
||| ||||| ||||| |||||
Db 3 TGCAGCGATGCGAGGGGG 20
RESULT 9
AX352247
LOCUS AX352247 20 bp DNA linear PAT 06-FEB-2002
DEFINITION Sequence 543 from Patent WO0193902.
ACCESSION AX352247
VERSION AX352247.1 GI:18617530
KEYWORDS
SOURCE
ORGANISM
synthetic construct
synthetic construct
artificial sequences.
REFERENCE
1
AUTHORS Mond,J.J., Flora,M. and Klinman,D.M.
TITLE Immunostimulatory rna/dna hybrid molecules
JOURNAL Patent: WO 0193902-A 543 13-DEC-2001;
Biosynexus Incorporated (US)
FEATURES
LOCATION/Qualifiers
1..20
/mol_type="synthetic construct"
/db_xref="taxon:32630"
/note="Synthetic HDR"
ORIGIN
Query Match 91.1%; Score 16.4; DB 6; Length 20;
Best Local Similarity 94.4%; Pred. No. 2.2e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 TGCAGCGATGCGAGGGGG 18
||| ||||| ||||| |||||
Db 3 TGCAGCGATGCGAGGGGG 20
RESULT 10
AX465390
LOCUS AX465390 20 bp DNA linear PAT 16-JUL-2002
DEFINITION Sequence 58 from Patent WO0211761.
ACCESSION AX465390
VERSION AX465390.1 GI:21899753
KEYWORDS
SOURCE
ORGANISM
synthetic construct
synthetic construct
artificial sequences.
REFERENCE
1
AUTHORS Mond,J.J., Prince,G. and Klinman,D.M.
TITLE Vaccine against RSV
JOURNAL Patent: WO 0211761-A 58 14-FEB-2002;
HENRY M. JACKSON FOUNDATION FOR THE ADVANCEMENT OF MILITARY
MEDICINE (US)
FEATURES
LOCATION/Qualifiers
1..20
/mol_type="synthetic construct"
/db_xref="taxon:32630"
/note="Synthetic HDR"
ORIGIN
Query Match 91.1%; Score 16.4; DB 6; Length 20;
Best Local Similarity 94.4%; Pred. No. 2.2e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 TGCAGCGATGCGAGGGGG 18
||| ||||| ||||| |||||
Db 3 TGCAGCGATGCGAGGGGG 20
```

```
artificial sequences.
REFERENCE
1
AUTHORS Mond,J.J., Flora,M. and Klinman,D.M.
TITLE Immunostimulatory rna/dna hybrid molecules
JOURNAL Patent: WO 0193902-A 510 13-DEC-2001;
Biosynexus Incorporated (US)
FEATURES
LOCATION/Qualifiers
1..20
/mol_type="synthetic construct"
/db_xref="taxon:32630"
/note="Synthetic HDR"
ORIGIN
Query Match 91.1%; Score 16.4; DB 6; Length 20;
Best Local Similarity 94.4%; Pred. No. 2.2e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 TGCAGCGATGCGAGGGGG 18
||| ||||| ||||| |||||
Db 3 TGCAGCGATGCGAGGGGG 20
RESULT 9
AX352247
LOCUS AX352247 20 bp DNA linear PAT 06-FEB-2002
DEFINITION Sequence 543 from Patent WO0193902.
ACCESSION AX352247
VERSION AX352247.1 GI:18617530
KEYWORDS
SOURCE
ORGANISM
synthetic construct
synthetic construct
artificial sequences.
REFERENCE
1
AUTHORS Mond,J.J., Flora,M. and Klinman,D.M.
TITLE Immunostimulatory rna/dna hybrid molecules
JOURNAL Patent: WO 0193902-A 543 13-DEC-2001;
Biosynexus Incorporated (US)
FEATURES
LOCATION/Qualifiers
1..20
/mol_type="synthetic construct"
/db_xref="taxon:32630"
/note="Synthetic HDR"
ORIGIN
Query Match 91.1%; Score 16.4; DB 6; Length 20;
Best Local Similarity 94.4%; Pred. No. 2.2e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 TGCAGCGATGCGAGGGGG 18
||| ||||| ||||| |||||
Db 3 TGCAGCGATGCGAGGGGG 20
RESULT 10
AX465390
LOCUS AX465390 20 bp DNA linear PAT 16-JUL-2002
DEFINITION Sequence 58 from Patent WO0211761.
ACCESSION AX465390
VERSION AX465390.1 GI:21899753
KEYWORDS
SOURCE
ORGANISM
synthetic construct
synthetic construct
artificial sequences.
REFERENCE
1
AUTHORS Mond,J.J., Prince,G. and Klinman,D.M.
TITLE Vaccine against RSV
JOURNAL Patent: WO 0211761-A 58 14-FEB-2002;
HENRY M. JACKSON FOUNDATION FOR THE ADVANCEMENT OF MILITARY
MEDICINE (US)
FEATURES
LOCATION/Qualifiers
1..20
/mol_type="synthetic construct"
/db_xref="taxon:32630"
/note="Synthetic HDR"
ORIGIN
Query Match 91.1%; Score 16.4; DB 6; Length 20;
Best Local Similarity 94.4%; Pred. No. 2.2e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 TGCAGCGATGCGAGGGGG 18
||| ||||| ||||| |||||
Db 3 TGCAGCGATGCGAGGGGG 20
```

/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic oligonucleotide"

ORIGIN

Query Match 91.1%; Score 16.4; DB 6; Length 20;
Best Local Similarity 94.4%; Pred. No. 2.2e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TCGCCCGATGCAGGGGG 18
||| ||||| ||||| |||||
Db 3 TCGTCGATGCAGGGGG 20

RESULT 11
AX465431
LOCUS AX465431 20 bp DNA linear PAT 16-JUL-2002
DEFINITION Sequence 99 from Patent WO0211761.
ACCESSION AX465431
VERSION AX465431.1 GI:21899794
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.

REFERENCE 1
AUTHORS Mond, J.J., Prince, G. and Klinman, D.M.
TITLE Vaccine against RSV
JOURNAL Patent: WO 0211761-A 99 14-FEB-2002;
HENRY M. JACKSON FOUNDATION FOR THE ADVANCEMENT OF MILITARY
MEDICINE (US)
FEATURES Location/Qualifiers
source 1..20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic oligonucleotide"

ORIGIN

Query Match 91.1%; Score 16.4; DB 6; Length 20;
Best Local Similarity 94.4%; Pred. No. 2.2e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic oligonucleotide"

Qy 1 TCGCCCGATGCAGGGGG 18
||| ||||| ||||| |||||
Db 3 TCGTCGATGCAGGGGG 20

RESULT 12
AX465432
LOCUS AX465432 20 bp DNA linear PAT 16-JUL-2002
DEFINITION Sequence 100 from Patent WO0211761.
ACCESSION AX465432
VERSION AX465432.1 GI:21899795
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.

REFERENCE 1
AUTHORS Mond, J.J., Prince, G. and Klinman, D.M.
TITLE Vaccine against RSV
JOURNAL Patent: WO 0211761-A 100 14-FEB-2002;
HENRY M. JACKSON FOUNDATION FOR THE ADVANCEMENT OF MILITARY
MEDICINE (US)
FEATURES Location/Qualifiers
source 1..20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic oligonucleotide"

ORIGIN

Query Match 91.1%; Score 16.4; DB 6; Length 20;
Best Local Similarity 94.4%; Pred. No. 2.2e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic oligonucleotide"

Best Local Similarity 94.4%; Pred. No. 2.2e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TCGCCCGATGCAGGGGG 18
||| ||||| ||||| |||||
Db 3 TCGTCGATGCAGGGGG 20

RESULT 13
AX352224
LOCUS AX352224 28 bp DNA linear PAT 06-FEB-2002
DEFINITION Sequence 520 from Patent WO0193902.
ACCESSION AX352224
VERSION AX352224.1 GI:18617507
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.

REFERENCE 1
AUTHORS Mond, J.J., Flora, M. and Klinman, D.M.
TITLE Immunostimulatory rna/dna hybrid molecules
JOURNAL Patent: WO 0193902-A 520 13-DEC-2001;
Biosynexus Incorporated (US)
FEATURES Location/Qualifiers
source 1..28
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic HDR"

ORIGIN

Query Match 91.1%; Score 16.4; DB 6; Length 28;
Best Local Similarity 94.4%; Pred. No. 2.1e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TCGCCCGATGCAGGGGG 18
||| ||||| ||||| |||||
Db 3 TGCACGATGCAGGGGG 20

RESULT 14
AX352236
LOCUS AX352236 28 bp DNA linear PAT 06-FEB-2002
DEFINITION Sequence 532 from Patent WO0193902.
ACCESSION AX352236
VERSION AX352236.1 GI:18617519
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.

REFERENCE 1
AUTHORS Mond, J.J., Flora, M. and Klinman, D.M.
TITLE Immunostimulatory rna/dna hybrid molecules
JOURNAL Patent: WO 0193902-A 532 13-DEC-2001;
Biosynexus Incorporated (US)
FEATURES Location/Qualifiers
source 1..28
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic HDR"

ORIGIN

Query Match 91.1%; Score 16.4; DB 6; Length 28;
Best Local Similarity 94.4%; Pred. No. 2.1e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TCGCCCGATGCAGGGGG 18
||| ||||| ||||| |||||
Db 11 TGCACGATGCAGGGGG 28

RESULT 15

```

/db xref="GI:21111652"
/translation="MALIEGFRVRYNRALRDIITGLRLSAEQEQDPLTPTFTVVIKNGYV
GKSTLPDAPQFVADCLSKSVESADCDQKGGPERMSLGTSEISIRDIYVREAKGERVS
ITYELAINDSRGPVSEVELKQRKGOKGHRPYPLRLHCHGVKVGWAGEARVETSS
GEDRQAEDELTLQALGTALGTLKEHPIKRFEDLKGWHLSEVHPDSARSIPSA
GAORHLDVHGENIGNVQYMERHKKERFKTILDRIAAKIPGVHSIRITVTQDKRVLIQ
FNGAFNDPIAGQSDGTLKIPAYLULLMEDPEPPFICIEBPENGLHRLDLSLASE
LRSHAGXKNAPQIFVYTHQPIYFDVALSTKEVWILBKXNGFSTICRASDIDLRVNLV
EELGPIGLGWYGDYLDTK"
complement(1664..2089)
/gene="holc"
/notes="holc"
complement(1664..2089)
/gene="holc"
/notes="identified by sequence similarity; putative; ORF
located using Blastx/Glimmer/Genemark"
/codon_start=1
/transl_table=11
/product="DNA polymerase III holoenzyme chi subunit"
/protein_id="AAM39964.1"
/db xref="GI:21111653"
/translation="MPRAFDYIAIKRPFIDELPRLVCELARKANDANLSTLILARDA
QACDLRLWADDEAYVPHQJADEDELAPVLIIATPEFAAPRPLVNLRDDPYL
GACDRVLEVPADPAAREPLRBRKQYKALGLELATYDM"
complement(2204..3685)
/gene="pepa"
/notes="synonyms: XCC0649, xerB, carP"
complement(2204..3685)
/gene="pepa"
/notes="identified by sequence similarity; putative; ORF
located using Blastx/Glimmer/Genemark"
/codon_start=1
/transl_table=11
/product="aminopeptidase A/I"
/protein_id="AAM39965.1"
/db xref="GI:21111654"
/translation="NALQFTLNQDAPASAHVDCIYVGAFADKTLSPAQAQLDSAQGR
LTALVARGDVATKGTITSLVHDLPGVQAPRLVWGLGDAAKFGVAPYLKAIQDAARAL
KTGPICTALLITELPVRKARDAAWNIROAVIVSDHAAYRYATLGGKVKDDTGLATLA
IAGDDARALVGATIAEGVFAEELGNLPPNVCCTPAYLAETATAAENGKFPGBAEILLD
EQOMALCHGSLLSVARGSANRPRLIIVLKNWGGGEARPYVVGKGITFDGCVNLKTKQ
GKIENKIDMCGANVIGTIVATYKAEPLINLVVVVPAVENAIDGNAYRPSDVIITMS
GXTIEVNTDAGEBRLICDALTYAEERPEALVDVATLTGACMVALGHQTACGLMSKSH
DANELLAGEHVPRVWRLPLWDBYQGLDSTPADVYNIIGRWGGAITAGCFLSRFT
ENORWHLIDAGVASDEGRKGMATCRPVCLLTQWLLDRAEGN"
3793..4875
/gene="XCC0650"
3793..4875
/gene="XCC0650"
/notes="identified by sequence similarity; putative; ORF
located using Blastx/Glimmer/Genemark"
/codon_start=1
/transl_table=11
/product="conserved hypothetical protein"
/protein_id="AAM39966.1"
/db xref="GI:21111655"
/translation="MPKDRYLLSDFTQSLFIATLIVLWVSGVVLVDILGNADGRI
PARLLSVQGLQFVAYLPILPIALMLGLALALRYLVDSEMAVITAIIGIPRMLRP
ILWLVVYVTVGACSLWGPWASTAEMLLEDANRYSVMAGLSEKGTPLSGGGVYV
LTTIPDCKGKGLKPMQCKDORIDVTAERGAMPECKTDYRLPLEDGRLEGCPAGA
CGLDYELMTPASNDVMDRYKAHDANDPVMWSFKLIGDARPTABELHRLRAPPLL
ALAPALLTLPUSRAPQQRIGRIKMLLAYLVNLMIVGTQWITANGKVPGLAUGLW
LTPLPLVASINWAYARDGRLSRPRA"
4872..5978
/gene="XCC0651"
4872..5978
/gene="XCC0651"
/notes="identified by sequence similarity; putative; ORF
located using Blastx/Glimmer/Genemark"
/codon_start=1
/transl_table=11
/product="conserved hypothetical protein"
/protein_id="AAM39967.1"

```

```

/db xref="GI:21111652"
/translation="MALIEGFRVRYNRALRDIITGLRLSAEQEQDPLTPTFTVVIKNGYV
GKSTLPDAPQFVADCLSKSVESADCDQKGGPERMSLGTSEISIRDIYVREAKGRVS
ITYELAINDDSSRPVSEVIELKQRKGOKGHRPYPLRLHCHGVKVGWAGEARVETS
GEDRAGDEVELTDLQGLATIGTLKEHPIKRFEDLKGWHLSEVHPDSARSIPSA
GAORHLDVHGENIGNVQYMERHKKERFKTILDRIAAKIPGVHSIRITVTQDKRVLIQ
FNGAFNDPIAGQSDGTLKIPAYLULLMEDPEPPFICIEBPENGLHRLDLSLASE
LRSHAGXKNAPQIFVYTHQPIYFVDALSTKEVWILBKGNKFSTICRASDIDLRVRLV
EELGPIGLGWYGDYLDTK"
complement(1664..2089)
/gene="holc"
/notes="holc"
complement(1664..2089)
/gene="holc"
/notes="holc"
located using Blastx/Glimmer/Genemark"
/codon_start=1
/transl_table=11
/product="DNA polymerase III holoenzyme chi subunit"
/protein_id="AAM39964.1"
/db xref="GI:21111653"
/translation="MPRAFDYIAIKRPFIDELPRLVCELARKANDANLSTLILARDA
QACDLRLWADDEAYVPHQJADEDELAPVLIIATPEFAAPRPLVNLRDDPYL
GACDRVLEVPADPAAREPLRBRKQYKALGLELATYDM"
complement(2204..3685)
/gene="pepa"
/notes="synonyms: XCC0649, xerB, carP"
complement(2204..3685)
/gene="pepa"
/notes="identified by sequence similarity; putative; ORF
located using Blastx/Glimmer/Genemark"
/codon_start=1
/transl_table=11
/product="aminopeptidase A/I"
/protein_id="AAM39965.1"
/db xref="GI:21111654"
/translation="NALQFTLNQDAPASAHVDCIYVGAFADKTLSPAQAQLDSAQGR
LTALVARGDVATKGTITSLVHDLPGVQAPRLVWGLGDAAKFGVAPYLKAIQDAARAL
KTGICITALLITELPVPKARDAAWNIROAVIVSDHAAYRYTATLGKKVDDTGLATLA
IAGDDARALVGATIAEGVFAEELGNLPPNVCCTPAYLAETATAAENGKFPGBAEILLD
EQOMALCHGSLLSVARGSANRPRLIILKNWGGGEARPYVVKGITITDGGVNLKTKQ
GKTEHNYDMCGANVIGTIVATYKAEPLINLVVVVPAVENAIDGNAYRPSDVIITMS
GKTIYVNTDAGEBRLICDALTAYERPEALVDVATLTGACMVALGHQTACGLMSKKH
ENORALLDAGEHVPYRWRLPLWDBYQGLDSTPADVYNIIGRWGGAITAGCFLSRFT
ENORALLDIAGVASDEGRKGMATCRPVCLLTQWLLDRAEGN"
3793..4875
/gene="XCC0650"
3793..4875
/gene="XCC0650"
/notes="identified by sequence similarity; putative; ORF
located using Blastx/Glimmer/Genemark"
/codon_start=1
/transl_table=11
/product="conserved hypothetical protein"
/protein_id="AAM39966.1"
/db xref="GI:21111655"
/translation="MPKDRYLLSDFTQSLATILVLVWSVGGVLDVILGNADGRI
PARLLSVQGVQFVAYLPILPILALMLALALRLYRDSMAVITAIIGIPRMLRP
ILWLVPVYVIGACSLWGPWASTAEMLLEDANRYSVMAGLSEKGTPLSGGGVYV
LTTIPDCKGKGLKPMQCKDORIDVTAERGAMPECKTDYRLPLEDGERLEGCPAGA
CGLDYELMTPASNDVMDRYKAHDANDPVMWSFKLIGDARPTABELHRLRAPPLL
ALAPALLTLPUSRAPQQRIGRIKMLLAYLVLNLMIVGTQMTIANGKVPGLAULMW
LTLPLLAVSINWAYARDGRLSRPRA"
4872..5978
/gene="XCC0651"
4872..5978
/gene="XCC0651"
/notes="identified by sequence similarity; putative; ORF
located using Blastx/Glimmer/Genemark"
/codon_start=1
/transl_table=11
/product="conserved hypothetical protein"
/protein_id="AAM39967.1"

```

```

/db_xref="GI:21111656"
/translation="MKLMPRVDHTVGRVLFVTLTWAVLLGLDVNAPASEKSG
QSSYFGALAVATVYPRRAYLPTTAAGVIGALMGLQLAATSELTALRALGVSRKR
MSAYVAVATVATVWISGETVGPWQASQADTLTSARYQSDMTSARYSGLMWREGD
TFLNALSDEQLLDNGQFALTLHDVLYHLDANGQOQLTYAAAEHREGRTLOVR
RDTFOARSQRETFPELFWQSOLNPKALAGLAKPRLSVHDLGOSIEYRRNGLDAS
DYEDQWSRWFPYPLAVLALCLAAIPFSPGSLRSGGLKRLFLGILFALGFLLQLFFG
RMAGALKDQYRIAYALPFMVLGVSAWLFRRSS"
5756..5310
/gene="XCC0652"
CDS
5756..5310
/gene="XCC0652"
/note="putative; ORF located using Glimmer/Genemark"
/codon_start=1
/transl_table=11
/product="hypothetical protein"
/protein_id="AAM39968.1"
/db_xref="GI:21111657"
/translation="MSGGDPVLRFVVAQRFPQALVPGHPVRAGLLAAAVRTHGRC
AARLPRLICLAAGDAGSLGVVPAQQLMRKRLWSVFLVLCVPAVLIVQCLRW
HDPOVDYKSLVWKQLPVLLQSMVAEGGLTULLGWLFWAYVLMMAAPMFVGLYLLG
KVVEDTIRGHPFWKDAENPGADK"
complement(6518..6985)
/gene="XCC0653"
CDS
complement(6518..6985)
/gene="XCC0653"
/note="identified by sequence similarity; putative; ORF
located using Blastx/Glimmer/Genemark"
/codon_start=1
/transl_table=11
/product="conserved hypothetical protein"
/protein_id="AAM39969.1"
/db_xref="GI:21111658"
/translation="MTSIPAPLTARAPALVGRLLALCYDAMPVLMMMSAGFTLG
FTLAGHPAPSPSGWQWLMCCWIAAGVYATVSWRHGQTLGMEPWRLSLTGPQ
ACWRALWTRYAVGTLALGGVGFWMWMLDRDLTWHDRASQTRLQRIAKPT"
7073..8044
/gene="xerD"
CDS
7073..8044
/note="synonym: XCC0654"
/gene="xerD"
/note="identified by sequence similarity; putative; ORF
located using Blastx/Glimmer/Genemark"
/codon_start=1
/transl_table=11
/product="integrase/recombinase"
/protein_id="AAM39970.1"
/db_xref="GI:21111659"
/translation="MSASPARRQRAQQLPPLRAEDDQAIORFLDLRWAEQGVARQT
LDSYRDLEGARWEDGAGGLQGADRSALFDYLRWTEARYAPRSNARLLSLRGFY
ALCLDGVSDPTALLDPLPRLPKALTESOIDALLAAPELGTPLGLDRAMLEL
MYAGLRVSELVTLPAVALINLRQGLVITGSKERLVPGLSEESCHWLERYLETARPT
LSERKAVPAVDGQVFLFIDAAARRPLSRQQFWGLVRYAAVAGIDPTVSPHGLRHSFA
THLNHGADLRALQMLGHSSLSLTQIYTLVARQHLQTLHARHPRG"
8296..9090

```

```

gene
Query Match          91.1%; Score 16.4; DB 1; Length 13936;
Best Local Similarity 94.4%; Pred No. 1.1e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1  TCGCGCATGCGAGGGGG 18
      |||||
DB     13832  TCGCAGATGCAGGGGG 13849

```

Search completed: July 2, 2004, 10:08:10
Job time : 636.732 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 2, 2004, 06:05:50 ; Search time 134.89 Seconds
(without alignments)
566.887 Million cell updates/sec

Title: US-10-068-160-18

Perfect score: 18

Sequence: 1 tgcgccgacgcagggggg 18

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_29Jan04:*

1: Geneseqn1980s:*

2: Geneseqn1990s:*

3: Geneseqn2000s:*

4: Geneseqn2001as:*

5: Geneseqn2001bs:*

6: Geneseqn2002as:*

7: Geneseqn2003as:*

8: Geneseqn2003bs:*

9: Geneseqn2003cs:*

10: Geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	18	100.0	20	7	ACC48303 CpG oligo
2	17	94.4	19	4	AAC80656 Immunogen
3	17	94.4	19	4	AAS09626 Immunorea
4	17	94.4	19	6	ABK46504 Immunosti
5	16.4	91.1	20	4	AAC80662 Immunogen
6	16.4	91.1	20	4	AAC80661 Immunogen
7	16.4	91.1	20	4	AAC80620 Immunogen
8	16.4	91.1	20	4	AAS09631 Immunorea
9	16.4	91.1	20	4	AAS09590 Immunorea
10	16.4	91.1	20	4	AAS09651 Immunorea
11	16.4	91.1	20	4	AAS09632 Immunorea
12	16.4	91.1	20	6	ABL35573 Immunosti
13	16.4	91.1	20	6	ABL35584 Immunosti
14	16.4	91.1	20	6	ABL35617 Immunosti
15	16.4	91.1	20	6	ABK46510 Immunosti
16	16.4	91.1	20	6	ABK46468 Immunosti
17	16.4	91.1	20	6	ABK46509 Immunosti
18	16.4	91.1	20	7	ACC48311 CpG oligo
19	16.4	91.1	20	7	ACC48298 CpG oligo
20	16.4	91.1	20	7	ACC48312 CpG oligo
21	16.4	91.1	20	7	ACC48306 CpG oligo
22	16.4	91.1	20	7	ACC48319 CpG oligo
23	16.4	91.1	20	8	ACC83116 D class C

24	16.4	91.1	20	8	ACC83117	ACC83117 D class C
25	16.4	91.1	20	8	ACC83124	ACC83124 D class C
26	16.4	91.1	20	9	ADD01050	ADD01050 CpG D oli
27	16.4	91.1	20	9	ADD01059	ADD01059 CpG D oli
28	16.4	91.1	28	6	ABL35594	ABL35594 Immunosti
29	16.4	91.1	28	6	ABL35606	ABL35606 Immunosti
30	15.4	85.6	19	4	AAC80602	AAC80602 Immunogen
31	15.4	85.6	19	4	AAC80653	AAC80653 Immunogen
32	15.4	85.6	19	4	AAS09633	AAS09633 Immunorea
33	15.4	85.6	19	4	AAS09572	AAS09572 Immunorea
34	15.4	85.6	19	6	ABK46450	ABK46450 Immunosti
35	15.4	85.6	19	6	ABK46511	ABK46511 Immunosti
c	36	15.4	675	6	AAS62113	AAS62113 Porcine m
37	15.4	85.6	682	5	AAS77915	AAS77915 DNA encod
38	15.4	85.6	755	3	AAR13360	AAR13360 Aspergill
c	39	15.4	759	9	ADE62051	ADE62051 Rat gene
c	40	15.4	759	9	ADE62051	ADE62051 Rat gene
41	15	83.3	2712	7	ACA26785	ACA26785 Prokaryot
42	14.8	82.2	18	6	ABL35587	ABL35587 Immunosti
43	14.8	82.2	18	6	ABL35577	ABL35577 Immunosti
44	14.8	82.2	18	6	ABL35625	ABL35625 Immunosti
45	14.8	82.2	18	9	ADD01052	ADD01052 CpG D oli

ALIGNMENTS

RESULT 1

ID ACC48303 standard; DNA; 20 BP.

XX

AC ACC48303;

XX

DT 11-AUG-2003 (first entry)

XX

DB CpG oligodeoxynucleotide used for dendritic cell maturation.

XX

KW CpG oligodeoxynucleotide; dendritic cell; tumour; immunotherapy; vaccine; cytostatic; immunostimulant; gene therapy; ss.

XX

OS Synthetic.

XX

PH Key Location/Qualifiers

FT misc_difference 1 /tag= a

FT /note= "N is any base (especially G) or no base"

FT misc_difference 2 /tag= b

FT /note= "N is any base (especially G) or no base"

XX

WO2003020884-A2.

PN

XX

PD 13-MAR-2003.

XX

PF 13-AUG-2002; 2002WO-US025732.

XX

PR 14-AUG-2001; 2001US-0312190P.

XX

PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX

PI Klinman DM, Gursel M, Verthelyi D;

XX

DR WPI; 2003-300874/29.

XX

PT Generating mature dendritic cells for tumor immunotherapy or as vaccines for activating the immune system to treat diseases such as cancer, comprises contacting a dendritic cell precursor with a D type oligodeoxynucleotide.

XX

PS Disclosure; Page 26; 69pp; English.

XX

CC The present sequence is that of a D type CpG oligodeoxynucleotide that is an example of claimed D type oligodeoxynucleotides (see ACC48294) of the

CC invention. Mature dendritic cells are obtained by contacting a dendritic
 CC cell precursor, such as a monocyte, with such an oligodeoxynucleotide.
 CC The method is useful for generating mature dendritic cells and enhancing
 CC T cell responses, thus enhancing antigen presentation. Mature dendritic
 CC cells are useful for tumour immunotherapy, for augmenting an immune
 CC response to an infectious agent or to a vaccine, and as vaccines to
 CC prevent future infection or to activate the immune system to treat
 CC diseases such as cancer. Mature dendritic cells may also be used to
 CC produce activated T lymphocytes

XX Sequence 20 BP; 2 A; 4 C; 10 G; 2 T; 0 U; 2 Other;
 SQ Query Match 100.0%; Score 18; DB 7; Length 20;
 Best Local Similarity 100.0%; Pred. No. 37;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCGCCGATGACGGGGG 18
 Db 3 TCGCCGATGACGGGGG 20
 |||||
 |||||

RESULT 2
 AAC80656
 ID AAC80656 standard; DNA; 19 BP.
 XX AC AAC80656;
 XX 14-FEB-2001 (first entry)
 DT
 DE Immunogenic CpG oligodeoxynucleotide, SEQ ID NO:76.
 XX

CpG oligodeoxynucleotide; unmethylated; antigen-presenting cell;
 immunogenic; cytokine release; natural killer cell; NK cell activation;
 cell-mediated immune response; T-cell response; humoral response;
 B-cell response; antibody production; immune response induction; vaccine;
 allergy; asthma; infection; bacterial; viral; fungal; protozoal;
 parasitic; tuberculosis; AIDS; autoimmune disease; lupus erythematosus;
 rheumatoid arthritis; multiple sclerosis; solid tumour; cancer;
 immune deficiency; biological warfare agent; cytostatic; antiarthritic;
 antimicrobial; antiallergic; protozoicide; tuberculostatic;
 antiasthmatic; dermatological; phosphorothioate; ss.
 Synthetic.
 OS
 XS
 WO200061151-A2.
 FN
 XX
 XX
 PD 19-OCT-2000.
 XX
 PF 12-APR-2000; 2000WO-US009839.
 XX
 XX 12-APR-1999; 99US-0128898P.
 PR
 XX (KLIN/) KLINMAN D.
 PA (ISHI/) ISHII K.
 PA (VERT/) VERTHELYI D.
 XX
 PI Klinman D, Ishii K, Verthelyi D;
 DR WPI; 2001-006880/01.
 XX
 XX Novel oligonucleotides useful for the prevention and treatment of
 FT allergies, cancer, and autoimmune disorders and for ameliorating symptoms
 PT resulting from exposure to a bio-warfare agent.
 PT
 XX
 XX Claim 4; Page 35; 46pp; English.
 PS
 XX The invention relates to novel immunogenic CpG oligodeoxynucleotides
 CC (AAC80581-C80723). The oligonucleotide are at least 10 bases long and
 CC comprise one of the generic sequences 5'-NNNT-CpG-WNNN-3' or 5'-RY-CpG-RY
 CC -3'. The central CpG motif is unmethylated, and the oligonucleotides
 CC optionally have phosphorothioate linkages which make them more resistant
 CC to degradation. The invention also relates to an oligonucleotide delivery
 CC complex comprising an oligonucleotide of the invention and a targeting

CC agent, and a pharmaceutical composition comprising the oligonucleotide
 CC delivery complex. The oligonucleotides are able to induce either a cell-
 CC mediated (T-cell) response or a humoral (B-cell, antibody) response, with
 CC oligonucleotides of the sequence 5'-RY-CpG-RY-3' being able to induce a
 CC cell-mediated response, and those of the sequence 5'-NNNT-CpG-WNNN-3',
 CC being able to induce a humoral response. It is thought that after
 CC administration, the oligonucleotide acts on antigen-presenting cells
 CC (e.g. macrophages and dendritic cells), which then release cytokines,
 CC leading to activation of natural killer (NK) cells. A cell-mediated or
 CC humoral response can then occur by activation of T- or B-cells. The
 CC induction of an immune response is useful for treating, preventing or
 CC ameliorating an allergic reaction (preferably asthma), or an infection,
 CC where an immunogenic CpG oligonucleotide is administered either alone or
 CC in combination with an anti-allergenic agent or anti-infectious agent.
 CC The allergic conditions which may be treated include eczema, allergic
 CC rhinitis, hayfever, urticaria, food allergies and other atopic
 CC conditions, and the infections which may be treated include viral,
 CC bacterial, fungal and protozoal infections such as tuberculosis, AIDS,
 CC leishmania and schistosomiasis. Immune response induction may also be
 CC used in the treatment of an autoimmune disorder (e.g., lupus
 CC erythematosus, rheumatoid arthritis and multiple sclerosis), a disease
 CC associated with immune system deficiency, and symptoms resulting from
 CC exposure to an agent of biological warfare. An immunogenic CpG
 CC oligonucleotide, either alone or in combination with an anti-cancer
 CC agent, is useful for treating solid tumour cancer. The induction of an
 CC immune response is used in antisense therapy and to improve the efficacy
 CC of a vaccine. The oligonucleotide is preferably administered to
 CC lymphocytes ex vivo, producing activated lymphocytes which are then
 CC administered to the host. The present sequence represents an immunogenic
 CC CpG oligodeoxynucleotide of the invention

XX Sequence 19 BP; 2 A; 4 C; 11 G; 2 T; 0 U; 0 Other;
 SQ Query Match 94.4%; Score 17; DB 4; Length 19;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCGCCGATGACGGGGG 17
 Db 3 TCGCCGATGACGGGGG 19
 |||||
 |||||

RESULT 3
 AAS09626
 ID AAS09626 standard; DNA; 19 BP.
 XX AC AAS09626;
 XX 26-SEP-2001 (first entry)
 DT
 DE Immunoreactive CpG sequence-containing oligonucleotide #76.
 XX

CpG sequence; immune response; non-B cell activation; interferon gamma;
 IFN-gamma; humoral; antibody production; interleukin-6 production;
 therapeutic; allergy; asthma; cancer; autoimmune disorder; infection;
 bio-warfare; vaccine; antisense therapy; eczema; allergic rhinitis;
 coryza; hay fever; urticaria; hives; food allergy; atopic condition;
 hepatitis; human immunodeficiency virus; HIV; malaria; Francisella;
 lupus erythematosus; rheumatoid arthritis; multiple sclerosis;
 schistosomiasis; tuberculosis; acquired immunodeficiency syndrome; AIDS;
 leishmania; Ebola; Anthrax; Listeria; ss.
 Synthetic.
 OS
 XX WO200151500-A1.
 PN
 XX 19-JUL-2001.
 PD
 XX 12-JAN-2001; 2001WO-US001122.
 PF
 XX 14-JAN-2000; 2000US-0176115P.
 PR
 XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
 PA

XX Klinman D, Ishii K, Verthelyi D;
 XX WPI; 2001-442129/47.
 XX
 XX Oligodeoxynucleotides for inducing an immune response to treat and
 PT prevent an allergic reaction, cancer, an autoimmune disorder, and symptoms
 PT resulting from exposure to bio-warfare agents, comprise multiple CpG
 PT sequences.
 XX
 XX Claim 5; Page 39; 48pp; English.
 XX
 XX AAS09551-AAS09662 represent oligodeoxynucleotides (ODN) of at least 10
 CC nucleotides comprising multiple CpG sequences, where one of the CpG
 CC sequences is different from another of the multiple CpG sequences. The
 CC ODN are useful for inducing an immune response, preferably a cell-
 CC mediated immune response, involving non-B cell activation, interferon
 CC gamma (IFN-gamma) production or a humoral immune response involving B
 CC cell activation, antibody and interleukin-6 production in a host, for
 CC treating, preventing or ameliorating an allergic reaction, e.g. asthma,
 CC cancer, e.g. solid tumour cancer, a disease associated with the immune
 CC system e.g. autoimmune disorder or an immune system deficiency, infection
 CC or a symptom resulting from exposure to bio-warfare agent in a human. The
 CC induction of immune response improves the efficacy of a vaccine and is
 CC used in antisense therapy. The ODN are useful for treating, preventing or
 CC ameliorating allergic reactions, including eczema, allergic rhinitis or
 CC coryza, hay fever, bronchial asthma, urticaria (hives), food allergies
 CC and other atopic conditions, for improving the efficacy of vaccines
 CC against hepatitis A, B and C, human immunodeficiency virus (HIV) and
 CC malaria, for treating immune system deficiencies, e.g. lupus
 CC erythematosus and autoimmune diseases such as rheumatoid arthritis and
 CC multiple sclerosis, infections including Francisella, schistosomiasis,
 CC tuberculosis, acquired immunodeficiency syndrome (AIDS), leishmania and
 CC symptoms resulting from exposure of bio-warfare agent, including Ebola,
 CC Anthrax and Listeria
 XX
 XX Sequence 19 BP; 2 A; 4 C; 11 G; 2 T; 0 U; 0 Other;
 SQ
 Query Match 94.4%; Score 17; DB 4; Length 19;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TGGCCCGATGCGAGGGG 17
 Db 3 TGGCCCGATGCGAGGGG 19
 RESULT 4
 ABK46504
 ID ABK46504 standard; DNA; 19 BP.
 XX
 XX ABK46504;
 AC
 XX
 XX 05-JUN-2002 (first entry)
 DT
 XX
 XX Immunostimulatory unmethylated CpG oligodeoxynucleotide #94.
 DE
 XX unmethylated CpG; oligodeoxynucleotide; ODN; virucide; vaccine;
 KW Paramyxoviridae; F protein; respiratory syncytial virus; RSV;
 KW viral bronchiolitis; pneumonia; infectious pulmonary disease;
 KW bronchopulmonary dysplasia; congenital heart condition; ss.
 XX
 OS Synthetic.
 XX
 XX WO200211761-A2.
 FN
 XX
 XX 14-FEB-2002.
 PD
 XX
 XX 09-AUG-2001; 2001WO-US041633.
 PF
 XX
 XX 10-AUG-2000; 2000US-0224011P.
 PR
 XX 01-SEP-2000; 2000US-0229307P.
 XX

XX (JACK-) JACKSON FOUND ADVANCEMENT MILITARY MED.
 PI Mond JJ, Prince G, Klinman DM;
 XX
 XX WPI; 2002-227118/28.
 DR
 XX
 XX Vaccine for immunizing patient against respiratory syncytial virus, has
 PT epitopes of Paramyxoviridae F protein, and cytosine followed by guanine
 PT linked by phosphate bond-oligodeoxynucleotides.
 PT
 XX
 XX Claim 4; Page 9; 30pp; English.
 PS
 XX
 XX The invention describes a vaccine comprising one or more epitopes of a
 CC Paramyxoviridae F protein, and one or more CpG (cytosine followed by
 CC guanine linked by phosphate bond)-oligodeoxynucleotides (ODNs). The
 CC vaccine is useful for vaccinating a patient especially against viruses of
 CC the Paramyxoviridae family e.g. respiratory syncytial virus (RSV), the
 CC primary cause of viral bronchiolitis and pneumonia in infants and
 CC children, and infectious pulmonary disease in infants.
 CC particularly implicated in death of infants that are premature, have
 CC bronchopulmonary dysplasia, or congenital heart conditions. This sequence
 CC represents an oligodeoxynucleotide that can be used in the creation of
 CC the vaccine
 XX
 XX Sequence 19 BP; 2 A; 4 C; 11 G; 2 T; 0 U; 0 Other;
 SQ
 Query Match 94.4%; Score 17; DB 6; Length 19;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TGGCCCGATGCGAGGGG 17
 Db 3 TGGCCCGATGCGAGGGG 19
 RESULT 5
 AAC80662
 ID AAC80662 standard; DNA; 20 BP.
 XX
 XX AAC80662;
 AC
 XX
 XX 14-FEB-2001 (first entry)
 DT
 XX
 XX Immunogenic CpG oligodeoxynucleotide, SEQ ID NO:82.
 DE
 XX CpG oligodeoxynucleotide; unmethylated; antigen-presenting cell;
 KW immunogenic; cytokine release; natural killer cell; NK cell activation;
 KW cell-mediated immune response; T-cell response; humoral response; vaccine;
 KW B-cell response; antibody production; immune response induction; protozoal;
 KW allergy; asthma; infection; bacterial; viral; fungal; protozoal;
 KW parasitic; tuberculosis; AIDS; autoimmune disease; lupus erythematosus;
 KW rheumatoid arthritis; multiple sclerosis; solid tumour; cancer;
 KW immune deficiency; biological warfare agent; cytostatic; antiarthritic;
 KW antimicrobial; antiallergic; protozoicide; tuberculostatic;
 KW antiasthmatic; dermatological; phosphorothioate; ss.
 XX
 OS Synthetic.
 XX
 XX WO2000061151-A2.
 FN
 XX
 XX 19-OCT-2000.
 PD
 XX
 XX 12-APR-2000; 2000WO-US009839.
 PF
 XX
 XX 12-APR-1999; 99US-0128898P.
 PR
 XX
 XX (KLIN/) KLINMAN D.
 PA (ISHI/) ISHII K.
 PA (VERT/) VERTHELYI D.
 XX
 XX Klinman D, Ishii K, Verthelyi D;
 PI WPI; 2001-006880/01.
 DR

XX Novel oligonucleotides useful for the prevention and treatment of
PT allergies, cancer, and autoimmune disorders and for ameliorating symptoms
PT resulting from exposure to a bio-warfare agent.

XX Claim 4; Page 36; 46pp; English.

XX The invention relates to novel immunogenic CpG oligodeoxynucleotides
XX (AAC80581-C80723). The oligonucleotides are at least 10 bases long and
XX comprise one of the generic sequences 5'-NNNT-CpG-WNNN-3' or 5'-RY-CpG-RY
XX -3'. The central CpG motif is unmethylated, and the oligonucleotides
XX optionally have phosphorothioate linkages which make them more resistant
XX to degradation. The invention also relates to an oligonucleotide delivery
XX complex comprising an oligonucleotide of the invention and a targeting
XX agent, and a pharmaceutical composition comprising the oligonucleotide
XX delivery complex. The oligonucleotides are able to induce either a cell-
XX mediated (T-cell) response or a humoral (B-cell, antibody) response, with
XX oligonucleotides of the sequence 5'-RY-CpG-RY-3' being able to induce a
XX cell-mediated response, and those of the sequence 5'-NNNT-CpG-WNNN-3'
XX being able to induce a humoral response. It is thought that after
XX administration, the oligonucleotide acts on antigen-presenting cells
XX (e.g., macrophages and dendritic cells), which then release cytokines,
XX leading to activation of natural killer (NK) cells. A cell-mediated or
XX humoral response can then occur by activation of T- or B-cells. The
XX induction of an immune response is useful for treating, preventing or
XX ameliorating an allergic reaction (preferably asthma), or an infection,
XX where an immunogenic CpG oligonucleotide is administered either alone or
XX in combination with an anti-allergic agent or anti-infectious agent.
XX The allergic conditions which may be treated include eczema, allergic
XX rhinitis, hayfever, urticaria, food allergies and other atopic
XX conditions, and the infections which may be treated include viral,
XX bacterial, fungal and protozoal infections such as tuberculosis, AIDS,
XX leishmania and schistosomiasis. Immune response induction may also be
XX used in the treatment of an autoimmune disorder (e.g., lupus
XX erythematosus, rheumatoid arthritis and multiple sclerosis), a disease
XX associated with immune system deficiency, and symptoms resulting from
XX exposure to an agent of biological warfare. An immunogenic CpG
XX oligonucleotide, either alone or in combination with an anti-cancer
XX agent, is useful for treating solid tumour cancer. The induction of an
XX immune response is used in antisense therapy and to improve the efficacy
XX of a vaccine. The oligonucleotide is preferably administered to
XX lymphocytes ex vivo, producing activated lymphocytes which are then
XX administered to the host. The present sequence represents an immunogenic
XX CpG oligodeoxynucleotide of the invention

XX Sequence 20 BP; 2 A; 3 C; 12 G; 3 T; 0 U; 0 Other;

Query Match 91.1%; Score 16.4; DB 4; Length 20;

Best Local Similarity 94.4%; Pred. No. 2.2e+02;

Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TGGCCGATGACGGGGG 18

DB 3 TGGCCGATGACGGGGG 20

RESULT 6

AAC80661

ID AAC80661 standard; DNA; 20 BP.

XX AAC80661;

XX AAC80661;

DT 14-FEB-2001 (first entry)

XX Immunogenic CpG oligodeoxynucleotide, SEQ ID NO:81.

XX CpG oligodeoxynucleotide; unmethylated; antigen-presenting cell;

XX immunogenic; cytokine release; natural killer cell; NK cell activation;

XX cell-mediated immune response; T-cell response; humoral response;

XX B-cell response; antibody production; immune response induction; vaccine;

XX allergy; asthma; infection; bacterial; viral; fungal; protozoal;

XX parasitic; tuberculosis; AIDS; autoimmune disease; lupus erythematosus;

XX rheumatoid arthritis; multiple sclerosis; solid tumour; cancer;

KW immune deficiency; biological warfare agent; cytostatic; antiarthritic;

KW antimicrobial; anti-allergic; protozoic; tuberculo-static;

KW antiasthmatic; dermatological; phosphorothioate; ss.

XX Synthetic.

OS WO200061151-A2.

PN 19-OCT-2000.

PD 12-APR-2000; 2000WO-US009839.

PF 12-APR-1999; 99US-0128898P.

PR {KLIN/} KLINMAN D.

XX {ISHI/} ISHII K.

PA {VERT/} VERTHELYI D.

PI Klinman D. Ishii K. Verthelyi D.

XX WPI; 2001-006880/01.

XX Novel oligonucleotides useful for the prevention and treatment of

XX allergies, cancer, and autoimmune disorders and for ameliorating symptoms

XX resulting from exposure to a bio-warfare agent.

XX Claim 4; Page 36; 46pp; English.

XX The invention relates to novel immunogenic CpG oligodeoxynucleotides

XX (AAC80581-C80723). The oligonucleotides are at least 10 bases long and

XX comprise one of the generic sequences 5'-NNNT-CpG-WNNN-3' or 5'-RY-CpG-RY

XX -3'. The central CpG motif is unmethylated, and the oligonucleotides

XX optionally have phosphorothioate linkages which make them more resistant

XX to degradation. The invention also relates to an oligonucleotide delivery

XX complex comprising an oligonucleotide of the invention and a targeting

XX agent, and a pharmaceutical composition comprising the oligonucleotide

XX delivery complex. The oligonucleotides are able to induce either a cell-

XX mediated (T-cell) response or a humoral (B-cell, antibody) response, with

XX oligonucleotides of the sequence 5'-RY-CpG-RY-3' being able to induce a

XX cell-mediated response, and those of the sequence 5'-NNNT-CpG-WNNN-3'

XX being able to induce a humoral response. It is thought that after

XX administration, the oligonucleotide acts on antigen-presenting cells

XX (e.g., macrophages and dendritic cells), which then release cytokines,

XX leading to activation of natural killer (NK) cells. A cell-mediated or

XX humoral response can then occur by activation of T- or B-cells. The

XX induction of an immune response is useful for treating, preventing or

XX ameliorating an allergic reaction (preferably asthma), or an infection,

XX where an immunogenic CpG oligonucleotide is administered either alone or

XX in combination with an anti-allergic agent or anti-infectious agent.

XX The allergic conditions which may be treated include eczema, allergic

XX rhinitis, hayfever, urticaria, food allergies and other atopic

XX conditions, and the infections which may be treated include viral,

XX bacterial, fungal and protozoal infections such as tuberculosis, AIDS,

XX leishmania and schistosomiasis. Immune response induction may also be

XX used in the treatment of an autoimmune disorder (e.g., lupus

XX erythematosus, rheumatoid arthritis and multiple sclerosis), a disease

XX associated with immune system deficiency, and symptoms resulting from

XX exposure to an agent of biological warfare. An immunogenic CpG

XX oligonucleotide, either alone or in combination with an anti-cancer

XX agent, is useful for treating solid tumour cancer. The induction of an

XX immune response is used in antisense therapy and to improve the efficacy

XX of a vaccine. The oligonucleotide is preferably administered to

XX lymphocytes ex vivo, producing activated lymphocytes which are then

XX administered to the host. The present sequence represents an immunogenic

XX CpG oligodeoxynucleotide of the invention

XX Sequence 20 BP; 2 A; 3 C; 12 G; 3 T; 0 U; 0 Other;

Query Match 91.1%; Score 16.4; DB 4; Length 20;

Best Local Similarity 94.4%; Pred. No. 2.2e+02;

Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TGGCCGATGACGGGGG 18

DB 3 TGGCCGATGACGGGGG 20

RESULT 6

AAC80661

ID AAC80661 standard; DNA; 20 BP.

XX AAC80661;

XX AAC80661;

DT 14-FEB-2001 (first entry)

XX Immunogenic CpG oligodeoxynucleotide, SEQ ID NO:81.

XX CpG oligodeoxynucleotide; unmethylated; antigen-presenting cell;

XX immunogenic; cytokine release; natural killer cell; NK cell activation;

XX cell-mediated immune response; T-cell response; humoral response;

XX B-cell response; antibody production; immune response induction; vaccine;

XX allergy; asthma; infection; bacterial; viral; fungal; protozoal;

XX parasitic; tuberculosis; AIDS; autoimmune disease; lupus erythematosus;

XX rheumatoid arthritis; multiple sclerosis; solid tumour; cancer;

Query Match 91.1%; Score 16.4; DB 4; Length 20;

Best Local Similarity 94.4%; Pred. No. 2.2e+02;

Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TGGCCGATGACGGGGG 18

Db 3 TGGCTCGATGCAGGGGG 20

RESULT 7
AAC80620
ID AAC80620 standard; DNA; 20 BP.
XX AAC80620;
AC AAC80620;
XX
DT 14-FEB-2001 (first entry)
XX Immunogenic CpG oligodeoxynucleotide, SEQ ID NO:40.
DE
XX CpG oligodeoxynucleotide; unmethylated; antigen-presenting cell;
KW immunogenic; cytokine release; natural killer cell; NK cell activation;
KW cell-mediated immune response; T-cell response; humoral response;
KW B-cell response; antibody production; immune response induction; vaccine;
KW allergy; asthma; infection; bacterial; viral; fungal; protozoal;
KW parasitic; tuberculosis; AIDS; autoimmune disease; lupus erythematosus;
KW rheumatoid arthritis; multiple sclerosis; solid tumour; cancer;
KW immune deficiency; biological warfare agent; cytostatic; antiarthritic;
KW antimicrobial; anciaallergic; protozoacide; tuberculoostatic;
KW antiasthmatic; dermatological; phosphorothioate; ss.
XX
OS Synthetic.
XX WO200061151-A2.
XX
XX 19-OCT-2000.
XX
XX 12-APR-2000; 2000NO-US009839.
XX
XX 12-APR-1999; 99US-01288989.
XX
XX (KLIN/) KLINMAN D.
PA (ISHI/) ISHII K.
PA (VERT/) VERTHELYI D.
XX
XX Klinman D, Ishii K, Verthelyi D;
PI WPI; 2001-006880/01.
XX
XX Novel oligonucleotides useful for the prevention and treatment of
PT allergies, cancer, and autoimmune disorders and for ameliorating symptoms
PT resulting from exposure to a bio-warfare agent.
XX
XX Claim 4; Page 30; 46pp; English.
XX
XX The invention relates to novel immunogenic CpG oligodeoxynucleotides
CC (AAC80581-C80723). The oligonucleotide are at least 10 bases long and
CC comprise one of the generic sequences 5'-NNNT-CpG-WNNN-3' or 5'-RY-CpG-RY
CC -3'. The central CpG motif is unmethylated, and the oligonucleotides
CC optionally have phosphorothioate linkages which make them more resistant
CC to degradation. The invention also relates to an oligonucleotide delivery
CC complex comprising an oligonucleotide of the invention and a targeting
CC agent, and a pharmaceutical composition comprising the oligonucleotide
CC delivery complex. The oligonucleotides are able to induce either a cell-
CC mediated (T-cell) response or a humoral (B-cell, antibody) response, with
CC oligonucleotides of the sequence 5'-RY-CpG-RY-3' being able to induce a
CC cell-mediated response, and those of the sequence 5'-NNNT-CpG-WNNN-3',
CC being able to induce a humoral response. It is thought that after
CC administration, the oligonucleotide acts on antigen-presenting cells
CC (e.g., macrophages and dendritic cells), which then release cytokines,
CC leading to activation of natural killer (NK) cells. A cell-mediated or
CC humoral response can then occur by activation of T- or B-cells. The
CC induction of an immune response is useful for treating, preventing or
CC ameliorating an allergic reaction (preferably asthma), or an infection,
CC where an immunogenic CpG oligonucleotide is administered either alone or
CC in combination with an anti-allergenic agent or anti-infectious agent.
CC The allergic conditions which may be treated include eczema, allergic
CC rhinitis, hayfever, urticaria, food allergies and other atopic
CC conditions, and the infections which may be treated include viral,
CC

CC bacterial, fungal and protozoal infections such as tuberculosis, AIDS,
CC leishmania and schistosomiasis. Immune response induction may also be
CC used in the treatment of an autoimmune disorder (e.g., lupus
CC erythematosus, rheumatoid arthritis and multiple sclerosis), a disease
CC associated with immune system deficiency, and symptoms resulting from
CC exposure to an agent of biological warfare. An immunogenic CpG
CC oligonucleotide, either alone or in combination with an anti-cancer
CC agent, is useful for treating solid tumour cancer. The induction of an
CC immune response is used in antisense therapy and to improve the efficacy
CC of a vaccine. The oligonucleotide is preferably administered to
CC lymphocytes ex vivo, producing activated lymphocytes which are then
CC administered to the host. The present sequence represents an immunogenic
CC CpG oligodeoxynucleotide of the invention
XX
XX Sequence 20 BP; 2 A; 3 C; 12 G; 3 T; 0 U; 0 Other;
SQ

Query Match 91.1%; Score 16.4; DB 4; Length 20;
Best Local Similarity 94.4%; Pred. No. 2.2e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 TGGCTCGATGCAGGGGG 18
DB 3 TGGCTCGATGCAGGGGG 20

RESULT 8
AAS09631
ID AAS09631 standard; DNA; 20 BP.
XX
XX AAS09631;
XX
XX 26-SEP-2001 (first entry)
XX Immunoreactive CpG sequence-containing oligonucleotide #81.
XX
XX CpG sequence; immune response; non-B cell activation; interferon gamma;
KW IFN-gamma; humoral; antibody production; interleukin-6 production;
KW therapeutic; allergy; asthma; cancer; autoimmune disorder; infection;
KW bio-warfare; vaccine; antisense therapy; eczema; allergic rhinitis;
KW coryza; hay fever; urticaria; hives; food allergy; atopic condition;
KW hepatitis; human immunodeficiency virus; HIV; malaria; Francisella;
KW lupus erythematosus; rheumatoid arthritis; multiple sclerosis;
KW schistosomiasis; tuberculosis; acquired immunodeficiency syndrome; AIDS;
KW Leishmania; Ebola; Anthrax; Listeria; ss.
XX
XX Synthetic.
XX WO200151500-A1.
XX
XX 19-JUL-2001.
XX
XX 12-JAN-2001; 2001WO-US001122.
XX
XX 14-JAN-2000; 2000US-0176115P.
XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
XX Klinman D, Ishii K, Verthelyi D;
PI WPI; 2001-442129/47.
XX
XX Oligodeoxynucleotides for inducing an immune response to treat and
PT prevent an allergic reaction, cancer, an autoimmune disorder and symptoms
PT resulting from exposure to bio-warfare agents, comprise multiple CpG
PT sequences.
XX
XX Claim 5; Page 40; 48pp; English.
XX
XX AAS09551-AAS09662 represent oligodeoxynucleotides (ODN) of at least 10
CC nucleotides comprising multiple CpG sequences, where one of the CpG
CC sequences is different from another of the multiple CpG sequences. The
CC ODN are useful for inducing an immune response, preferably a cell-
CC mediated immune response, involving non-B cell activation, interferon

CC gamma (IFN-gamma) production or a humoral immune response involving B
 CC cell activation, antibody and interleukin-6 production in a host, for
 CC treating, preventing or ameliorating an allergic reaction, e.g. asthma,
 CC cancer, e.g. solid tumour cancer, a disease associated with the immune
 CC system e.g. autoimmune disorder or an immune system deficiency, infection
 CC or a symptom resulting from exposure to bio-warfare agent in a human. The
 CC induction of immune response improves the efficacy of a vaccine and is
 CC used in antisense therapy. The ODN are useful for treating, preventing or
 CC ameliorating allergic reactions, including eczema, allergic rhinitis or
 CC coryza, hay fever, bronchial asthma, urticaria (hives), food allergies
 CC and other atopic conditions, for improving the efficacy of vaccines
 CC against hepatitis A, B and C, human immunodeficiency virus (HIV) and
 CC malaria, for treating immune system deficiencies, e.g. lupus
 CC erythematosus and autoimmune diseases such as rheumatoid arthritis and
 CC multiple sclerosis, infections including Francisella, schistosomiasis,
 CC tuberculosis, acquired immunodeficiency syndrome (AIDS), Leishmania and
 CC symptoms resulting from exposure of bio-warfare agent, including Ebola,
 CC Anthrax and Listeria
 XX
 SQ Sequence 20 BP; 2 A; 3 C; 12 G; 3 T; 0 U; 0 Other;
 Query Match 91.1%; Score 16.4; DB 4; Length 20;
 Best Local Similarity 94.4%; Pred. No. 2.2e+02;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 TCGCCGATGCGAGGGGG 18
 DB 3 TCGTCGATGCGAGGGGG 20
 RESULT 9
 AAS09590
 ID AAS09590 standard; DNA; 20 BP.
 AC AAS09590;
 XX
 DT 26-SEP-2001 (first entry)
 XX
 DE Immunoreactive CpG sequence-containing oligonucleotide #40.
 KW CpG sequence; immune response; non-B cell activation; interferon gamma;
 KW IFN-gamma; humoral; antibody production; interleukin-6 production;
 KW therapeutic; allergy; asthma; cancer; autoimmune disorder; infection;
 KW bio-warfare; vaccine; antisense therapy; eczema; allergic rhinitis;
 KW coryza; hay fever; urticaria; hives; food allergy; atopic condition;
 KW hepatitis; human immunodeficiency virus; HIV; malaria; Francisella;
 KW lupus erythematosus; rheumatoid arthritis; multiple sclerosis;
 KW schistosomiasis; tuberculosis; acquired immunodeficiency syndrome; AIDS;
 KW Leishmania; Ebola; Anthrax; Listeria; ss.
 OS Synthetic.
 XX
 PN WO200151500-A1.
 XX
 PD 19-JUL-2001.
 XX
 PF 12-JAN-2001; 2001WO-US001122.
 XX
 PR 14-JAN-2000; 2000US-0176115P.
 XX
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX
 PI Klinman D, Ishii K, Verthelyi D;
 XX
 DR WPI; 2001-442129/47.
 XX
 PT Oligodeoxynucleotides for inducing an immune response to treat and
 PT prevent an allergic reaction, cancer, an autoimmune disorder and symptoms
 PT resulting from exposure to bio-warfare agents, comprise multiple CpG
 PT sequences.
 XX
 PS Claim 5; Page 33; 48pp; English.
 XX

CC AAS09551-AAS09662 represent oligodeoxynucleotides (ODN) of at least 10
 CC nucleotides comprising multiple CpG sequences, where one of the CpG
 CC sequences is different from another of the multiple CpG sequences. The
 CC ODN are useful for inducing an immune response, preferably a cell-
 CC mediated immune response, involving non-B cell activation, interferon
 CC gamma (IFN-gamma) production or a humoral immune response involving B
 CC cell activation, antibody and interleukin-6 production in a host, for
 CC treating, preventing or ameliorating an allergic reaction, e.g. asthma,
 CC cancer, e.g. solid tumour cancer, a disease associated with the immune
 CC system e.g. autoimmune disorder or an immune system deficiency, infection
 CC or a symptom resulting from exposure to bio-warfare agent in a human. The
 CC induction of immune response improves the efficacy of a vaccine and is
 CC used in antisense therapy. The ODN are useful for treating, preventing or
 CC ameliorating allergic reactions, including eczema, allergic rhinitis or
 CC coryza, hay fever, bronchial asthma, urticaria (hives), food allergies
 CC and other atopic conditions, for improving the efficacy of vaccines
 CC against hepatitis A, B and C, human immunodeficiency virus (HIV) and
 CC malaria, for treating immune system deficiencies, e.g. lupus
 CC erythematosus and autoimmune diseases such as rheumatoid arthritis and
 CC multiple sclerosis, infections including Francisella, schistosomiasis,
 CC tuberculosis, acquired immunodeficiency syndrome (AIDS), Leishmania and
 CC symptoms resulting from exposure of bio-warfare agent, including Ebola,
 CC Anthrax and Listeria
 XX
 SQ Sequence 20 BP; 2 A; 3 C; 12 G; 3 T; 0 U; 0 Other;
 Query Match 91.1%; Score 16.4; DB 4; Length 20;
 Best Local Similarity 94.4%; Pred. No. 2.2e+02;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 TCGCCGATGCGAGGGGG 18
 DB 3 TCGTCGATGCGAGGGGG 20
 RESULT 10
 AAS09651
 ID AAS09651 standard; DNA; 20 BP.
 AC AAS09651;
 XX
 DT 26-SEP-2001 (first entry)
 XX
 DE Immunoreactive CpG sequence-containing oligonucleotide #101.
 KW CpG sequence; immune response; non-B cell activation; interferon gamma;
 KW IFN-gamma; humoral; antibody production; interleukin-6 production;
 KW therapeutic; allergy; asthma; cancer; autoimmune disorder; infection;
 KW bio-warfare; vaccine; antisense therapy; eczema; allergic rhinitis;
 KW coryza; hay fever; urticaria; hives; food allergy; atopic condition;
 KW hepatitis; human immunodeficiency virus; HIV; malaria; Francisella;
 KW lupus erythematosus; rheumatoid arthritis; multiple sclerosis;
 KW schistosomiasis; tuberculosis; acquired immunodeficiency syndrome; AIDS;
 KW Leishmania; Ebola; Anthrax; Listeria; ss.
 OS Synthetic.
 XX
 PN WO200151500-A1.
 XX
 PD 19-JUL-2001.
 XX
 PF 12-JAN-2001; 2001WO-US001122.
 XX
 PR 14-JAN-2000; 2000US-0176115P.
 XX
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX
 PI Klinman D, Ishii K, Verthelyi D;
 XX
 DR WPI; 2001-442129/47.
 XX
 PT Oligodeoxynucleotides for inducing an immune response to treat and
 PT prevent an allergic reaction, cancer, an autoimmune disorder and symptoms

PT resulting from exposure to bio-warfare agents, comprise multiple CpG
 PT sequences.
 XX
 XX
 PS Claim 5; Page 44; 48pp; English.
 CC AAS09551-AAS09662 represent oligodeoxynucleotides (ODN) of at least 10
 CC nucleotides comprising multiple CpG sequences, where one of the CpG
 CC sequences is different from another of the multiple CpG sequences. The
 CC ODN are useful for inducing an immune response, preferably a cell-
 CC mediated immune response, involving non-B cell activation, interferon
 CC gamma (IFN-gamma) production or a humoral immune response involving B
 CC cell activation, antibody and interleukin-6 production in a host, for
 CC treating, preventing or ameliorating an allergic reaction, e.g. asthma,
 CC cancer, e.g. solid tumour cancer, a disease associated with the immune
 CC system e.g. autoimmune disorder or an immune system deficiency, infection
 CC or a symptom resulting from exposure to bio-warfare agent in a human. The
 CC induction of immune response improves the efficacy of a vaccine and is
 CC used in antisense therapy. The ODN are useful for treating, preventing or
 CC ameliorating allergic reactions, including eczema, allergic rhinitis or
 CC coryza, hay fever, bronchial asthma, urticaria (hives), food allergies
 CC and other atopic conditions, for improving the efficacy of vaccines
 CC against hepatitis A, B and C, human immunodeficiency virus (HIV) and
 CC malaria, for treating immune system deficiencies, e.g. lupus
 CC erythematosus and autoimmune diseases such as rheumatoid arthritis and
 CC multiple sclerosis, infections including Francisella, schistosomiasis,
 CC tuberculosis, acquired immunodeficiency syndrome (AIDS), Leishmania and
 CC symptoms resulting from exposure of bio-warfare agent, including Ebola,
 CC Anthrax and Listeria
 XX
 SQ Sequence 20 BP; 3 A; 4 C; 11 G; 2 T; 0 U; 0 Other;
 Query Match 91.1%; Score 16.4; DB 4; Length 20;
 Best Local Similarity 94.4%; Pred. No. 2.2e+02;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 TGCGCCGATCGACGGGGG 18
 Db 3 TGACCGATCGACGGGGG 20
 RESULT 11
 ID AAS09632
 AC AAS09632;
 XX
 XX 26-SEP-2001 (first entry)
 DE
 DE Immunoreactive CpG sequence-containing oligonucleotide #82.
 KW CpG sequence; immune response; non-B cell activation; interferon gamma;
 KW IFN-gamma; humoral; antibody production; interleukin-6 production;
 KW therapeutic; allergy; asthma; cancer; autoimmune disorder; infection;
 KW bio-warfare; vaccine; antisense therapy; eczema; allergic rhinitis;
 KW coryza; hay fever; urticaria; hives; food allergy; atopic condition;
 KW hepatitis; human immunodeficiency virus; HIV; malaria; Francisella;
 KW lupus erythematosus; rheumatoid arthritis; multiple sclerosis;
 KW schistosomiasis; tuberculosis; acquired immunodeficiency syndrome; AIDS;
 KW Leishmania; Ebola; Anthrax; Listeria; ss.
 XX
 OS Synthetic.
 XX
 XX WO200151500-A1.
 PN
 XX
 XX 19-JUL-2001.
 PD
 XX
 XX 12-JAN-2001; 2001WO-US001122.
 PF
 XX
 PR 14-JAN-2000; 2000US-0176115P.
 XX
 XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
 PA
 XX
 PI Klinman D, Ishii K, Verthelyi D;

XX
 DR WPI; 2001-442129/47.
 XX
 PT Oligodeoxynucleotides for inducing an immune response to treat and
 PT prevent an allergic reaction, cancer, an autoimmune disorder and symptoms
 PT resulting from exposure to bio-warfare agents, comprise multiple CpG
 PT sequences.
 XX
 PS Claim 5; Page 40; 48pp; English.
 CC AAS09551-AAS09662 represent oligodeoxynucleotides (ODN) of at least 10
 CC nucleotides comprising multiple CpG sequences, where one of the CpG
 CC sequences is different from another of the multiple CpG sequences. The
 CC ODN are useful for inducing an immune response, preferably a cell-
 CC mediated immune response, involving non-B cell activation, interferon
 CC gamma (IFN-gamma) production or a humoral immune response involving B
 CC cell activation, antibody and interleukin-6 production in a host, for
 CC treating, preventing or ameliorating an allergic reaction, e.g. asthma,
 CC cancer, e.g. solid tumour cancer, a disease associated with the immune
 CC system e.g. autoimmune disorder or an immune system deficiency, infection
 CC or a symptom resulting from exposure to bio-warfare agent in a human. The
 CC induction of immune response improves the efficacy of a vaccine and is
 CC used in antisense therapy. The ODN are useful for treating, preventing or
 CC ameliorating allergic reactions, including eczema, allergic rhinitis or
 CC coryza, hay fever, bronchial asthma, urticaria (hives), food allergies
 CC and other atopic conditions, for improving the efficacy of vaccines
 CC against hepatitis A, B and C, human immunodeficiency virus (HIV) and
 CC malaria, for treating immune system deficiencies, e.g. lupus
 CC erythematosus and autoimmune diseases such as rheumatoid arthritis and
 CC multiple sclerosis, infections including Francisella, schistosomiasis,
 CC tuberculosis, acquired immunodeficiency syndrome (AIDS), Leishmania and
 CC symptoms resulting from exposure of bio-warfare agent, including Ebola,
 CC Anthrax and Listeria
 XX
 SQ Sequence 20 BP; 2 A; 3 C; 12 G; 3 T; 0 U; 0 Other;
 Query Match 91.1%; Score 16.4; DB 4; Length 20;
 Best Local Similarity 94.4%; Pred. No. 2.2e+02;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 TGCGCCGATCGACGGGGG 18
 Db 3 TGCGTCGATCGACGGGGG 20
 RESULT 12
 ID ABL35573
 AC ABL35573;
 XX
 XX 04-APR-2002 (first entry)
 DE
 DE Immunostimulatory oligonucleotide SEQ ID NO: 499.
 KW DNA/RNA hybrid; phosphorothioate backbone; immunostimulatory; vaccine;
 KW infection; allergy; cancer; hypersensitivity; bio-warfare;
 KW immunostimulant; antiallergic; cytostatic; antimicrobial; anti-HIV;
 KW immunosuppressive; protozoacide; virucide; hepatotropic; gene therapy;
 KW antiinflammatory; antibacterial; ss.
 XX
 OS Synthetic.
 XX
 XX
 PH Key Location/Qualifiers
 FT misc_RNA 1..20
 FT /+tag= a
 FT /note= "optionally thymidine is replaced by uracil to
 FT form RNA or DNA/RNA hybrids. Thymidine is linked to at
 FT least one other base through a ribose sugar"
 XX
 XX WO200193902-A2.
 PN
 XX
 PD 13-DEC-2001.

```

XX 07-JUN-2001; 2001WO-US018276.
XX 07-JUN-2000; 2000US-0209797P.
XX (BIOS-) BIOSYNEXUS INC.
XX Mond JJ, Flora M, Klinman DM;
XX WPI; 2002-130570/17.
XX New immunostimulatory compositions comprising RNA/DNA hybrid
XX oligonucleotides, useful for enhancing an immune response or inducing
XX cytokines, particularly for treating diseases, e.g. cancer, allergy or
XX HIV infection.
XX Example 11; Page 61; 68pp; English.
XX The present invention relates to an immunostimulatory composition, which
XX comprises at least one oligonucleotide comprising both an RNA region and
XX a DNA region. The composition is useful for enhancing an immune response
XX or inducing cytokines. It can be used as a vaccine adjuvant and in
XX treating diseases, including pathogenic infection, (non-)malignant
XX tumours (e.g. cancers of the brain, lung, ovary, breast, prostate or
XX colon, or carcinomas and sarcomas), autoimmune diseases or allergies
XX (e.g. allergic rhinitis, hay fever or food allergies), Lyme disease,
XX hepatitis, HIV or malaria. The composition is also useful for treating,
XX preventing or ameliorating the symptoms resulting from exposure to a bio-
XX warfare agent, e.g. Ebola, Anthrax or Listeria. The present sequence is
XX an immunostimulatory oligonucleotide described in the exemplification of
XX the invention
XX Sequence 20 BP; 3 A; 4 C; 11 G; 2 T; 0 U; 0 Other;
XX Query Match 91.1%; Score 16.4; DB 6; Length 20;
XX Best Local Similarity 94.4%; Pred. No. 2.2e+02;
XX Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX QY 1 TGGCCCGATGCAGGGGGG 18
XX ||| ||||| |||||
XX Db 3 TGCACCGATGCAGGGGGG 20
XX ||| ||||| |||||
XX RESULT 13
XX ABL35584
XX ID ABL35584 standard; DNA; 20 BP.
XX AC ABL35584;
XX DT 04-APR-2002 (first entry)
XX DE Immunostimulatory oligonucleotide SEQ ID NO: 510.
XX DNA/RNA hybrid; phosphorothioate backbone; immunostimulatory; vaccine;
XX infection; allergy; cancer; hypersensitivity; bio-warfare;
XX immunostimulant; antiallergic; cytostatic; antimicrobial; anti-HIV;
XX immunosuppressive; protozoacide; virucide; hepatotropic; gene therapy;
XX antiinflammatory; antibacterial; ss.
XX Synthetic.
XX Key Location/Qualifiers
XX Key misc_RNA 1..20
XX /tag= a
XX /note= "optionally thymidine is replaced by uracil to
XX form RNA or DNA/RNA hybrids. Thymidine is linked to at
XX least one other base through a ribose sugar"
XX WO200193902-A2.
XX 13-DEC-2001.
XX 07-JUN-2001; 2001WO-US018276.
XX PF
XX 07-JUN-2000; 2000US-0209797P.
XX PF

```

```

XX 07-JUN-2000; 2000US-0209797P.
XX (BIOS-) BIOSYNEXUS INC.
XX Mond JJ, Flora M, Klinman DM;
XX WPI; 2002-130570/17.
XX New immunostimulatory compositions comprising RNA/DNA hybrid
XX oligonucleotides, useful for enhancing an immune response or inducing
XX cytokines, particularly for treating diseases, e.g. cancer, allergy or
XX HIV infection.
XX Example 11; Page 61; 68pp; English.
XX The present invention relates to an immunostimulatory composition, which
XX comprises at least one oligonucleotide comprising both an RNA region and
XX a DNA region. The composition is useful for enhancing an immune response
XX or inducing cytokines. It can be used as a vaccine adjuvant and in
XX treating diseases, including pathogenic infection, (non-)malignant
XX tumours (e.g. cancers of the brain, lung, ovary, breast, prostate or
XX colon, or carcinomas and sarcomas), autoimmune diseases or allergies
XX (e.g. allergic rhinitis, hay fever or food allergies), Lyme disease,
XX hepatitis, HIV or malaria. The composition is also useful for treating,
XX preventing or ameliorating the symptoms resulting from exposure to a bio-
XX warfare agent, e.g. Ebola, Anthrax or Listeria. The present sequence is
XX an immunostimulatory oligonucleotide described in the exemplification of
XX the invention
XX Sequence 20 BP; 3 A; 4 C; 11 G; 2 T; 0 U; 0 Other;
XX Query Match 91.1%; Score 16.4; DB 6; Length 20;
XX Best Local Similarity 94.4%; Pred. No. 2.2e+02;
XX Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX QY 1 TGGCCCGATGCAGGGGGG 18
XX ||| ||||| |||||
XX Db 3 TGCACCGATGCAGGGGGG 20
XX ||| ||||| |||||
XX RESULT 14
XX ABL35617
XX ID ABL35617 standard; DNA; 20 BP.
XX AC ABL35617;
XX DT 04-APR-2002 (first entry)
XX DE Immunostimulatory oligonucleotide SEQ ID NO: 543.
XX DNA/RNA hybrid; phosphorothioate backbone; immunostimulatory; vaccine;
XX infection; allergy; cancer; hypersensitivity; bio-warfare;
XX immunostimulant; antiallergic; cytostatic; antimicrobial; anti-HIV;
XX immunosuppressive; protozoacide; virucide; hepatotropic; gene therapy;
XX antiinflammatory; antibacterial; ss.
XX Synthetic.
XX Key Location/Qualifiers
XX Key misc_RNA 1..20
XX /tag= a
XX /note= "optionally thymidine is replaced by uracil to
XX form RNA or DNA/RNA hybrids. Thymidine is linked to at
XX least one other base through a ribose sugar"
XX WO200193902-A2.
XX 13-DEC-2001.
XX 07-JUN-2001; 2001WO-US018276.
XX PF
XX 07-JUN-2000; 2000US-0209797P.
XX PF

```

XX PA (BIOS-) BIOSNEXUS INC.
 XX PI Mond JJ, Flora M, Klinman DM;
 XX DR WPI; 2002-130570/17.
 XX PT New immunostimulatory compositions comprising RNA/DNA hybrid
 PT oligonucleotides, useful for enhancing an immune response or inducing
 PT cytokines, particularly for treating diseases, e.g. cancer, allergy or
 PT HIV infection.
 XX PS Example 11; Page 62; 68pp; English.
 XX CC The present invention relates to an immunostimulatory composition, which
 CC comprises at least one oligonucleotide comprising both an RNA region and
 CC a DNA region. The composition is useful for enhancing an immune response
 CC or inducing cytokines. It can be used as a vaccine adjuvant and in
 CC treating diseases, including pathogenic infection, (non-)malignant
 CC tumours (e.g. cancers of the brain, lung, ovary, breast, prostate or
 CC colon, or carcinomas and sarcomas), autoimmune diseases or allergies
 CC (e.g. allergic rhinitis, hay fever or food allergies), Lyme disease,
 CC hepatitis, HIV or malaria. The composition is also useful for treating,
 CC preventing or ameliorating the symptoms resulting from exposure to a bio-
 CC warfare agent, e.g. Ebola, Anthrax or Listeria. The present sequence is
 CC an immunostimulatory oligonucleotide described in the exemplification of
 CC the invention
 XX SQ Sequence 20 BP; 3 A; 4 C; 11 G; 2 T; 0 U; 0 Other;
 Query Match 91.1%; Score 16.4; DB 6; Length 20;
 Best Local Similarity 94.4%; Pred. No. 2.2e+02;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 TGGCCCGATGCAGGGGG 18
 ||| |||||
 Db 3 TGCACCGATGCAGGGGG 20
 Search completed: July 2, 2004, 08:31:38
 Job time : 134.89 secs

PT linked by phosphate bond-oligodideoxynucleotides.
 XX Claim 4; Page 9; 30pp; English.
 XX CC The invention describes a vaccine comprising one or more epitopes of a
 CC Paramyxoviridae F protein, and one or more CpG (cytosine followed by
 CC guanine linked by phosphate bond)-oligodideoxynucleotides (ODNs). The
 CC vaccine is useful for vaccinating a patient especially against viruses of
 CC the Paramyxoviridae family e.g. respiratory syncytial virus (RSV), the
 CC primary cause of viral bronchiolitis and pneumonia in infants and
 CC children, and infectious pulmonary disease in infants. RSV has been
 CC particularly implicated in death of infants that are premature, have
 CC bronchopulmonary dysplasia, or congenital heart conditions. This sequence
 CC represents an oligodideoxynucleotide that can be used in the creation of
 CC the vaccine
 XX SQ Sequence 20 BP; 2 A; 3 C; 12 G; 3 T; 0 U; 0 Other;
 Query Match 91.1%; Score 16.4; DB 6; Length 20;
 Best Local Similarity 94.4%; Pred. No. 2.2e+02;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 TGGCCCGATGCAGGGGG 18
 ||| |||||
 Db 3 TGCACCGATGCAGGGGG 20
 Search completed: July 2, 2004, 08:31:38
 Job time : 134.89 secs

RESULT 15
 ID ABK46510
 XX ABK46510 standard; DNA; 20 BP.
 XX AC ABK46510;
 XX DT 05-JUN-2002 (first entry)
 XX DE Immunostimulatory unmethylated CpG oligodideoxynucleotide #100.
 XX KW unmethylated CpG; oligodideoxynucleotide; ODN; virucide; vaccine;
 KW Paramyxoviridae; F protein; respiratory syncytial virus; RSV;
 KW viral bronchiolitis; pneumonia; infectious pulmonary disease;
 KW bronchopulmonary dysplasia; congenital heart condition; ss.
 XX OS Synthetic.
 XX PN WO200211761-A2.
 XX PD 14-FEB-2002.
 XX PF 09-AUG-2001; 2001WO-US041633.
 XX PR 10-AUG-2000; 2000US-0224011P.
 XX PR 01-SEP-2000; 2000US-0229307P.
 XX PA (JACK-) JACKSON FOUND ADVANCEMENT MILITARY MED.
 XX PI Mond JJ, Prince G, Klinman DM;
 XX DR WPI; 2002-227118/28.
 XX PT Vaccine for immunizing patient against respiratory syncytial virus, has
 PT epitopes of Paramyxoviridae F protein, and cytosine followed by guanine

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 2, 2004, 08:09:30 ; Search time 28.2073 Seconds
(without alignments)
354.132 Million cell updates/sec

Title: US-10-068-160-18
Perfect score: 18
Sequence: 1 tgcgcgatgcaggggg 18

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA:
1: /cgn2_6/prodata/2/ina/5A COMB.seq:
2: /cgn2_6/prodata/2/ina/5B COMB.seq:
3: /cgn2_6/prodata/2/ina/6A COMB.seq:
4: /cgn2_6/prodata/2/ina/6B COMB.seq:
5: /cgn2_6/prodata/2/ina/6C COMB.seq:
6: /cgn2_6/prodata/2/ina/6D COMB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	14.8	82.2	3358	3	US-09-248-571-2
2	14.8	82.2	3358	4	US-09-553-736-2
3	14.8	82.2	3728	1	US-08-111-939-1
4	14.8	82.2	10380	3	US-09-077-354B-3
5	14.8	82.2	33529	3	US-09-144-085-3
6	14.8	82.2	4403765	3	US-09-103-840A-2
7	14.8	82.2	441529	3	US-09-103-840A-1
8	14.4	80.0	648	4	US-09-252-991A-4236
9	14.4	80.0	756	3	US-09-175-014-1
10	14.4	80.0	771	4	US-09-252-991A-4440
11	14.4	80.0	1024	4	US-09-328-475C-59
12	14.4	80.0	1488	4	US-09-252-991A-4168
13	14.4	80.0	1503	4	US-09-252-991A-4643
14	14.4	80.0	2870	4	US-09-799-875-16
15	14.4	80.0	2891	4	US-09-578-441-1
16	14.4	77.8	519	4	US-09-252-991A-2220
17	14.4	77.8	615	4	US-09-252-991A-5794
18	14.4	77.8	879	4	US-09-252-991A-2380
19	14.4	77.8	1407	4	US-09-252-991A-2455
20	14.4	77.8	1617	4	US-09-252-991A-5856
21	14.4	77.8	2019	4	US-09-252-991A-5836
22	14.4	77.8	2391	4	US-09-252-991A-5912
23	14.4	77.8	2814	4	US-09-252-991A-5912
24	13.8	76.7	20	4	US-09-659-845A-106
25	13.8	76.7	236	4	US-09-621-976-18710
26	13.8	76.7	382	4	US-09-833-381-178
27	13.8	76.7	462	4	US-09-252-991A-9628

28	13.8	76.7	468	4	US-09-252-991A-9670	Sequence 9670, Ap
29	13.8	76.7	594	4	US-09-489-039A-7023	Sequence 7023, Ap
30	13.8	76.7	597	4	US-09-252-991A-14469	Sequence 14469, A
31	13.8	76.7	630	4	US-09-252-991A-9630	Sequence 9630, Ap
32	13.8	76.7	633	4	US-09-489-039A-2752	Sequence 2752, Ap
33	13.8	76.7	699	4	US-09-252-991A-11367	Sequence 11367, A
34	13.8	76.7	885	4	US-09-252-991A-7532	Sequence 7532, Ap
35	13.8	76.7	912	4	US-09-252-991A-7811	Sequence 7811, Ap
36	13.8	76.7	1011	4	US-09-252-991A-9228	Sequence 9228, Ap
37	13.8	76.7	1017	4	US-09-252-991A-11322	Sequence 11322, A
38	13.8	76.7	1020	4	US-09-252-991A-9145	Sequence 9145, Ap
39	13.8	76.7	1119	4	US-09-252-991A-11028	Sequence 11028, A
40	13.8	76.7	1146	4	US-09-252-991A-9710	Sequence 9710, Ap
41	13.8	76.7	1188	4	US-09-252-991A-8025	Sequence 8025, Ap
42	13.8	76.7	1242	4	US-09-252-991A-7949	Sequence 7949, Ap
43	13.8	76.7	1255	4	US-09-659-845A-104	Sequence 104, App
44	13.8	76.7	1287	4	US-09-252-991A-8820	Sequence 8820, Ap
45	13.8	76.7	1293	4	US-09-252-991A-15351	Sequence 15351, A

ALIGNMENTS

RESULT 1

US-09-248-571-2
; Sequence 2, Application US/09248571
; Patent No. 6136539
; GENERAL INFORMATION:
; APPLICANT: BASBAUM, CAROL
; APPLICANT: GALLUP, MARIANNE
; APPLICANT: DAIZONG, LI
; APPLICANT: GEBREMICHAEL, ASSEFA
; TITLE OF INVENTION: GENSCHE, ERIN
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR INHIBITION OF MUC-5 MUCIN
; FILE REFERENCE: UCSF12/02
; CURRENT APPLICATION NUMBER: US/09/248,571
; CURRENT FILING DATE: 1999-02-11
; EARLIER APPLICATION NUMBER: 60/074,398
; EARLIER FILING DATE: 1998-02-11
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 3358
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-248-571-2

Query Match 82.2%; Score 14.8; DB 3; Length 3358;
Best Local Similarity 88.9%; Pred. No. 2.3e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 TGC GCGATG CAGGGGG 18
DB 999 TGC ACCATG CAGGGGG 1016

RESULT 2

US-09-553-736-2
; Sequence 2, Application US/09553736
; Patent No. 6440672
; GENERAL INFORMATION:
; APPLICANT: BASBAUM, CAROL
; APPLICANT: GALLUP, MARIANNE
; APPLICANT: DAIZONG, LI
; APPLICANT: GEBREMICHAEL, ASSEFA
; TITLE OF INVENTION: GENSCHE, ERIN
; TITLE OF INVENTION: MUCIN GENE EXPRESSION
; FILE REFERENCE: UCSF-012/03US
; CURRENT APPLICATION NUMBER: US/09/553,736
; CURRENT FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 09/248,571


```
; PRIOR FILING DATE: 1999-02-11
; PRIOR APPLICATION NUMBER: US 60/074,398
; PRIOR FILING DATE: 1998-02-11
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 3358
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-553-736-2

Query Match      82.2%; Score 14.8; DB 4; Length 3358;
Best Local Similarity 88.9%; Pred. No. 2.3e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 TGGCCCGATGCAGGGGG 18
Db      999 TGCACCCATGCAGGGGG 1016

RESULT 3
US-08-111-939-1/c
; Sequence 1, Application US/08111939
; Patent No. 5460951
; GENERAL INFORMATION:
; APPLICANT: Kawai, Shinji
; APPLICANT: Takeshita, Sunao
; APPLICANT: Okazaki, Makoto
; APPLICANT: Amann, Egon
; TITLE OF INVENTION: Bone-Related Carboxypeptidase-Like
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESSEE: Dunner
; STREET: 1300 I Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/08/111,939
; FILING DATE: 26-AUG-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 324033/92
; FILING DATE: 03-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 230029/92
; FILING DATE: 28-AUG-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Forman, David S.
; REGISTRATION NUMBER: 33,694
; REFERENCE/DOCKET NUMBER: 02481.1321-00000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-408-4000
; TELEFAX: 202-408-4000
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3728 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cdna to mRNA
; ORIGINAL SOURCE:
; ORGANISM: Mus musculus
; STRAIN: osteoblastic cell line MC3T3E1
; FEATURE:
; NAME/KEY: exon 1
; LOCATION: 202..4000
; FEATURE:
; NAME/KEY: exon 2
; LOCATION: 2115..2262
; FEATURE:
; NAME/KEY: exon 3
; LOCATION: 3056..3202
; FEATURE:
; NAME/KEY: exon 4
; LOCATION: 3387..3472
; FEATURE:
; NAME/KEY: exon 5
```

```
; NAME/KEY: CDS
; LOCATION: 69...3452
; US-08-111-939-1

Query Match      82.2%; Score 14.8; DB 1; Length 3728;
Best Local Similarity 88.9%; Pred. No. 2.3e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 TGGCCCGATGCAGGGGG 18
Db      3093 TGGCCCGCTGCTGGGGG 3076

RESULT 4
US-07-077-354B-3/c
; Sequence 3, Application US/09077354B
; Patent No. 6255096
; GENERAL INFORMATION:
; APPLICANT: HOPWOOD, JOHN JOSEPH; SCOTT, HAMISH STEELE;
; APPLICANT: WEBER, BIRGIT; BLANCH, LIANNE; ANSON, DONALD STEWART
; TITLE OF INVENTION: SYNTHETIC MAMMALIAN
; TITLE OF INVENTION: -N-ACETYLGLUCOSAMINIDASE AND GENETIC SEQUENCES ENCODING SAM
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 GARDEN CITY PLAZA
; CITY: GARDEN CITY
; STATE: NEW YORK
; COUNTRY: UNITED STATES
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/077,354B
; FILING DATE: 22-APRIL-1999
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/00747
; FILING DATE: 22-NOV-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: POKALSKY, ANN R.
; REGISTRATION NUMBER: 34,697
; REFERENCE/DOCKET NUMBER: 12416
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 516 742 4343
; TELEFAX: 516 742 4366
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10380 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT: Chromosome 17
; FEATURE:
; NAME/KEY: exon 1
; LOCATION: 990..1372
; FEATURE:
; NAME/KEY: exon 2
; LOCATION: 2115..2262
; FEATURE:
; NAME/KEY: exon 3
; LOCATION: 3056..3202
; FEATURE:
; NAME/KEY: exon 4
; LOCATION: 3387..3472
; FEATURE:
; NAME/KEY: exon 5
```

LOCATION: 5667..5923
FEATURE:
NAME/KEY: exon 6
LOCATION: 7745..8955
US-09-077-354B-3

Query Match 82.2%; Score 14.8; DB 3; Length 10380;
Best Local Similarity 88.9%; Pred. No. 2.2e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TGGCCCGATGCAGGGGG 18
DB 2346 TGGCCCATGCTGGGGG 2329

RESULT 5

US-09-144-085-3
; Sequence 3, Application US/09144085
; Patent No. 6280999
; GENERAL INFORMATION:
; APPLICANT: Gustafsson, Claes
; APPLICANT: Betlach, Mary C.
; APPLICANT: Ashley, Gary
; APPLICANT: Julien, Bryan
; APPLICANT: Ziermann, Rainer
; TITLE OF INVENTION: SORANGIUM POLYKETIDE SYNTHASES AND ENCODING DNA
; TITLE OF INVENTION: THEREFOR
; FILE REFERENCE: 30062-20020.20
; CURRENT APPLICATION NUMBER: US/09/144,085
; EARLIER FILING DATE: 1998-08-31
; EARLIER APPLICATION NUMBER: 09/010,809
; EARLIER FILING DATE: 1998-01-22
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 33529
; TYPE: DNA
; ORGANISM: Sorangium cellulosum
US-09-144-085-3

Query Match 82.2%; Score 14.8; DB 3; Length 33529;
Best Local Similarity 88.9%; Pred. No. 2.1e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TGGCCCGATGCAGGGGG 18
DB 30209 TGGCCAGATGCAGGGG 30226

RESULT 6

US-09-103-840A-2/c
; Sequence 2, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; TITLE OF INVENTION: TUBERCULOSIS
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 4403765
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; FEATURE:
; OTHER INFORMATION: CDC 1551
; OTHER INFORMATION: "n" bases at various positions throughout the sequence
; OTHER INFORMATION: represent a, t, c or g

US-09-103-840A-2

Query Match 82.2%; Score 14.8; DB 3; Length 4403765;
Best Local Similarity 88.9%; Pred. No. 97;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TGGCCCGATGCAGGGGG 18
DB 173979 TGGCCGATGCAGCGCG 173962

RESULT 7

US-09-103-840A-1/c
; Sequence 1, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; TITLE OF INVENTION: TUBERCULOSIS
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 4411529
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; OTHER INFORMATION: H37Rv
US-09-103-840A-1

Query Match 82.2%; Score 14.8; DB 3; Length 4411529;
Best Local Similarity 88.9%; Pred. No. 96;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TGGCCCGATGCAGGGGG 18
DB 173810 TGGCCGATGCAGCGCG 173793

RESULT 8

US-09-252-991A-4236/c
; Sequence 4236, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 4236
; LENGTH: 648
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-4236

Query Match 80.0%; Score 14.4; DB 4; Length 648;
Best Local Similarity 93.8%; Pred. No. 3.7e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TGGCCCGATGCAGGGG 16
DB 263 TGGCCGAGGCAGGGG 248

RESULT 9
US-09-175-014-1
; Sequence 1, Application US/09175014
; Patent No. 6261802
; GENERAL INFORMATION:
; APPLICANT: Huang, Jianzhong
; APPLICANT: Jiang, Xinhe
; APPLICANT: McDevitt, Damien
; TITLE OF INVENTION: ups (ugc)
; FILE REFERENCE: GMI0171
; CURRENT APPLICATION NUMBER: US/09/175,014
; CURRENT FILING DATE: 1998-10-19
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Fast-SEQ for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 756
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(753)
US-09-175-014-1

Query Match 80.0%; Score 14.4; DB 3; Length 756;
Best Local Similarity 93.8%; Pred. No. 3.7e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TGGCCCGATGCGGGG 16
|||||
Db 148 TGGCCCGAGCGGGG 163
|||||

RESULT 10
US-09-252-991A-4440
; Sequence 4440, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 4440
; LENGTH: 771
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-4440

Query Match 80.0%; Score 14.4; DB 4; Length 771;
Best Local Similarity 93.8%; Pred. No. 3.7e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TGGCCCGATGCGGGG 16
|||||
Db 163 TGGCCCGAGCGGGG 178
|||||

RESULT 11
US-09-328-475C-59/C
; Sequence 59, Application US/09328475C
; Patent No. 6476207
; GENERAL INFORMATION:
; APPLICANT: Zhang, Jimmy
; APPLICANT: Astel, Jon H.
; APPLICANT: Carroll III, Eddie
; APPLICANT: Endege, Wilson O.

; APPLICANT: Ford, Donna M.
; APPLICANT: Monahan, John E.
; APPLICANT: Schlegel, Robert
; APPLICANT: Steinmann, Kathleen E.
; TITLE OF INVENTION: GENES AND GENE EXPRESSION PRODUCTS THAT
; FILE REFERENCE: 1532.002/200130.463
; CURRENT APPLICATION NUMBER: US/09/328,475C
; CURRENT FILING DATE: 1999-06-09
; NUMBER OF SEQ ID NOS: 341
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 59
; LENGTH: 1024
; TYPE: DNA
; ORGANISM: Homo Sapien
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(1024)
; OTHER INFORMATION: n = A,T,C or G
US-09-328-475C-59

Query Match 80.0%; Score 14.4; DB 4; Length 1024;
Best Local Similarity 83.3%; Pred. No. 3.6e+02;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 TGGCCCGATGCGGGG 18
|||||
Db 805 TGGCCGNTACAGGGG 788
|||||

RESULT 12
US-09-252-991A-4168/c
; Sequence 4168, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 4168
; LENGTH: 1488
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-4168

Query Match 80.0%; Score 14.4; DB 4; Length 1488;
Best Local Similarity 93.8%; Pred. No. 3.6e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TGGCCCGATGCGGGG 16
|||||
Db 600 TGGCCGAGCGGGG 585
|||||

RESULT 13
US-09-252-991A-4643
; Sequence 4643, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18

TITLE OF INVENTION: HUMAN HEME-REGULATED INITIATION FACTOR 2. ALPHA KINASE
 FILE REFERENCE: 176/60571
 CURRENT APPLICATION NUMBER: US/09/578,441
 CURRENT FILING DATE: 2000-05-25
 PRIOR APPLICATION NUMBER: 60/135,713
 PRIOR FILING DATE: 1999-05-25
 NUMBER OF SEQ ID NOS: 5

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 2, 2004, 08:11:05 ; Search time 138.732 Seconds
(without alignments)
625.926 Million cell updates/sec

Title: US-10-068-160-18

Perfect score: 18

Sequence: 1 tgcgcgatgcaggggg 18

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searched: 3163042 seqs, 2412103800 residues

Total number of hits satisfying chosen parameters: 6326084

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:*

- 1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
- 6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
- 7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
- 8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
- 10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
- 12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
- 13: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
- 14: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
- 15: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
- 16: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
- 17: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
- 18: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
- 19: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	18	100.0	18	15	US-10-068-160-18
2	18	100.0	20	17	US-10-666-022-16
3	17	94.4	19	15	US-10-194-035-76
4	16.4	91.1	18	15	US-10-068-160-16
5	16.4	91.1	20	13	US-09-874-991C-499
6	16.4	91.1	20	13	US-09-874-991C-510
7	16.4	91.1	20	13	US-09-874-991C-543
8	16.4	91.1	20	15	US-10-068-160-7
9	16.4	91.1	20	15	US-10-068-160-37
10	16.4	91.1	20	15	US-10-194-035-40
11	16.4	91.1	20	15	US-10-194-035-81
12	16.4	91.1	20	15	US-10-194-035-82
13	16.4	91.1	20	15	US-10-194-035-101
14	16.4	91.1	20	17	US-10-666-022-4

15	16.4	91.1	20	17	US-10-666-022-16	Sequence 16, Appl
16	16.4	91.1	28	13	US-09-874-991C-520	Sequence 520, App
17	16.4	91.1	28	13	US-09-874-991C-532	Sequence 532, App
18	15.4	85.6	19	15	US-10-194-035-22	Sequence 22, Appl
19	15.4	85.6	19	15	US-10-194-035-83	Sequence 83, Appl
20	15.4	85.6	675	15	US-10-257-826A-239	Sequence 239, Appl
21	15.4	85.6	1668	17	US-10-437-963-47855	Sequence 47855, A
22	15	83.3	2712	13	US-10-282-122A-14655	Sequence 14655, A
23	14.8	82.2	18	13	US-09-874-991C-503	Sequence 503, App
24	14.8	82.2	18	13	US-09-874-991C-513	Sequence 513, App
25	14.8	82.2	18	13	US-09-874-991C-551	Sequence 551, App
26	14.8	82.2	18	15	US-10-068-160-12	Sequence 12, Appl
27	14.8	82.2	18	15	US-10-068-160-13	Sequence 13, Appl
28	14.8	82.2	18	15	US-10-068-160-14	Sequence 14, Appl
29	14.8	82.2	18	15	US-10-068-160-17	Sequence 17, Appl
30	14.8	82.2	18	15	US-10-068-160-20	Sequence 20, Appl
31	14.8	82.2	20	13	US-09-874-991C-494	Sequence 494, App
32	14.8	82.2	20	13	US-09-874-991C-496	Sequence 496, App
33	14.8	82.2	20	13	US-09-874-991C-497	Sequence 497, App
34	14.8	82.2	20	13	US-09-874-991C-502	Sequence 502, App
35	14.8	82.2	20	13	US-09-874-991C-504	Sequence 504, App
36	14.8	82.2	20	13	US-09-874-991C-505	Sequence 505, App
37	14.8	82.2	20	13	US-09-874-991C-507	Sequence 507, App
38	14.8	82.2	20	13	US-09-874-991C-508	Sequence 508, App
39	14.8	82.2	20	13	US-09-874-991C-512	Sequence 512, App
40	14.8	82.2	20	13	US-09-874-991C-514	Sequence 514, App
41	14.8	82.2	20	13	US-09-874-991C-538	Sequence 538, App
42	14.8	82.2	20	13	US-09-874-991C-540	Sequence 540, App
43	14.8	82.2	20	13	US-09-874-991C-541	Sequence 541, App
44	14.8	82.2	20	13	US-09-874-991C-546	Sequence 546, App
45	14.8	82.2	20	13	US-09-874-991C-550	Sequence 550, App

ALIGNMENTS

RESULT 1
US-10-068-160-18
; Sequence 18, Application US/10068160
; Publication No. US20030060440A1
; GENERAL INFORMATION:
; APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA, REPRESENTED BY THE
; APPLICANT: SECRETARY, DEPARTMENT OF HEALTH AND HUMAN SERVICES
; APPLICANT: KLINMAN, Dennis
; APPLICANT: ISHII, Ken
; APPLICANT: VERTHELYI, Daniela
; TITLE OF INVENTION: OLIGODEOXYNUCLEOTIDE AND ITS USE TO INDUCE AN IMMUNE RESPONSE
; FILE REFERENCE: 4239-61999
; CURRENT APPLICATION NUMBER: US/10/068,160
; CURRENT FILING DATE: 2002-02-06
; PRIOR APPLICATION NUMBER: 60/128,898
; PRIOR FILING DATE: 1999-04-12
; NUMBER OF SEQ ID NOS: 120
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURES:
; OTHER INFORMATION: Oligonucleotide
US-10-068-160-18

Query Match 100.0%; Score 18; DB 15; Length 18;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TCGCGCATGCAGGGGG 18
Db 1 TCGCGCATGCAGGGGG 18

RESULT 2
US-10-666-022-6

Sequence 6, Application US/10666022
Publication No. US20040105872A1
GENERAL INFORMATION:
APPLICANT: The Government of the United States of America, as represented by the
Secretary of the Department of Health and Human Services
APPLICANT: KLINMAN, Dennis M.
APPLICANT: VERTHELYI, Daniela
TITLE OF INVENTION: METHOD OF TREATING AND PREVENTING INFECTIONS IN IMMUNOCOMPROMISED
SUBJECTS WITH IMMUNOSTIMULATORY CPG
FILE REFERENCE: 4239-66899
CURRENT APPLICATION NUMBER: US/10/666,022
PRIOR FILING DATE: 2003-09-17
PRIOR APPLICATION NUMBER: US 60/411,944
PRIOR FILING DATE: 2002-09-18
NUMBER OF SEQ ID NOS: 191
SOFTWARE: PatentIn version 3.1
SEQ ID NO 6
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: synthetic
NAME/KEY: misc feature
LOCATION: (1)..(20)
OTHER INFORMATION: n is a, c, g, or t, or no nucleotide
US-10-666-022-6

Query Match 100.0%; Score 18; DB 17; Length 20;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGGCCCGATCGAGGGGG 18
DB 3 TGGCCCGATCGAGGGGG 20

RESULT 3
US-10-194-035-76
Sequence 76, Application US/10194035
Publication No. US20030144229A1
GENERAL INFORMATION:
APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS REPRESENTED BY THE
SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES
APPLICANT: KLINMAN, Dennis
APPLICANT: ISHII, Ken
TITLE OF INVENTION: OLIGODEOXYNUCLEOTIDE AND ITS USE TO INDUCE AN IMMUNE RESPONSE
FILE REFERENCE: 4239-63317
CURRENT APPLICATION NUMBER: US/10/194,035
PRIOR FILING DATE: 2002-07-12
CURRENT APPLICATION NUMBER: PCT/US01/01122
PRIOR FILING DATE: 2001-07-19
PRIOR APPLICATION NUMBER: US 60/176,115
PRIOR FILING DATE: 2000-01-14
NUMBER OF SEQ ID NOS: 119
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 76
LENGTH: 19
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
US-10-194-035-76

Query Match 94.4%; Score 17; DB 15; Length 19;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGGCCCGATCGAGGGGG 17
DB 3 TGGCCCGATCGAGGGGG 19

RESULT 4
US-10-068-160-16
Sequence 16, Application US/10068160
Publication No. US2003006040A1
GENERAL INFORMATION:
APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA, REPRESENTED BY THE
SECRETARY, DEPARTMENT OF HEALTH AND HUMAN SERVICES
APPLICANT: KLINMAN, Dennis
APPLICANT: ISHII, Ken
TITLE OF INVENTION: OLIGODEOXYNUCLEOTIDE AND ITS USE TO INDUCE AN IMMUNE RESPONSE
FILE REFERENCE: 4239-61999
CURRENT APPLICATION NUMBER: US/10/068,160
CURRENT FILING DATE: 2002-02-06
PRIOR APPLICATION NUMBER: 60/128,898
PRIOR FILING DATE: 1999-04-12
NUMBER OF SEQ ID NOS: 120
SOFTWARE: PatentIn version 3.1
SEQ ID NO 16
LENGTH: 18
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Oligonucleotide
US-10-068-160-16

Query Match 91.1%; Score 15.4; DB 15; Length 18;
Best Local Similarity 94.4%; Pred. No. 1.4e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TGGCCCGATCGAGGGGG 18
DB 1 TGGCCCGATCGAGGGGG 18

RESULT 5
US-09-874-991C-499
Sequence 499, Application US/09874991C
Publication No. US20040052763A1
GENERAL INFORMATION:
APPLICANT: MOND, JAMES J.
APPLICANT: FLORA, MICHAEL
APPLICANT: KLINMAN, DENNIS M.
TITLE OF INVENTION: IMMUNOSTIMULATORY RNA/DNA HYBRID MOLECULES
FILE REFERENCE: 07787,0042-0
CURRENT APPLICATION NUMBER: US/09/874,991C
CURRENT FILING DATE: 2001-06-07
PRIOR APPLICATION NUMBER: 60/209,797
PRIOR FILING DATE: 2000-06-07
NUMBER OF SEQ ID NOS: 620
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 499
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic HDR
US-09-874-991C-499

Query Match 91.1%; Score 15.4; DB 13; Length 20;
Best Local Similarity 94.4%; Pred. No. 1.4e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TGGCCCGATCGAGGGGG 18
DB 3 TGGCCCGATCGAGGGGG 20

RESULT 6
US-09-874-991C-510
Sequence 510, Application US/09874991C
Publication No. US20040052763A1

GENERAL INFORMATION:
APPLICANT: MOND, JAMES J.
APPLICANT: FLORA, MICHAEL
APPLICANT: KLINMAN, DENNIS M.
TITLE OF INVENTION: IMMUNOSTIMULATORY RNA/DNA HYBRID MOLECULES
FILE REFERENCE: 07787.0042-0
CURRENT APPLICATION NUMBER: US/09/874.991C
CURRENT FILING DATE: 2001-06-07
PRIOR APPLICATION NUMBER: 60/209,797
PRIOR FILING DATE: 2000-06-07
NUMBER OF SEQ ID NOS: 620
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 510
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic HDR
US-09-874-991C-510

Query Match 91.1%; Score 16.4; DB 13; Length 20;
Best Local Similarity 94.4%; Pred. No. 1.4e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TGGCCCGATGCGAGGGG 18
Db 3 TGCACCGATGCGAGGGG 20

RESULT 7
US-09-874-991C-543
Sequence 543, Application US/09874991C
Publication No. US20040052763A1
GENERAL INFORMATION:
APPLICANT: MOND, JAMES J.
APPLICANT: FLORA, MICHAEL
APPLICANT: KLINMAN, DENNIS M.
TITLE OF INVENTION: IMMUNOSTIMULATORY RNA/DNA HYBRID MOLECULES
FILE REFERENCE: 07787.0042-0
CURRENT APPLICATION NUMBER: US/09/874.991C
CURRENT FILING DATE: 2001-06-07
PRIOR APPLICATION NUMBER: 60/209,797
PRIOR FILING DATE: 2000-06-07
NUMBER OF SEQ ID NOS: 620
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 543
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic HDR
US-09-874-991C-543

Query Match 91.1%; Score 16.4; DB 13; Length 20;
Best Local Similarity 94.4%; Pred. No. 1.4e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TGGCCCGATGCGAGGGG 18
Db 3 TGCACCGATGCGAGGGG 20

RESULT 8
US-10-068-160-7
Sequence 7, Application US/10068160
Publication No. US2003006040A1
GENERAL INFORMATION:
APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA, REPRESENTED BY THE
APPLICANT: SECRETARY, DEPARTMENT OF HEALTH AND HUMAN SERVICES
APPLICANT: KLINMAN, Dennis
APPLICANT: ISHII, Ken
TITLE OF INVENTION: OLIGODEOXYNUCLEOTIDE AND ITS USE TO INDUCE AN IMMUNE RESPONSE
FILE REFERENCE: 4239-61999
CURRENT APPLICATION NUMBER: US/10/194.035
CURRENT FILING DATE: 2002-07-12

FILE REFERENCE: 4239-61999
CURRENT APPLICATION NUMBER: US/10/068.160
CURRENT FILING DATE: 2002-02-06
PRIOR APPLICATION NUMBER: 60/128,898
PRIOR FILING DATE: 1999-04-12
NUMBER OF SEQ ID NOS: 120
SOFTWARE: Patentin version 3.1
SEQ ID NO 7
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Oligonucleotide
US-10-068-160-7

Query Match 91.1%; Score 16.4; DB 15; Length 20;
Best Local Similarity 94.4%; Pred. No. 1.4e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TGGCCCGATGCGAGGGG 18
Db 3 TGCCTCGATGCGAGGGG 20

RESULT 9
US-10-068-160-37
Sequence 37, Application US/10068160
Publication No. US20030060440A1
GENERAL INFORMATION:
APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA, REPRESENTED BY THE
APPLICANT: SECRETARY, DEPARTMENT OF HEALTH AND HUMAN SERVICES
APPLICANT: KLINMAN, Dennis
APPLICANT: ISHII, Ken
APPLICANT: VERHELXI, Daniela
TITLE OF INVENTION: OLIGODEOXYNUCLEOTIDE AND ITS USE TO INDUCE AN IMMUNE RESPONSE
FILE REFERENCE: 4239-61999
CURRENT APPLICATION NUMBER: US/10/068.160
CURRENT FILING DATE: 2002-02-06
PRIOR APPLICATION NUMBER: 60/128,898
PRIOR FILING DATE: 1999-04-12
NUMBER OF SEQ ID NOS: 120
SOFTWARE: Patentin version 3.1
SEQ ID NO 37
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Oligonucleotide
US-10-068-160-37

Query Match 91.1%; Score 16.4; DB 15; Length 20;
Best Local Similarity 94.4%; Pred. No. 1.4e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TGGCCCGATGCGAGGGG 18
Db 3 TGCACCGATGCGAGGGG 20

RESULT 10
US-10-194-035-40
Sequence 40, Application US/10194035
Publication No. US20030144229A1
GENERAL INFORMATION:
APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS REPRESENTED BY THE
APPLICANT: SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES
APPLICANT: KLINMAN, Dennis
APPLICANT: ISHII, Ken
APPLICANT: VERHELXI, Daniela
TITLE OF INVENTION: OLIGODEOXYNUCLEOTIDE AND ITS USE TO INDUCE AN IMMUNE RESPONSE
FILE REFERENCE: 4239-63317
CURRENT APPLICATION NUMBER: US/10/194.035
CURRENT FILING DATE: 2002-07-12

; PRIOR APPLICATION NUMBER: PCT/US01/01122
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: US 60/176,115
; PRIOR FILING DATE: 2000-01-14
; NUMBER OF SEQ ID NOS: 119
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 40
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
US-10-194-035-40

Query Match 91.1%; Score 16.4; DB 15; Length 20;
Best Local Similarity 94.4%; Pred. No. 1.4e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TGGCCCGATGCAGGGGG 18
||| ||||| ||||| |||||
Db 3 TGGTCGATGCAGGGGG 20

RESULT 11
US-10-194-035-81
; Sequence 81, Application US/10194035
; Publication No. US20030144229A1
; GENERAL INFORMATION:
; APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS REPRESENTED BY THE
; APPLICANT: SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES
; APPLICANT: KLINMAN, Dennis
; APPLICANT: ISHII, Ken
; APPLICANT: VERTHELYI, Daniela
; TITLE OF INVENTION: OLIGODEOXYNUCLEOTIDE AND ITS USE TO INDUCE AN IMMUNE RESPONSE
; FILE REFERENCE: 4239-63317
; CURRENT APPLICATION NUMBER: US/10/194,035
; PRIOR FILING DATE: 2002-07-12
; PRIOR APPLICATION NUMBER: PCT/US01/01122
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: US 60/176,115
; PRIOR FILING DATE: 2000-01-14
; NUMBER OF SEQ ID NOS: 119
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 81
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
US-10-194-035-81

Query Match 91.1%; Score 16.4; DB 15; Length 20;
Best Local Similarity 94.4%; Pred. No. 1.4e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TGGCCCGATGCAGGGGG 18
||| ||||| ||||| |||||
Db 3 TGGTCGATGCAGGGGG 20

RESULT 12
US-10-194-035-82
; Sequence 82, Application US/10194035
; Publication No. US20030144229A1
; GENERAL INFORMATION:
; APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS REPRESENTED BY THE
; APPLICANT: SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES
; APPLICANT: KLINMAN, Dennis
; APPLICANT: ISHII, Ken
; APPLICANT: VERTHELYI, Daniela
; TITLE OF INVENTION: OLIGODEOXYNUCLEOTIDE AND ITS USE TO INDUCE AN IMMUNE RESPONSE
; FILE REFERENCE: 4239-63317
; CURRENT APPLICATION NUMBER: US/10/194,035

; CURRENT FILING DATE: 2002-07-12
; PRIOR APPLICATION NUMBER: PCT/US01/01122
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: US 60/176,115
; PRIOR FILING DATE: 2000-01-14
; NUMBER OF SEQ ID NOS: 119
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 82
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
US-10-194-035-82

Query Match 91.1%; Score 16.4; DB 15; Length 20;
Best Local Similarity 94.4%; Pred. No. 1.4e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TGGCCCGATGCAGGGGG 18
||| ||||| ||||| |||||
Db 3 TGGTCGATGCAGGGGG 20

RESULT 13
US-10-194-035-101
; Sequence 101, Application US/10194035
; Publication No. US20030144229A1
; GENERAL INFORMATION:
; APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS REPRESENTED BY THE
; APPLICANT: SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES
; APPLICANT: KLINMAN, Dennis
; APPLICANT: ISHII, Ken
; APPLICANT: VERTHELYI, Daniela
; TITLE OF INVENTION: OLIGODEOXYNUCLEOTIDE AND ITS USE TO INDUCE AN IMMUNE RESPONSE
; FILE REFERENCE: 4239-63317
; CURRENT APPLICATION NUMBER: US/10/194,035
; PRIOR FILING DATE: 2002-07-12
; PRIOR APPLICATION NUMBER: PCT/US01/01122
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: US 60/176,115
; PRIOR FILING DATE: 2000-01-14
; NUMBER OF SEQ ID NOS: 119
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 101
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
US-10-194-035-101

Query Match 91.1%; Score 16.4; DB 15; Length 20;
Best Local Similarity 94.4%; Pred. No. 1.4e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TGGCCCGATGCAGGGGG 18
||| ||||| ||||| |||||
Db 3 TGGTCGATGCAGGGGG 20

RESULT 14
US-10-666-022-4
; Sequence 4, Application US/10666022
; Publication No. US20040105872A1
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America, as represented by the
; APPLICANT: Secretary of the Department of Health and Human Services
; APPLICANT: KLINMAN, Dennis M.
; APPLICANT: VERTHELYI, Daniela
; TITLE OF INVENTION: METHOD OF TREATING AND PREVENTING INFECTIONS IN IMMUNOCOMPROMIS
; FILE REFERENCE: 4239-66899

; CURRENT APPLICATION NUMBER: US/10/666,022
; CURRENT FILING DATE: 2003-09-17
; PRIOR APPLICATION NUMBER: US 60/411,944
; PRIOR FILING DATE: 2002-09-18
; NUMBER OF SEQ ID NOS: 181
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(20)
; OTHER INFORMATION: n is a, c, g, or t, or no nucleotide
US-10-666-022-4

Query Match 91.1%; Score 16.4; DB 17; Length 20;
Best Local Similarity 94.4%; Pred. No. 1.4e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TGGCCGATGCAGGGGG 18
Db 3 TGGTCGATGCAGGGGG 20

RESULT 15
US-10-666-022-16
; Sequence 16, Application US/10666022
; Publication No. US20040105872A1
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America, as represented by the
; APPLICANT: Secretary of the Department of Health and Human Services
; APPLICANT: Klinman, Dennis M.
; APPLICANT: Verhelmi, Daniela
; TITLE OF INVENTION: METHOD OF TREATING AND PREVENTING INFECTIONS IN IMMUNOCOMPROMISED
; TITLE OF INVENTION: SUBJECTS WITH IMMUNOSTIMULATORY CPG
; FILE REFERENCE: 4239-66899
; CURRENT APPLICATION NUMBER: US/10/666,022
; CURRENT FILING DATE: 2003-09-17
; PRIOR APPLICATION NUMBER: US 60/411,944
; PRIOR FILING DATE: 2002-09-18
; NUMBER OF SEQ ID NOS: 181
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic
US-10-666-022-16

Query Match 91.1%; Score 16.4; DB 17; Length 20;
Best Local Similarity 94.4%; Pred. No. 1.4e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TGGCCGATGCAGGGGG 18
Db 3 TGGTCGATGCAGGGGG 20

Search completed: July 2, 2004, 13:58:26
Job time : 139.732 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 2, 2004, 07:36:05 ; Search time 704.146 Seconds
(without alignments)
1231.080 Million cell updates/sec

Title: US-10-068-160-1

Perfect score: 20

Sequence: 1 ggtgcatcgatgcaggggg 20

Scoring table:

IDENTITY_NUC

Gapop 10.0, Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.*

1: gb.ba.*

2: gb.hcg.*

3: gb.in.*

4: gb.om.*

5: gb.ov.*

6: gb.pat.*

7: gb.ph.*

8: gb.pl.*

9: gb.pr.*

10: gb.ro.*

11: gb.sts.*

12: gb.sy.*

13: gb.un.*

14: gb.vi.*

15: em.ba.*

16: em.fun.*

17: em.hum.*

18: em.in.*

19: em.mu.*

20: em.or.*

21: em.ov.*

22: em.pat.*

23: em.ph.*

24: em.pl.*

25: em.ro.*

26: em.sts.*

27: em.un.*

28: em.vi.*

29: em.yi.*

30: em.htg.hum.*

31: em.htg.inv.*

32: em.htg.other.*

33: em.htg.mus.*

34: em.htg.pln.*

35: em.htg.pln.*

36: em.htg.rod.*

37: em.htg.mam.*

38: em.htg.vrt.*

39: em.ey.*

40: em.htgo.hum.*

41: em.htgo.mus.*

42: em.htgo.other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	20	100.0	20	6	AX194432	Sequence
2	20	100.0	20	6	AX194434	Sequence
3	20	100.0	20	6	AX194437	Sequence
4	20	100.0	20	6	AX194438	Sequence
5	20	100.0	20	6	AX194443	Sequence
6	20	100.0	20	6	AX194472	Sequence
7	20	100.0	20	6	AX194472	Sequence
8	20	100.0	20	6	AX352198	Sequence
9	20	100.0	20	6	AX352209	Sequence
10	20	100.0	20	6	AX352242	Sequence
11	20	100.0	20	6	AX465382	Sequence
12	20	100.0	20	6	AX465384	Sequence
13	20	100.0	20	6	AX465387	Sequence
14	20	100.0	20	6	AX465388	Sequence
15	20	100.0	20	6	AX465393	Sequence
16	20	100.0	20	6	AX465422	Sequence
17	20	100.0	20	6	AX816067	Sequence
18	20	100.0	22	6	AX352204	Sequence
19	20	100.0	22	6	AX352248	Sequence
20	20	100.0	28	6	AX352219	Sequence
21	20	100.0	28	6	AX352231	Sequence
22	20	100.0	29	6	AX352237	Sequence
23	20	100.0	30	6	AX352225	Sequence
24	20	100.0	30	6	AX352230	Sequence
25	19	95.0	13	6	AX352167	Sequence
26	19	95.0	19	6	AX194453	Sequence
27	19	95.0	19	6	AX194473	Sequence
28	19	95.0	19	6	AX465403	Sequence
29	18.4	92.0	20	6	AX465423	Sequence
30	18.4	92.0	20	6	AX194440	Sequence
31	18.4	92.0	20	6	AX194481	Sequence
32	18.4	92.0	20	6	AX194482	Sequence
33	18.4	92.0	20	6	AX194500	Sequence
34	18.4	92.0	20	6	AX194501	Sequence
35	18.4	92.0	20	6	AX194504	Sequence
36	18.4	92.0	20	6	AX194506	Sequence
37	18.4	92.0	20	6	AX194507	Sequence
38	18.4	92.0	20	6	AX352202	Sequence
39	18.4	92.0	20	6	AX352203	Sequence
40	18.4	92.0	20	6	AX352213	Sequence
41	18.4	92.0	20	6	AX352214	Sequence
42	18.4	92.0	20	6	AX352246	Sequence
43	18.4	92.0	20	6	AX352247	Sequence
44	18.4	92.0	20	6	AX465390	Sequence
45	18.4	92.0	20	6	AX465431	Sequence
					AX465432	Sequence

ALIGNMENTS

RESULT 1
AX194432
LOCUS AX194432
DEFINITION Sequence 32 from Patent WO0151500.
ACCESSION AX194432
VERSION AX194432.1 GI:15385088
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL

AX194432
Sequence 32 from Patent WO0151500.
AX194432
AX194432.1 GI:15385088
synthetic construct
synthetic construct
artificial sequences.
1
Klimman,D., Ishii,K. and Verthelyi,D.
Oligodeoxynucleotide and its use to induce an immune response
Patent: WO 0151500-A 32 19-JUL-2001;
Secretary of the Department of Health and Human Services (US)

20 bp
DNA
linear
PAT 28-AUG-2001

```

FEATURES
  source
    1..20
      /organism="synthetic construct"
      /mol_type="unassigned DNA"
      /db_xref="taxon:32630"
      /note="Synthetic DNA"
ORIGIN
  Query Match
    Best Local Similarity 100.0%; Score 20; DB 6; Length 20;
    Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
  QY
    1 GGTGCATCGATCGAGGGGG 20
    |||||
  Db
    1 GGTGCATCGATCGAGGGGG 20
    |||||
RESULT 2
AX194434
LOCUS
  AX194434
  Sequence 34 from Patent WO0151500.
  20 bp DNA linear PAT 28-AUG-2001
ACCESSION
  AX194434
VERSION
  AX194434.1 GI:15385090
KEYWORDS
  synthetic construct
SOURCE
  synthetic construct
  artificial sequences.
REFERENCE
  1
  Klinman,D., Ishii,K. and Verthelyi,D.
  Oligodeoxynucleotide and its use to induce an immune response
  TITLE
  Patent: WO 0151500-A 34 19-JUL-2001;
  JOURNAL
  Secretary of the Department of Health and Human Services (US)
FEATURES
  source
    1..20
      /organism="synthetic construct"
      /mol_type="unassigned DNA"
      /db_xref="taxon:32630"
      /note="Synthetic DNA"
ORIGIN
  Query Match
    Best Local Similarity 100.0%; Score 20; DB 6; Length 20;
    Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
  QY
    1 GGTGCATCGATCGAGGGGG 20
    |||||
  Db
    1 GGTGCATCGATCGAGGGGG 20
    |||||
RESULT 3
AX194437
LOCUS
  AX194437
  Sequence 37 from Patent WO0151500.
  20 bp DNA linear PAT 28-AUG-2001
ACCESSION
  AX194437
VERSION
  AX194437.1 GI:15385093
KEYWORDS
  synthetic construct
SOURCE
  synthetic construct
  artificial sequences.
REFERENCE
  1
  Klinman,D., Ishii,K. and Verthelyi,D.
  Oligodeoxynucleotide and its use to induce an immune response
  TITLE
  Patent: WO 0151500-A 37 19-JUL-2001;
  JOURNAL
  Secretary of the Department of Health and Human Services (US)
FEATURES
  source
    1..20
      /organism="synthetic construct"
      /mol_type="unassigned DNA"
      /db_xref="taxon:32630"
      /note="Synthetic DNA"
ORIGIN
  Query Match
    Best Local Similarity 100.0%; Score 20; DB 6; Length 20;
    Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
  QY
    1 GGTGCATCGATCGAGGGGG 20
    |||||
  Db
    1 GGTGCATCGATCGAGGGGG 20
    |||||
RESULT 4
AX194438
LOCUS
  AX194438
  Sequence 38 from Patent WO0151500.
  20 bp DNA linear PAT 28-AUG-2001
ACCESSION
  AX194438
VERSION
  AX194438.1 GI:15385094
KEYWORDS
  synthetic construct
SOURCE
  synthetic construct
  artificial sequences.
REFERENCE
  1
  Klinman,D., Ishii,K. and Verthelyi,D.
  Oligodeoxynucleotide and its use to induce an immune response
  TITLE
  Patent: WO 0151500-A 38 19-JUL-2001;
  JOURNAL
  Secretary of the Department of Health and Human Services (US)
FEATURES
  source
    1..20
      /organism="synthetic construct"
      /mol_type="unassigned DNA"
      /db_xref="taxon:32630"
      /note="Synthetic DNA"
ORIGIN
  Query Match
    Best Local Similarity 100.0%; Score 20; DB 6; Length 20;
    Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
  QY
    1 GGTGCATCGATCGAGGGGG 20
    |||||
  Db
    1 GGTGCATCGATCGAGGGGG 20
    |||||
RESULT 5
AX194443
LOCUS
  AX194443
  Sequence 43 from Patent WO0151500.
  20 bp DNA linear PAT 28-AUG-2001
ACCESSION
  AX194443
VERSION
  AX194443.1 GI:15385099
KEYWORDS
  synthetic construct
SOURCE
  synthetic construct
  artificial sequences.
REFERENCE
  1
  Klinman,D., Ishii,K. and Verthelyi,D.
  Oligodeoxynucleotide and its use to induce an immune response
  TITLE
  Patent: WO 0151500-A 43 19-JUL-2001;
  JOURNAL
  Secretary of the Department of Health and Human Services (US)
FEATURES
  source
    1..20
      /organism="synthetic construct"
      /mol_type="unassigned DNA"
      /db_xref="taxon:32630"
      /note="Synthetic DNA"
ORIGIN
  Query Match
    Best Local Similarity 100.0%; Score 20; DB 6; Length 20;
    Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
  QY
    1 GGTGCATCGATCGAGGGGG 20
    |||||
  Db
    1 GGTGCATCGATCGAGGGGG 20
    |||||
RESULT 6
AX194437
LOCUS
  AX194437
  Sequence 37 from Patent WO0151500.
  20 bp DNA linear PAT 28-AUG-2001
ACCESSION
  AX194437
VERSION
  AX194437.1 GI:15385093
KEYWORDS
  synthetic construct
SOURCE
  synthetic construct
  artificial sequences.
REFERENCE
  1
  Klinman,D., Ishii,K. and Verthelyi,D.
  Oligodeoxynucleotide and its use to induce an immune response
  TITLE
  Patent: WO 0151500-A 37 19-JUL-2001;
  JOURNAL
  Secretary of the Department of Health and Human Services (US)
FEATURES
  source
    1..20
      /organism="synthetic construct"
      /mol_type="unassigned DNA"
      /db_xref="taxon:32630"
      /note="Synthetic DNA"
ORIGIN
  Query Match
    Best Local Similarity 100.0%; Score 20; DB 6; Length 20;
    Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
  QY
    1 GGTGCATCGATCGAGGGGG 20
    |||||
  Db
    1 GGTGCATCGATCGAGGGGG 20
    |||||

```

AX194472
 LOCUS AX194472 20 bp DNA linear PAT 28-AUG-2001
 DEFINITION Sequence 72 from Patent WO0151500.
 ACCESSION AX194472
 VERSION AX194472.1 GI:15385128
 KEYWORDS
 SOURCE synthetic construct
 ORGANISM synthetic construct
 ORGANISM artificial sequences.
 REFERENCE
 AUTHORS Klinman,D., Ishii,K. and Verthelyi,D.
 JOURNAL Oligodeoxynucleotide and its use to induce an immune response
 TITLE Patent: WO 0151500-A 72 19-JUL-2001;
 SECRETARY of the Department of Health and Human Services (US)
 FEATURES
 source Location/Qualifiers
 1..20
 /organism="synthetic construct"
 /mol_type="unassigned DNA"
 /db_xref="taxon:32630"
 /note="Synthetic DNA"
 ORIGIN
 Query Match 100.0%; Score 20; DB 6; Length 20;
 Best Local Similarity 100.0%; Pred. No. 16;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 GGTGCATCGATCGAGGGGG 20
 |||||
 Db 1 GGTGCATCGATCGAGGGGG 20
 |||||
 RESULT 7
 AX352198
 LOCUS AX352198 20 bp DNA linear PAT 06-FEB-2002
 DEFINITION Sequence 494 from Patent WO0193902.
 ACCESSION AX352198
 VERSION AX352198.1 GI:18617481
 KEYWORDS
 SOURCE synthetic construct
 ORGANISM synthetic construct
 ORGANISM artificial sequences.
 REFERENCE
 AUTHORS Mond,J.J., Flora,M. and Klimman,D.M.
 JOURNAL Immunostimulatory rna/dna hybrid molecules
 TITLE Patent: WO 0193902-A 494 13-DEC-2001;
 Biosynexus Incorporated (US)
 FEATURES
 source Location/Qualifiers
 1..20
 /organism="synthetic construct"
 /mol_type="unassigned DNA"
 /db_xref="taxon:32630"
 /note="Synthetic HDR"
 ORIGIN
 Query Match 100.0%; Score 20; DB 6; Length 20;
 Best Local Similarity 100.0%; Pred. No. 16;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 GGTGCATCGATCGAGGGGG 20
 |||||
 Db 1 GGTGCATCGATCGAGGGGG 20
 |||||
 RESULT 8
 AX352209
 LOCUS AX352209 20 bp DNA linear PAT 06-FEB-2002
 DEFINITION Sequence 505 from Patent WO0193902.
 ACCESSION AX352209
 VERSION AX352209.1 GI:18617492
 KEYWORDS
 SOURCE synthetic construct
 ORGANISM synthetic construct
 ORGANISM artificial sequences.

AX194472
 LOCUS AX194472 20 bp DNA linear PAT 28-AUG-2001
 DEFINITION Sequence 72 from Patent WO0151500.
 ACCESSION AX194472
 VERSION AX194472.1 GI:15385128
 KEYWORDS
 SOURCE synthetic construct
 ORGANISM synthetic construct
 ORGANISM artificial sequences.
 REFERENCE
 AUTHORS Klinman,D., Ishii,K. and Verthelyi,D.
 JOURNAL Oligodeoxynucleotide and its use to induce an immune response
 TITLE Patent: WO 0151500-A 72 19-JUL-2001;
 SECRETARY of the Department of Health and Human Services (US)
 FEATURES
 source Location/Qualifiers
 1..20
 /organism="synthetic construct"
 /mol_type="unassigned DNA"
 /db_xref="taxon:32630"
 /note="Synthetic DNA"
 ORIGIN
 Query Match 100.0%; Score 20; DB 6; Length 20;
 Best Local Similarity 100.0%; Pred. No. 16;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 GGTGCATCGATCGAGGGGG 20
 |||||
 Db 1 GGTGCATCGATCGAGGGGG 20
 |||||
 RESULT 7
 AX352198
 LOCUS AX352198 20 bp DNA linear PAT 06-FEB-2002
 DEFINITION Sequence 494 from Patent WO0193902.
 ACCESSION AX352198
 VERSION AX352198.1 GI:18617481
 KEYWORDS
 SOURCE synthetic construct
 ORGANISM synthetic construct
 ORGANISM artificial sequences.
 REFERENCE
 AUTHORS Mond,J.J., Flora,M. and Klimman,D.M.
 JOURNAL Immunostimulatory rna/dna hybrid molecules
 TITLE Patent: WO 0193902-A 494 13-DEC-2001;
 Biosynexus Incorporated (US)
 FEATURES
 source Location/Qualifiers
 1..20
 /organism="synthetic construct"
 /mol_type="unassigned DNA"
 /db_xref="taxon:32630"
 /note="Synthetic HDR"
 ORIGIN
 Query Match 100.0%; Score 20; DB 6; Length 20;
 Best Local Similarity 100.0%; Pred. No. 16;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 GGTGCATCGATCGAGGGGG 20
 |||||
 Db 1 GGTGCATCGATCGAGGGGG 20
 |||||
 RESULT 8
 AX352209
 LOCUS AX352209 20 bp DNA linear PAT 06-FEB-2002
 DEFINITION Sequence 505 from Patent WO0193902.
 ACCESSION AX352209
 VERSION AX352209.1 GI:18617492
 KEYWORDS
 SOURCE synthetic construct
 ORGANISM synthetic construct
 ORGANISM artificial sequences.

AX194472
 LOCUS AX194472 20 bp DNA linear PAT 28-AUG-2001
 DEFINITION Sequence 72 from Patent WO0151500.
 ACCESSION AX194472
 VERSION AX194472.1 GI:15385128
 KEYWORDS
 SOURCE synthetic construct
 ORGANISM synthetic construct
 ORGANISM artificial sequences.
 REFERENCE
 AUTHORS Klinman,D., Ishii,K. and Verthelyi,D.
 JOURNAL Oligodeoxynucleotide and its use to induce an immune response
 TITLE Patent: WO 0151500-A 72 19-JUL-2001;
 SECRETARY of the Department of Health and Human Services (US)
 FEATURES
 source Location/Qualifiers
 1..20
 /organism="synthetic construct"
 /mol_type="unassigned DNA"
 /db_xref="taxon:32630"
 /note="Synthetic DNA"
 ORIGIN
 Query Match 100.0%; Score 20; DB 6; Length 20;
 Best Local Similarity 100.0%; Pred. No. 16;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 GGTGCATCGATCGAGGGGG 20
 |||||
 Db 1 GGTGCATCGATCGAGGGGG 20
 |||||
 RESULT 7
 AX352198
 LOCUS AX352198 20 bp DNA linear PAT 06-FEB-2002
 DEFINITION Sequence 494 from Patent WO0193902.
 ACCESSION AX352198
 VERSION AX352198.1 GI:18617481
 KEYWORDS
 SOURCE synthetic construct
 ORGANISM synthetic construct
 ORGANISM artificial sequences.
 REFERENCE
 AUTHORS Mond,J.J., Flora,M. and Klimman,D.M.
 JOURNAL Immunostimulatory rna/dna hybrid molecules
 TITLE Patent: WO 0193902-A 494 13-DEC-2001;
 Biosynexus Incorporated (US)
 FEATURES
 source Location/Qualifiers
 1..20
 /organism="synthetic construct"
 /mol_type="unassigned DNA"
 /db_xref="taxon:32630"
 /note="Synthetic HDR"
 ORIGIN
 Query Match 100.0%; Score 20; DB 6; Length 20;
 Best Local Similarity 100.0%; Pred. No. 16;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 GGTGCATCGATCGAGGGGG 20
 |||||
 Db 1 GGTGCATCGATCGAGGGGG 20
 |||||
 RESULT 8
 AX352209
 LOCUS AX352209 20 bp DNA linear PAT 06-FEB-2002
 DEFINITION Sequence 505 from Patent WO0193902.
 ACCESSION AX352209
 VERSION AX352209.1 GI:18617492
 KEYWORDS
 SOURCE synthetic construct
 ORGANISM synthetic construct
 ORGANISM artificial sequences.

AX194472
 LOCUS AX194472 20 bp DNA linear PAT 28-AUG-2001
 DEFINITION Sequence 72 from Patent WO0151500.
 ACCESSION AX194472
 VERSION AX194472.1 GI:15385128
 KEYWORDS
 SOURCE synthetic construct
 ORGANISM synthetic construct
 ORGANISM artificial sequences.
 REFERENCE
 AUTHORS Klinman,D., Ishii,K. and Verthelyi,D.
 JOURNAL Oligodeoxynucleotide and its use to induce an immune response
 TITLE Patent: WO 0151500-A 72 19-JUL-2001;
 SECRETARY of the Department of Health and Human Services (US)
 FEATURES
 source Location/Qualifiers
 1..20
 /organism="synthetic construct"
 /mol_type="unassigned DNA"
 /db_xref="taxon:32630"
 /note="Synthetic DNA"
 ORIGIN
 Query Match 100.0%; Score 20; DB 6; Length 20;
 Best Local Similarity 100.0%; Pred. No. 16;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 GGTGCATCGATCGAGGGGG 20
 |||||
 Db 1 GGTGCATCGATCGAGGGGG 20
 |||||
 RESULT 7
 AX352198
 LOCUS AX352198 20 bp DNA linear PAT 06-FEB-2002
 DEFINITION Sequence 494 from Patent WO0193902.
 ACCESSION AX352198
 VERSION AX352198.1 GI:18617481
 KEYWORDS
 SOURCE synthetic construct
 ORGANISM synthetic construct
 ORGANISM artificial sequences.
 REFERENCE
 AUTHORS Mond,J.J., Flora,M. and Klimman,D.M.
 JOURNAL Immunostimulatory rna/dna hybrid molecules
 TITLE Patent: WO 0193902-A 494 13-DEC-2001;
 Biosynexus Incorporated (US)
 FEATURES
 source Location/Qualifiers
 1..20
 /organism="synthetic construct"
 /mol_type="unassigned DNA"
 /db_xref="taxon:32630"
 /note="Synthetic HDR"
 ORIGIN
 Query Match 100.0%; Score 20; DB 6; Length 20;
 Best Local Similarity 100.0%; Pred. No. 16;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 GGTGCATCGATCGAGGGGG 20
 |||||
 Db 1 GGTGCATCGATCGAGGGGG 20
 |||||
 RESULT 8
 AX352209
 LOCUS AX352209 20 bp DNA linear PAT 06-FEB-2002
 DEFINITION Sequence 505 from Patent WO0193902.
 ACCESSION AX352209
 VERSION AX352209.1 GI:18617492
 KEYWORDS
 SOURCE synthetic construct
 ORGANISM synthetic construct
 ORGANISM artificial sequences.

/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic oligonucleotide"

ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTGCATCGATCGAGGGGG 20
Db 1 GGTGCATCGATCGAGGGGG 20

RESULT 11

AX465384
LOCUS AX465384 20 bp DNA linear PAT 16-JUL-2002
DEFINITION Sequence 52 from Patent WO0211761.
ACCESSION AX465384
VERSION AX465384.1 GI:21899747
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Mond, J.J., Prince, G. and Klinman, D.M.
TITLE Vaccine against RSV
JOURNAL Patent: WO 0211761-A 52 14-FEB-2002;
HENRY M. JACKSON FOUNDATION FOR THE ADVANCEMENT OF MILITARY
MEDICINE (US)
FEATURES Location/Qualifiers
source 1..20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic oligonucleotide"

ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTGCATCGATCGAGGGGG 20
Db 1 GGTGCATCGATCGAGGGGG 20

RESULT 12

AX465387
LOCUS AX465387 20 bp DNA linear PAT 16-JUL-2002
DEFINITION Sequence 55 from Patent WO0211761.
ACCESSION AX465387
VERSION AX465387.1 GI:21899750
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Mond, J.J., Prince, G. and Klinman, D.M.
TITLE Vaccine against RSV
JOURNAL Patent: WO 0211761-A 55 14-FEB-2002;
HENRY M. JACKSON FOUNDATION FOR THE ADVANCEMENT OF MILITARY
MEDICINE (US)
FEATURES Location/Qualifiers
source 1..20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic oligonucleotide"

ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTGCATCGATCGAGGGGG 20
Db 1 GGTGCATCGATCGAGGGGG 20

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTGCATCGATCGAGGGGG 20
Db 1 GGTGCATCGATCGAGGGGG 20

RESULT 13

AX465388
LOCUS AX465388 20 bp DNA linear PAT 16-JUL-2002
DEFINITION Sequence 56 from Patent WO0211761.
ACCESSION AX465388
VERSION AX465388.1 GI:21899751
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Mond, J.J., Prince, G. and Klinman, D.M.
TITLE Vaccine against RSV
JOURNAL Patent: WO 0211761-A 56 14-FEB-2002;
HENRY M. JACKSON FOUNDATION FOR THE ADVANCEMENT OF MILITARY
MEDICINE (US)
FEATURES Location/Qualifiers
source 1..20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic oligonucleotide"

ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTGCATCGATCGAGGGGG 20
Db 1 GGTGCATCGATCGAGGGGG 20

RESULT 14

AX465393
LOCUS AX465393 20 bp DNA linear PAT 16-JUL-2002
DEFINITION Sequence 61 from Patent WO0211761.
ACCESSION AX465393
VERSION AX465393.1 GI:21899756
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Mond, J.J., Prince, G. and Klinman, D.M.
TITLE Vaccine against RSV
JOURNAL Patent: WO 0211761-A 61 14-FEB-2002;
HENRY M. JACKSON FOUNDATION FOR THE ADVANCEMENT OF MILITARY
MEDICINE (US)
FEATURES Location/Qualifiers
source 1..20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic oligonucleotide"

ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTGCATCGATCGAGGGGG 20
Db 1 GGTGCATCGATCGAGGGGG 20

```

RESULT 15
AX465422
LOCUS      AX465422          20 bp  DNA      linear  PAT 16-JUL-2002
DEFINITION Sequence 90 from Patent WO0211761.
ACCESSION  AX465422
VERSION    AX465422.1  GI:21899785
KEYWORDS   .
SOURCE     synthetic construct
           synthetic construct
           artificial sequences.
ORGANISM   1
REFERENCE  1
AUTHORS   Mond, J.J., Prince, G. and Klinman, D.M.
TITLE     Vaccine against RSV.
JOURNAL   Patent: WO 0211761-A 90 14-FEB-2002;
          HENRY M. JACKSON FOUNDATION FOR THE ADVANCEMENT OF MILITARY
          MEDICINE (US)
FEATURES   Location/Qualifiers
           1..20
            /organism="synthetic construct"
            /mol_type="unassigned DNA"
            /db_xref="taxon:32630"
            /note="Synthetic oligonucleotide"

ORIGIN
Query Match      100.0%; Score 20; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy  1  GGTGCATCGATCGAGGGGG 20
    ||||||||||||||||
Db   1  GGTGCATCGATCGAGGGGG 20

```

Search completed: July 2, 2004, 10:07:54
Job time : 705.146 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 2, 2004, 06:05:50 ; Search time 149.878 Seconds
(without alignments)
566.887 Million cell updates/sec

Title: US-10-068-160-1

Perfect score: 20

Sequence: 1 ggtgcatgacgagggggg 20

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 212409041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_23Jan04.*

- 1: Geneseqn1980s.*
- 2: Geneseqn1990s.*
- 3: Geneseqn2000s.*
- 4: Geneseqn2001as.*
- 5: Geneseqn2001bs.*
- 6: Geneseqn2002as.*
- 7: Geneseqn2003as.*
- 8: Geneseqn2003bs.*
- 9: Geneseqn2003cs.*
- 10: Geneseqn2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	100.0	20	AAC80652	Immunogen
2	20	100.0	20	AAC80614	Immunogen
3	20	100.0	20	AAC80612	Immunogen
4	20	100.0	20	AAC80617	Immunogen
5	20	100.0	20	AAC80618	Immunogen
6	20	100.0	20	AAC80623	Immunogen
7	20	100.0	20	AAC80622	Immunogen
8	20	100.0	20	AAS09582	Immunoreg
9	20	100.0	20	AAS09587	Immunoreg
10	20	100.0	20	AAS09583	Immunoreg
11	20	100.0	20	AAS09584	Immunoreg
12	20	100.0	20	AAS09588	Immunoreg
13	20	100.0	20	AAS09588	Immunoreg
14	20	100.0	20	ABL35579	Immunoreg
15	20	100.0	20	ABL35568	Immunoreg
16	20	100.0	20	ABL35612	Immunoreg
17	20	100.0	20	ABK46500	Immunoreg
18	20	100.0	20	ABK46465	Immunoreg
19	20	100.0	20	ABK46471	Immunoreg
20	20	100.0	20	ABK46462	Immunoreg
21	20	100.0	20	ABK46466	Immunoreg
22	20	100.0	20	ACC48309	CpG oligo
23	20	100.0	20	ACC48295	CpG oligo

24	20	100.0	20	7	ACC48310	CpG oligo
25	20	100.0	20	7	ACC48316	CpG oligo
26	20	100.0	20	8	ACC83150	D class O
27	20	100.0	20	8	ACC83115	D class C
28	20	100.0	20	8	ACC83151	D class O
29	20	100.0	20	8	ACC83114	D class C
30	20	100.0	20	8	ACC83121	D class C
31	20	100.0	20	9	ADB84186	CpG conta
32	20	100.0	20	9	ADC51789	D19 SEQ I
33	20	100.0	20	9	ADD01074	CpG D oli
34	20	100.0	20	9	ADD01048	CpG D oli
35	20	100.0	22	6	ABL35574	Immunosti
36	20	100.0	22	6	ABL35618	Immunosti
37	20	100.0	28	6	ABL35601	Immunosti
38	20	100.0	28	6	ABL35589	Immunosti
39	20	100.0	29	6	ABL35607	Immunosti
40	20	100.0	30	6	ABL35600	Immunosti
41	20	100.0	30	6	ABL35595	Immunosti
42	20	100.0	32	6	ABL35537	Immunosti
43	20	100.0	32	7	ACC48325	CpG oligo
44	20	100.0	32	7	ACC48323	CpG oligo
45	20	100.0	32	7	ACC48324	CpG oligo

ALIGNMENTS

RESULT 1

AAC80652

ID AAC80652 standard; DNA; 20 BP.

XX

AC AAC80652;

XX

DT 14-FEB-2001 (first entry)

XX

DE Immunogenic CpG oligodeoxynucleotide, SEQ ID NO:72.

XX

KW CpG oligodeoxynucleotide; unmethylated; antigen-presenting cell;
KW immunogenic; cytokine release; natural killer cell; NK cell activation;
KW cell-mediated immune response; T-cell response; humoral response;
KW B-cell response; antibody production; immune response induction; vaccine;
KW allergy; asthma; infection; bacterial; viral; fungal; protozoal;
KW parasitic; tuberculosis; AIDS; autoimmune disease; lupus erythematosus;
KW rheumatoid arthritis; multiple sclerosis; solid tumour; cancer;
KW immune deficiency; biological warfare agent; cytostatic; antiarthritic;
KW antimicrobial; antiallergic; protozoacide; tuberculostatic;
KW antiasthmatic; dermatological; phosphorothioate; ss.
XX Synthetic.
OS

XX WO200061151-A2.

XX 19-OCT-2000.

XX 12-APR-2000; 2000WO-US009839.

XX 12-APR-1999; 99US-0128898P.

XX (KLIN/) KLINMAN D.

XX (ISHI/) ISHII K.

XX (VERT/) VERTHELYI D.

XX Klinman D, Ishii K, Verthelyi D;

XX WPI; 2001-006880/01.

XX Novel oligonucleotides useful for the prevention and treatment of

XX allergies, cancer, and autoimmune disorders and for ameliorating symptoms

XX resulting from exposure to a bio-warfare agent.

XX Claim 4; Page 35; 46pp; English.

XX The invention relates to novel immunogenic CpG oligodeoxynucleotides

CC

(AAC80581-C80723). The oligonucleotide are at least 10 bases long and comprise one of the generic sequences 5'-NNNT-CpG-WNNN-3' or 5'-RV-CpG-RY-3'. The central CpG motif is unmethylated, and the oligonucleotides optionally have phosphorothioate linkages which make them more resistant to degradation. The invention also relates to an oligonucleotide delivery complex comprising an oligonucleotide of the invention and a targeting agent, and a pharmaceutical composition comprising the oligonucleotide delivery complex. The oligonucleotides are able to induce either a cell-mediated (T-cell) response or a humoral (B-cell, antibody) response, with oligonucleotides of the sequence 5'-RV-CpG-RY-3' being able to induce a cell-mediated response, and those of the sequence 5'-NNNT-CpG-WNNN-3' being able to induce a humoral response. It is thought that after administration, the oligonucleotide acts on antigen-presenting cells (e.g., macrophages and dendritic cells), which then release cytokines, leading to activation of natural killer (NK) cells. A cell-mediated or humoral response can then occur by activation of T- or B-cells. The induction of an immune response is useful for treating, preventing or ameliorating an allergic reaction (preferably asthma), or an infection, where an immunogenic CpG oligonucleotide is administered either alone or in combination with an anti-allergenic agent or anti-infectious agent. The allergic conditions which may be treated include eczema, allergic rhinitis, hayfever, urticaria, food allergies and other atopic conditions, and the infections which may be treated include viral, bacterial, fungal and protozoal infections such as tuberculosis, AIDS, leishmania and schistosomiasis. Immune response induction may also be used in the treatment of an autoimmune disorder (e.g., lupus erythematosus, rheumatoid arthritis and multiple sclerosis), a disease associated with immune system deficiency, and symptoms resulting from exposure to an agent of biological warfare. An immunogenic CpG oligonucleotide, either alone or in combination with an anti-cancer agent, is useful for treating solid tumour cancer. The induction of an immune response is used in antisense therapy and to improve the efficacy of a vaccine. The oligonucleotide is preferably administered to lymphocytes ex vivo, producing activated lymphocytes which are then administered to the host. The present sequence represents an immunogenic CpG oligodeoxynucleotide of the invention

Sequence 20 BP; 3 A; 3 C; 11 G; 3 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 4; Length 20;
 Best Local Similarity 100.0%; Pred. No. 3;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTCATCGATGCGAGGGGG 20
 |||||
 DB 1 GGTCATCGATGCGAGGGGG 20
 |||||

RESULT 2
 AAC80614
 ID AAC80614 standard; DNA; 20 BP.
 AC AAC80614;
 XX
 DT 14-FEB-2001 (first entry)
 XX
 DE Immunogenic CpG oligodeoxynucleotide, SEQ ID NO:34.
 XX
 KW CpG oligodeoxynucleotide; unmethylated; antigen-presenting cell;
 immunogenic; cytokine release; natural killer cell; NK cell activation;
 cell-mediated immune response; T-cell response; humoral response; vaccine;
 B-cell response; antibody production; immune response induction; allergic
 allergy; asthma; infection; bacterial; viral; fungal; protozoal;
 parasitic; tuberculosis; AIDS; autoimmune disease; lupus erythematosus;
 rheumatoid arthritis; multiple sclerosis; solid tumor; cancer;
 immune deficiency; biological warfare agent; cytostatic; antiarthritic;
 antimicrobial; antiallergic; protozoicide; tuberculostatic;
 antiasthmatic; dermatological; phosphorothioate; ss.
 XX
 OS Synthetic.
 XX
 XX WO200061151-A2.
 XX

PD 19-OCT-2000.
 XX 12-APR-2000; 2000WO-US009839.
 XX 12-APR-1999; 99US-0128898P.
 XX (KLIN/) KLINMAN D.
 PA (ISHI/) ISHII K.
 PA (VERT/) VERTHELYI D.
 XX Kliman D, Ishii K, Verthelyi D;
 PI WPI; 2001-006880/01.
 XX Novel oligonucleotides useful for the prevention and treatment of
 DR allergies, cancer, and autoimmune disorders and for ameliorating symptoms
 XX resulting from exposure to a bio-warfare agent.
 PT
 PT
 PT
 XX Claim 4; Page 29; 45pp; English.
 PS
 XX The invention relates to novel immunogenic CpG oligodeoxynucleotides
 CC (AAC80581-C80723). The oligonucleotide are at least 10 bases long and
 CC comprise one of the generic sequences 5'-NNNT-CpG-WNNN-3' or 5'-RV-CpG-RY-
 CC -3'. The central CpG motif is unmethylated, and the oligonucleotides
 CC optionally have phosphorothioate linkages which make them more resistant
 CC to degradation. The invention also relates to an oligonucleotide delivery
 CC complex comprising an oligonucleotide of the invention and a targeting
 CC agent, and a pharmaceutical composition comprising the oligonucleotide
 CC delivery complex. The oligonucleotides are able to induce either a cell-
 CC mediated (T-cell) response or a humoral (B-cell, antibody) response, with
 CC oligonucleotides of the sequence 5'-RV-CpG-RY-3' being able to induce a
 CC cell-mediated response, and those of the sequence 5'-NNNT-CpG-WNNN-3'
 CC being able to induce a humoral response. It is thought that after
 CC administration, the oligonucleotide acts on antigen-presenting cells
 CC (e.g., macrophages and dendritic cells), which then release cytokines,
 CC leading to activation of natural killer (NK) cells. A cell-mediated or
 CC humoral response can then occur by activation of T- or B-cells. The
 CC induction of an immune response is useful for treating, preventing or
 CC ameliorating an allergic reaction (preferably asthma), or an infection,
 CC where an immunogenic CpG oligonucleotide is administered either alone or
 CC in combination with an anti-allergenic agent or anti-infectious agent.
 CC The allergic conditions which may be treated include eczema, allergic
 CC rhinitis, hayfever, urticaria, food allergies and other atopic
 CC conditions, and the infections which may be treated include viral,
 CC bacterial, fungal and protozoal infections such as tuberculosis, AIDS,
 CC leishmania and schistosomiasis. Immune response induction may also be
 CC used in the treatment of an autoimmune disorder (e.g., lupus
 CC erythematosus, rheumatoid arthritis and multiple sclerosis), a disease
 CC associated with immune system deficiency, and symptoms resulting from
 CC exposure to an agent of biological warfare. An immunogenic CpG
 CC oligonucleotide, either alone or in combination with an anti-cancer
 CC agent, is useful for treating solid tumour cancer. The induction of an
 CC immune response is used in antisense therapy and to improve the efficacy
 CC of a vaccine. The oligonucleotide is preferably administered to
 CC lymphocytes ex vivo, producing activated lymphocytes which are then
 CC administered to the host. The present sequence represents an immunogenic
 CC CpG oligodeoxynucleotide of the invention

Sequence 20 BP; 3 A; 3 C; 11 G; 3 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 4; Length 20;
 Best Local Similarity 100.0%; Pred. No. 3;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTCATCGATGCGAGGGGG 20
 |||||
 DB 1 GGTCATCGATGCGAGGGGG 20
 |||||

RESULT 3
 AAC80612
 ID AAC80612 standard; DNA; 20 BP.
 XX

CC AAC80612;
 XX 14-FEB-2001 (first entry)
 XX Immunogenic CpG oligodeoxynucleotide, SEQ ID NO:32.
 KW CpG oligodeoxynucleotide; unmethylated; antigen-presenting cell;
 KW immunogenic; cytokine release; natural killer cell; NK cell activation;
 KW cell-mediated immune response; T-cell response; humoral response;
 KW B-cell response; antibody production; immune response induction; vaccine;
 KW allergy; asthma; infection; bacterial; viral; fungal; protozoal;
 KW parasitic; tuberculosis; AIDS; autoimmune disease; lupus erythematosus;
 KW rheumatoid arthritis; multiple sclerosis; solid tumour; cancer;
 KW immune deficiency; biological warfare agent; cytostatic; antiarthritic;
 KW antimicrobial; antiallergic; protozoacide; tuberculostatic;
 KW antiasthmatic; dermatological; phosphorothioate; ss.
 XX Synthetic.
 OS WO2000061151-A2.
 XX 19-OCT-2000.
 XX 12-APR-2000; 2000WO-US009839.
 XX 12-APR-1999; 99US-0128898P.
 XX (KLIN/) KLINMAN D.
 XX (ISHI/) ISHII K.
 XX (VERT/) VERTHELYI D.
 XX Klinman D, Ishii K, Verthelyi D;
 XX WPI; 2001-006880/01.
 XX Novel oligonucleotides useful for the prevention and treatment of
 XX allergies, cancer, and autoimmune disorders and for ameliorating symptoms
 XX resulting from exposure to a bio-warfare agent.
 XX Claim 4; Page 29; 46pp; English.
 XX The invention relates to novel immunogenic CpG oligodeoxynucleotides
 XX (AAC80581-C80723). The oligonucleotide are at least 10 bases long and
 XX comprise one of the generic sequences 5'-NNNT-CpG-WNNN-3' or 5'-RY-CpG-RY
 XX -3'. The central CpG motif is unmethylated, and the oligonucleotides
 XX optionally have phosphorothioate linkages which make them more resistant
 XX to degradation. The invention also relates to an oligonucleotide delivery
 XX agent, and a pharmaceutical composition comprising the oligonucleotide
 XX delivery complex. The oligonucleotides are able to induce either a cell-
 XX mediated (T-cell) response or a humoral (B-cell, antibody) response, with
 XX oligonucleotides of the sequence 5'-RY-CpG-RY-3', being able to induce a
 XX cell-mediated response, and those of the sequence 5'-NNNT-CpG-WNNN-3',
 XX being able to induce a humoral response. It is thought that after
 XX administration, the oligonucleotide acts on antigen-presenting cells
 XX (e.g., macrophages and dendritic cells), which then release cytokines,
 XX leading to activation of natural killer (NK) cells. A cell-mediated or
 XX humoral response can then occur by activation of T- or B-cells. The
 XX induction of an immune response is useful for treating, preventing or
 XX ameliorating an allergic reaction (preferably asthma), or an infection,
 XX where an immunogenic CpG oligonucleotide is administered either alone or
 XX in combination with an anti-allergenic agent or anti-infectious agent.
 XX The allergic conditions which may be treated include eczema, allergic
 XX rhinitis, hayfever, urticaria, food allergies and other atopic
 XX conditions, and the infections which may be treated include viral,
 XX bacterial, fungal and protozoal infections such as tuberculosis, AIDS,
 XX leishmania and schistosomiasis. Immune response induction may also be
 XX used in the treatment of an autoimmune disorder (e.g., lupus
 XX erythematosus, rheumatoid arthritis and multiple sclerosis), a disease
 XX associated with immune system deficiency, and symptoms resulting from
 XX exposure to an agent of biological warfare. An immunogenic CpG
 XX oligonucleotide, either alone or in combination with an anti-cancer
 XX agent, is useful for treating solid tumour cancer. The induction of an

CC immune response is used in antisense therapy and to improve the efficacy
 CC of a vaccine. The oligonucleotide is preferably administered to
 CC lymphocytes ex vivo, producing activated lymphocytes which are then
 CC administered to the host. The present sequence represents an immunogenic
 CC CpG oligodeoxynucleotide of the invention
 XX SQ Sequence 20 BP; 3 A; 3 C; 11 G; 3 T; 0 U; 0 Other;
 Query Match 100.0%; Score 20; DB 4; Length 20;
 Best Local Similarity 100.0%; Pred. No. 3;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GGTGATCATGATCGACGGGGG 20
 DB 1 GGTGATCATGATCGACGGGGG 20
 RESULT 4
 AAC80617
 ID AAC80617 standard; DNA; 20 BP.
 XX AC AAC80617;
 XX 14-FEB-2001 (first entry)
 XX Immunogenic CpG oligodeoxynucleotide, SEQ ID NO:37.
 KW CpG oligodeoxynucleotide; unmethylated; antigen-presenting cell;
 KW immunogenic; cytokine release; natural killer cell; NK cell activation;
 KW cell-mediated immune response; T-cell response; humoral response;
 KW B-cell response; antibody production; immune response induction; vaccine;
 KW allergy; asthma; infection; bacterial; viral; fungal; protozoal;
 KW parasitic; tuberculosis; AIDS; autoimmune disease; lupus erythematosus;
 KW rheumatoid arthritis; multiple sclerosis; solid tumour; cancer;
 KW immune deficiency; biological warfare agent; cytostatic; antiarthritic;
 KW antimicrobial; antiallergic; protozoacide; tuberculostatic;
 KW antiasthmatic; dermatological; phosphorothioate; ss.
 XX Synthetic.
 OS WO2000061151-A2.
 XX 19-OCT-2000.
 XX 12-APR-2000; 2000WO-US009839.
 XX 12-APR-1999; 99US-0128898P.
 XX (KLIN/) KLINMAN D.
 XX (ISHI/) ISHII K.
 XX (VERT/) VERTHELYI D.
 XX Klinman D, Ishii K, Verthelyi D;
 XX WPI; 2001-006880/01.
 XX Novel oligonucleotides useful for the prevention and treatment of
 XX allergies, cancer, and autoimmune disorders and for ameliorating symptoms
 XX resulting from exposure to a bio-warfare agent.
 XX Claim 4; Page 29; 46pp; English.
 XX The invention relates to novel immunogenic CpG oligodeoxynucleotides
 XX (AAC80581-C80723). The oligonucleotide are at least 10 bases long and
 XX comprise one of the generic sequences 5'-NNNT-CpG-WNNN-3' or 5'-RY-CpG-RY
 XX -3'. The central CpG motif is unmethylated, and the oligonucleotides
 XX optionally have phosphorothioate linkages which make them more resistant
 XX to degradation. The invention also relates to an oligonucleotide delivery
 XX agent, and a pharmaceutical composition comprising the oligonucleotide
 XX delivery complex. The oligonucleotides are able to induce either a cell-
 XX mediated (T-cell) response or a humoral (B-cell, antibody) response, with
 XX oligonucleotides of the sequence 5'-RY-CpG-RY-3', being able to induce a
 XX cell-mediated response, and those of the sequence 5'-NNNT-CpG-WNNN-3',
 XX being able to induce a humoral response. It is thought that after
 XX administration, the oligonucleotide acts on antigen-presenting cells
 XX (e.g., macrophages and dendritic cells), which then release cytokines,
 XX leading to activation of natural killer (NK) cells. A cell-mediated or
 XX humoral response can then occur by activation of T- or B-cells. The
 XX induction of an immune response is useful for treating, preventing or
 XX ameliorating an allergic reaction (preferably asthma), or an infection,
 XX where an immunogenic CpG oligonucleotide is administered either alone or
 XX in combination with an anti-allergenic agent or anti-infectious agent.
 XX The allergic conditions which may be treated include eczema, allergic
 XX rhinitis, hayfever, urticaria, food allergies and other atopic
 XX conditions, and the infections which may be treated include viral,
 XX bacterial, fungal and protozoal infections such as tuberculosis, AIDS,
 XX leishmania and schistosomiasis. Immune response induction may also be
 XX used in the treatment of an autoimmune disorder (e.g., lupus
 XX erythematosus, rheumatoid arthritis and multiple sclerosis), a disease
 XX associated with immune system deficiency, and symptoms resulting from
 XX exposure to an agent of biological warfare. An immunogenic CpG
 XX oligonucleotide, either alone or in combination with an anti-cancer
 XX agent, is useful for treating solid tumour cancer. The induction of an

CC cell-mediated response, and those of the sequence 5'-NNNT-CpG-WNNN-3'
 CC being able to induce a humoral response. It is thought that after
 CC administration, the oligonucleotide acts on antigen-presenting cells
 CC (e.g., macrophages and dendritic cells), which then release cytokines,
 CC leading to activation of natural killer (NK) cells. A cell-mediated or
 CC humoral response can then occur by activation of T- or B-cells. The
 CC induction of an immune response is useful for treating, preventing or
 CC ameliorating an allergic reaction (preferably asthma), or an infection,
 CC where an immunogenic CpG oligonucleotide is administered either alone or
 CC in combination with an anti-allergenic agent or anti-infectious agent.
 CC The allergic conditions which may be treated include eczema, allergic
 CC rhinitis, hayfever, urticaria, food allergies and other atopic
 CC conditions, and the infections which may be treated include viral,
 CC bacterial, fungal and protozoal infections such as tuberculosis, AIDS,
 CC leishmania and schistosomiasis. Immune response induction may also be
 CC used in the treatment of an autoimmune disorder (e.g., lupus
 CC erythematosus, rheumatoid arthritis and multiple sclerosis), a disease
 CC associated with immune system deficiency, and symptoms resulting from
 CC exposure to an agent of biological warfare. An immunogenic CpG
 CC oligonucleotide, either alone or in combination with an anti-cancer
 CC agent, is useful for treating solid tumour cancer. The induction of an
 CC immune response is used in antisense therapy and to improve the efficacy
 CC of a vaccine. The oligonucleotide is preferably administered to
 CC lymphocytes ex vivo, producing activated lymphocytes which are then
 CC administered to the host. The present sequence represents an immunogenic
 CC CpG oligodeoxynucleotide of the invention
 XX
 SQ Sequence 20 BP; 3 A; 3 C; 11 G; 3 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 4; Length 20;

Best Local Similarity 100.0%; Pred. No. 3;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTGCATCGATGCAGGGGG 20

DB 1 GGTGCATCGATGCAGGGGG 20

RESULT 5

AAC80618

ID AAC80618 standard; DNA; 20 BP.

XX

AC AAC80618;

XX

DT 14-FEB-2001 (first entry)

XX

DE Immunogenic CpG oligodeoxynucleotide, SEQ ID NO:38.

XX

KW CpG oligodeoxynucleotide; unmethylated; antigen-presenting cell;
 KW immunogenic; cytokine release; natural killer cell; NK cell activation;
 KW cell-mediated immune response; T-cell response; humoral response;
 KW B-cell response; antibody production; immune response induction; vaccine;
 KW allergy; asthma; infection; bacterial; viral; fungal; protozoal;
 KW parasitic; tuberculosis; AIDS; autoimmune disease; lupus erythematosus;
 KW rheumatoid arthritis; multiple sclerosis; solid tumour; cancer;
 KW immune deficiency; biological warfare agent; cytostatic; antiarthritic;
 KW antimicrobial; antiallergic; protozoicide; tuberculostatic;
 KW antiasthmatic; dermatological; phosphorothioate; ss.

OS Synthetic.

XX

PN WO200061151-A2.

XX

PD 19-OCT-2000.

XX

PF 12-APR-2000; 2000WO-US0009839.

XX

PR 12-APR-1999; 99US-0128898P.

XX

PA (KLIN/) KLIMAN D.

PA (ISHI/) ISHII K.

PA (VERT/) VERTHELYI D.

XX

PI Kliman D, Ishii K, Verthelyi D;

XX

DR WPI; 2001-006880/01.

XX

PT Novel oligonucleotides useful for the prevention and treatment of
 PT allergies, cancer, and autoimmune disorders and for ameliorating symptoms
 PT resulting from exposure to a bio-warfare agent.

XX

PS Claim 4; Page 30; 46pp; English.

XX

CC The invention relates to novel immunogenic CpG oligodeoxynucleotides
 CC (AAC8061-C80723). The oligonucleotide are at least 10 bases long and
 CC comprise one of the generic sequences 5'-NNNT-CpG-WNNN-3' or 5'-RY-CpG-RY
 CC -3'. The central CpG motif is unmethylated, and the oligonucleotides
 CC optionally have phosphorothioate linkages which make them more resistant
 CC to degradation. The invention also relates to an oligonucleotide delivery
 CC complex comprising an oligonucleotide of the invention and a targeting
 CC agent, and a pharmaceutical composition comprising the oligonucleotide
 CC delivery complex. The oligonucleotides are able to induce either a cell-
 CC mediated (T-cell) response or a humoral (B-cell, antibody) response, with
 CC oligonucleotides of the sequence 5'-RY-CpG-RY-3' being able to induce a
 CC cell-mediated response, and those of the sequence 5'-NNNT-CpG-WNNN-3'
 CC being able to induce a humoral response. It is thought that after
 CC administration, the oligonucleotide acts on antigen-presenting cells
 CC (e.g., macrophages and dendritic cells), which then release cytokines,
 CC leading to activation of natural killer (NK) cells. A cell-mediated or
 CC humoral response can then occur by activation of T- or B-cells. The
 CC induction of an immune response is useful for treating, preventing or
 CC ameliorating an allergic reaction (preferably asthma), or an infection,
 CC where an immunogenic CpG oligonucleotide is administered either alone or
 CC in combination with an anti-allergenic agent or anti-infectious agent.
 CC The allergic conditions which may be treated include eczema, allergic
 CC rhinitis, hayfever, urticaria, food allergies and other atopic
 CC conditions, and the infections which may be treated include viral, AIDS,
 CC bacterial, fungal and protozoal infections such as tuberculosis, AIDS,
 CC leishmania and schistosomiasis. Immune response induction may also be
 CC used in the treatment of an autoimmune disorder (e.g., lupus
 CC erythematosus, rheumatoid arthritis and multiple sclerosis), a disease
 CC associated with immune system deficiency, and symptoms resulting from
 CC exposure to an agent of biological warfare. An immunogenic CpG
 CC oligonucleotide, either alone or in combination with an anti-cancer
 CC agent, is useful for treating solid tumour cancer. The induction of an
 CC immune response is used in antisense therapy and to improve the efficacy
 CC of a vaccine. The oligonucleotide is preferably administered to
 CC lymphocytes ex vivo, producing activated lymphocytes which are then
 CC administered to the host. The present sequence represents an immunogenic
 CC CpG oligodeoxynucleotide of the invention
 XX

SQ Sequence 20 BP; 3 A; 3 C; 11 G; 3 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 4; Length 20;

Best Local Similarity 100.0%; Pred. No. 3;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTGCATCGATGCAGGGGG 20

DB 1 GGTGCATCGATGCAGGGGG 20

RESULT 6

AAC80623

ID AAC80623 standard; DNA; 20 BP.

XX

AC AAC80623;

XX

DT 14-FEB-2001 (first entry)

XX

DE Immunogenic CpG oligodeoxynucleotide, SEQ ID NO:43.

XX

KW CpG oligodeoxynucleotide; unmethylated; antigen-presenting cell;
 KW immunogenic; cytokine release; natural killer cell; NK cell activation;
 KW cell-mediated immune response; T-cell response; humoral response;
 KW B-cell response; antibody production; immune response induction; vaccine;

allergy; asthma; infection; bacterial; viral; fungal; protozoal; parasitic; tuberculosis; AIDS; autoimmune disease; lupus erythematosus; rheumatoid arthritis; multiple sclerosis; solid tumour; cancer; immune deficiency; biological warfare agent; cytostatic; antiarthritic; antimicrobial; antiallergic; protozoacide; tuberculostatic; antiasthmatic; dermatological; phosphorothioate; ss.

Synthetic.

WO200061151-A2.

19-OCT-2000.

12-APR-2000; 2000WO-US009839.

12-APR-1999; 99US-0128998P.

(KLIN/) KLINMAN D.

(ISHI/) ISHII K.

(VERT/) VERTHELYI D.

Klinman D, Ishii K, Verthelyi D;

WPI; 2001-006880/01.

Novel oligonucleotides useful for the prevention and treatment of allergies, cancer, and autoimmune disorders and for ameliorating symptoms resulting from exposure to a bio-warfare agent.

Claim 4; Page 30; 46pp; English.

The invention relates to novel immunogenic CpG oligodeoxynucleotides (AAC80581-C80723). The oligonucleotide are at least 10 bases long and comprise one of the generic sequences 5'-NNNT-CpG-WNNN-3' or 5'-RY-CpG-RY-3'. The central CpG motif is unmethylated, and the oligonucleotides optionally have phosphorothioate linkages which make them more resistant to degradation. The invention also relates to an oligonucleotide delivery complex comprising an oligonucleotide of the invention and a targeting agent, and a pharmaceutical composition comprising the oligonucleotide delivery complex. The oligonucleotides are able to induce either a cell-mediated (T-cell) response or a humoral (B-cell, antibody) response, with oligonucleotides of the sequence 5'-RY-CpG-RY-3' being able to induce a cell-mediated response, and those of the sequence 5'-NNNT-CpG-WNNN-3' being able to induce a humoral response. It is thought that after administration, the oligonucleotide acts on antigen-presenting cells (e.g., macrophages and dendritic cells), which then release cytokines, leading to activation of natural killer (NK) cells. A cell-mediated or humoral response can then occur by activation of T- or B-cells. The induction of an immune response is useful for treating, preventing or ameliorating an allergic reaction (preferably asthma), or an infection, where an immunogenic CpG oligonucleotide is administered either alone or in combination with an anti-allergenic agent or anti-infectious agent. The allergic conditions which may be treated include eczema, allergic rhinitis, hayfever, urticaria, food allergies and other atopic conditions, and the infections which may be treated include viral, bacterial, fungal and protozoal infections such as tuberculosis, AIDS, leishmania and schistosomiasis. Immune response induction may also be used in the treatment of an autoimmune disorder (e.g., lupus erythematosus, rheumatoid arthritis and multiple sclerosis), a disease associated with immune system deficiency, and symptoms resulting from exposure to an agent of biological warfare. An immunogenic CpG oligonucleotide, either alone or in combination with an anti-cancer agent, is useful for treating solid tumour cancer. The induction of an immune response is used in antisense therapy and to improve the efficacy of a vaccine. The oligonucleotide is preferably administered to lymphocytes ex vivo, producing activated lymphocytes which are then administered to the host. The present sequence represents an immunogenic CpG oligodeoxynucleotide of the invention

Sequence 20 BP; 3 A; 3 C; 11 G; 3 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 4; Length 20;

Best Local Similarity 100.0%; Pred. No. 3;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTGATCATGTCAGGGGGG 20
|||||

DB 1 GGTGATCATGTCAGGGGGG 20
|||||

RESULT 7

AAS09622

ID AAS09622 standard; DNA; 20 BP.

AC AAS09622;

XX 26-SEP-2001 (first entry)

XX Immunoreactive CpG sequence-containing oligonucleotide #72.

XX CpG sequence; immune response; non-B cell activation; interferon gamma; IFN-gamma; humoral; antibody production; interleukin-6 production; therapeutic; allergy; asthma; cancer; autoimmune disorder; infection; bio-warfare; vaccine; urticaria; hives; food allergy; allergic rhinitis; coryza; hay fever; urticaria; food allergy; atopic condition; hepatitis; human immunodeficiency virus; HIV; malaria; Francisella; lupus erythematosus; rheumatoid arthritis; multiple sclerosis; schistosomiasis; tuberculosis; acquired immunodeficiency syndrome; AIDS; Leishmania; Ebola; Anthrax; Listeria; ss.

XX Synthetic.

XX WO200151500-A1.

XX 19-JUL-2001.

XX 12-JAN-2001; 2001WO-US001122.

XX 14-JAN-2000; 2000US-0176115P.

(USSH) US DEPT HEALTH & HUMAN SERVICES.

Klinman D, Ishii K, Verthelyi D;

WPI; 2001-442129/47.

Oligodeoxynucleotides for inducing an immune response to treat and prevent an allergic reaction, cancer, an autoimmune disorder and symptoms resulting from exposure to bio-warfare agents, comprise multiple CpG sequences.

Claim 5; Page 39; 48pp; English.

AAS09551-AAS09662 represent oligodeoxynucleotides (ODN) of at least 10 nucleotides comprising multiple CpG sequences, where one of the CpG sequences is different from another of the multiple CpG sequences. The ODN are useful for inducing an immune response, preferably a cell-mediated immune response, involving non-B cell activation, interferon gamma (IFN-gamma) production or a humoral immune response involving B cell activation, antibody and interleukin-6 production in a host, for treating, preventing or ameliorating an allergic reaction, e.g. asthma, cancer, e.g. solid tumour cancer, a disease associated with the immune system e.g. autoimmune disorder or an immune system deficiency, infection or a symptom resulting from exposure to bio-warfare agent in a human. The induction of immune response improves the efficacy of a vaccine and is used in antisense therapy. The ODN are useful for treating, preventing or ameliorating allergic reactions, including eczema, allergic rhinitis or coryza, hay fever, bronchial asthma, urticaria (hives), food allergies and other atopic conditions, for improving the efficacy of vaccines against hepatitis A, B and C, human immunodeficiency virus (HIV) and malaria, for treating immune system deficiencies, e.g. lupus erythematosus and autoimmune diseases such as rheumatoid arthritis and multiple sclerosis, infections including Francisella, schistosomiasis, tuberculosis, acquired immunodeficiency syndrome (AIDS), Leishmania and symptoms resulting from exposure of bio-warfare agent, including Ebola, Anthrax and Listeria

XX SQ Sequence 20 BP; 3 A; 3 C; 11 G; 3 T; 0 U; 0 Other;
 Query Match 100.0%; Score 20; DB 4; Length 20;
 Best Local Similarity 100.0%; Pred. No. 3;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTGTCATCGATCGAGGGGG 20
 |||||
 Db 1 GGTGTCATCGATCGAGGGGG 20

RESULT 8
 AAS09582
 ID AAS09582 standard; DNA; 20 BP.
 XX AAS09582;
 AC
 XX
 XX
 XX 26-SEP-2001 (first entry)
 XX
 XX Immunoactive CpG sequence-containing oligonucleotide #32.

XX CpG sequence; immune response; non-B cell activation; interferon gamma;
 KW IFN-gamma; humoral; antibody production; interleukin-6 production;
 KW therapeutic; allergy; asthma; cancer; autoimmune disorder; infection;
 KW bio-warfare; vaccine; antitense therapy; eczema; allergic rhinitis;
 KW coryza; hay fever; urticaria; hives; food allergy; atopic condition;
 KW hepatitis; human immunodeficiency virus; HIV; malaria; Francisella;
 KW lupus erythematosus; rheumatoid arthritis; multiple sclerosis;
 KW schistosomiasis; tuberculosis; acquired immunodeficiency syndrome; AIDS;
 KW Leishmania; Ebola; Anthrax; Listeria; ss.
 XX Synthetic.
 OS
 XX
 XX WQ200151500-A1.
 XX 19-JUL-2001.
 XX
 XX 12-JAN-2001; 2001WO-US001122.
 XX
 XX 14-JAN-2000; 2000US-0176115P.
 XX
 XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX
 XX Klinman D, Ishii K, Verthelyi D;
 XX WPI; 2001-442129/47.
 XX
 XX Oligodeoxynucleotides for inducing an immune response to treat and
 PT prevent an allergic reaction; cancer, an autoimmune disorder and symptoms
 PT resulting from exposure to bio-warfare agents, comprise multiple CpG
 PT sequences.
 XX
 XX Claim 5; Page 32; 48pp; English.

XX AAS09551-AAS09662 represent oligodeoxynucleotides (ODN) of at least 10
 CC nucleotides comprising multiple CpG sequences, where one of the CpG
 CC sequences is different from another of the multiple CpG sequences. The
 CC ODN are useful for inducing an immune response, preferably a cell-
 CC mediated immune response, involving non-B cell activation, interferon
 CC gamma (IFN-gamma) production or a humoral immune response involving B
 CC cell activation, antibody and interleukin-6 production in a host, for
 CC treating, preventing or ameliorating an allergic reaction, e.g. asthma,
 CC cancer, e.g. solid tumour cancer, a disease associated with the immune
 CC system e.g. autoimmune disorder or an immune system deficiency, infection
 CC or a symptom resulting from exposure to bio-warfare agent in a human. The
 CC induction of immune response improves the efficacy of a vaccine and is
 CC used in antitense therapy. The ODN are useful for treating, preventing or
 CC ameliorating allergic reactions, including eczema, allergic rhinitis or
 CC coryza, hay fever, bronchial asthma, urticaria (hives), food allergies
 CC and other atopic conditions, for improving the efficacy of vaccines
 CC against hepatitis A, B and C, human immunodeficiency virus (HIV) and
 CC malaria, for treating immune system deficiencies, e.g. lupus

CC erythematosus and autoimmune diseases such as rheumatoid arthritis and
 CC multiple sclerosis, infections including Francisella, schistosomiasis,
 CC tuberculosis, acquired immunodeficiency syndrome (AIDS), Leishmania and
 CC symptoms resulting from exposure of bio-warfare agent, including Ebola,
 CC Anthrax and Listeria
 XX SQ Sequence 20 BP; 3 A; 3 C; 11 G; 3 T; 0 U; 0 Other;
 Query Match 100.0%; Score 20; DB 4; Length 20;
 Best Local Similarity 100.0%; Pred. No. 3;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTGTCATCGATCGAGGGGG 20
 |||||
 Db 1 GGTGTCATCGATCGAGGGGG 20

RESULT 9
 AAS09587
 ID AAS09587 standard; DNA; 20 BP.
 XX AAS09587;
 AC
 XX
 XX 26-SEP-2001 (first entry)
 XX
 XX Immunoactive CpG sequence-containing oligonucleotide #37.

XX CpG sequence; immune response; non-B cell activation; interferon gamma;
 KW IFN-gamma; humoral; antibody production; interleukin-6 production;
 KW therapeutic; allergy; asthma; cancer; autoimmune disorder; infection;
 KW bio-warfare; vaccine; antitense therapy; eczema; allergic rhinitis;
 KW coryza; hay fever; urticaria; hives; food allergy; atopic condition;
 KW hepatitis; human immunodeficiency virus; HIV; malaria; Francisella;
 KW lupus erythematosus; rheumatoid arthritis; multiple sclerosis;
 KW schistosomiasis; tuberculosis; acquired immunodeficiency syndrome; AIDS;
 KW Leishmania; Ebola; Anthrax; Listeria; ss.
 XX Synthetic.
 OS
 XX
 XX WQ200151500-A1.
 XX 19-JUL-2001.
 XX
 XX 12-JAN-2001; 2001WO-US001122.
 XX
 XX 14-JAN-2000; 2000US-0176115P.
 XX
 XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX
 XX Klinman D, Ishii K, Verthelyi D;
 XX WPI; 2001-442129/47.
 XX
 XX Oligodeoxynucleotides for inducing an immune response to treat and
 PT prevent an allergic reaction; cancer, an autoimmune disorder and symptoms
 PT resulting from exposure to bio-warfare agents, comprise multiple CpG
 PT sequences.
 XX
 XX Claim 5; Page 33; 48pp; English.

XX AAS09551-AAS09662 represent oligodeoxynucleotides (ODN) of at least 10
 CC nucleotides comprising multiple CpG sequences, where one of the CpG
 CC sequences is different from another of the multiple CpG sequences. The
 CC ODN are useful for inducing an immune response, preferably a cell-
 CC mediated immune response, involving non-B cell activation, interferon
 CC gamma (IFN-gamma) production or a humoral immune response involving B
 CC cell activation, antibody and interleukin-6 production in a host, for
 CC treating, preventing or ameliorating an allergic reaction, e.g. asthma,
 CC cancer, e.g. solid tumour cancer, a disease associated with the immune
 CC system e.g. autoimmune disorder or an immune system deficiency, infection
 CC or a symptom resulting from exposure to bio-warfare agent in a human. The
 CC induction of immune response improves the efficacy of a vaccine and is
 CC used in antitense therapy. The ODN are useful for treating, preventing or
 CC ameliorating allergic reactions, including eczema, allergic rhinitis or
 CC coryza, hay fever, bronchial asthma, urticaria (hives), food allergies
 CC and other atopic conditions, for improving the efficacy of vaccines
 CC against hepatitis A, B and C, human immunodeficiency virus (HIV) and
 CC malaria, for treating immune system deficiencies, e.g. lupus

CC ameliorating allergic reactions, including eczema, allergic rhinitis or
 CC coryza, hay fever, bronchial asthma, urticaria (hives), food allergies
 CC and other atopic conditions, for improving the efficacy of vaccines
 CC against hepatitis A, B and C, human immunodeficiency virus (HIV) and
 CC malaria, for treating immune system deficiencies, e.g. lupus
 CC erythematous and autoimmune diseases such as rheumatoid arthritis and
 CC multiple sclerosis, infections including Francisella, schistosomiasis,
 CC tuberculosis, acquired immunodeficiency syndrome (AIDS), Leishmania and
 CC symptoms resulting from exposure of bio-warfare agent, including Ebola,
 CC Anthrax and Listeria
 XX
 SQ Sequence 20 BP; 3 A; 3 C; 11 G; 3 T; 0 U; 0 Other;
 Query Match 100.0%; Score 20; DB 4; Length 20;
 Best Local Similarity 100.0%; Pred. No. 3;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GGTGCATCGATCGAGGGGG 20
 Db 1 GGTGCATCGATCGAGGGGG 20
 RESULT 10
 ID AAS09593
 XX AAS09593 standard; DNA; 20 BP.
 AC AAS09593;
 XX
 DT 26-SEP-2001 (first entry)
 XX
 DE Immunoreactive CpG sequence-containing oligonucleotide #43.
 XX
 KW CpG sequence; immune response; non-B cell activation; interferon gamma;
 KW IFN-gamma; humoral; antibody production; interleukin-6 production;
 KW therapeutic; allergy; asthma; cancer; autoimmune disorder; infection;
 KW bio-warfare; vaccine; antisense therapy; eczema; allergic rhinitis;
 KW coryza; hay fever; urticaria; hives; food allergy; atopic condition;
 KW hepatitis; human immunodeficiency virus; HIV; malaria; Francisella;
 KW lupus erythematosus; rheumatoid arthritis; multiple sclerosis;
 KW schistosomiasis; tuberculosis; acquired immunodeficiency syndrome; AIDS;
 KW Leishmania; Ebola; Anthrax; Listeria; ss.
 XX
 OS Synthetic.
 XX
 PN WO200151500-A1.
 XX
 PD 19-JUL-2001.
 XX
 PF 12-JAN-2001; 2001WO-US001122.
 XX
 PR 14-JAN-2000; 2000US-0176115P.
 XX
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX
 PI Klinman D, Ishii K, Verthelyi D;
 XX
 DR WPI; 2001-442129/47.
 XX
 PT Oligodeoxynucleotides for inducing an immune response to treat and
 PT prevent an allergic reaction, cancer, an autoimmune disorder and symptoms
 PT resulting from exposure to bio-warfare agents, comprise multiple CpG
 sequences.
 XX
 PS Claim 5; Page 34; 49pp; English.
 XX
 CC AAS09551-AAS09662 represent oligodeoxynucleotides (ODN) of at least 10
 CC nucleotides comprising multiple CpG sequences, where one of the CpG
 CC sequences is different from another of the multiple CpG sequences. The
 CC ODN are useful for inducing an immune response, preferably a cell-
 CC mediated immune response, involving non-B cell activation, interferon
 CC gamma (IFN-gamma) production or a humoral immune response involving B
 CC cell activation, antibody and interleukin-6 production in a host, for
 CC treating, preventing or ameliorating an allergic reaction, e.g. asthma,

CC cancer, e.g. solid tumour cancer, a disease associated with the immune
 CC system e.g. autoimmune disorder or an immune system deficiency, infection
 CC or a symptom resulting from exposure to bio-warfare agent in a human. The
 CC induction of immune response improves the efficacy of a vaccine and is
 CC used in antisense therapy. The ODN are useful for treating, preventing or
 CC ameliorating allergic reactions, including eczema, allergic rhinitis or
 CC coryza, hay fever, bronchial asthma, urticaria (hives), food allergies
 CC and other atopic conditions, for improving the efficacy of vaccines
 CC against hepatitis A, B and C, human immunodeficiency virus (HIV) and
 CC malaria, for treating immune system deficiencies, e.g. lupus
 CC erythematous and autoimmune diseases such as rheumatoid arthritis and
 CC multiple sclerosis, infections including Francisella, schistosomiasis,
 CC tuberculosis, acquired immunodeficiency syndrome (AIDS), Leishmania and
 CC symptoms resulting from exposure of bio-warfare agent, including Ebola,
 CC Anthrax and Listeria
 XX
 SQ Sequence 20 BP; 3 A; 3 C; 11 G; 3 T; 0 U; 0 Other;
 Query Match 100.0%; Score 20; DB 4; Length 20;
 Best Local Similarity 100.0%; Pred. No. 3;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GGTGCATCGATCGAGGGGG 20
 Db 1 GGTGCATCGATCGAGGGGG 20
 RESULT 11
 ID AAS09584
 XX AAS09584 standard; DNA; 20 BP.
 AC AAS09584;
 XX
 DT 26-SEP-2001 (first entry)
 XX
 DE Immunoreactive CpG sequence-containing oligonucleotide #34.
 XX
 KW CpG sequence; immune response; non-B cell activation; interferon gamma;
 KW IFN-gamma; humoral; antibody production; interleukin-6 production;
 KW therapeutic; allergy; asthma; cancer; autoimmune disorder; infection;
 KW bio-warfare; vaccine; antisense therapy; eczema; allergic rhinitis;
 KW coryza; hay fever; urticaria; hives; food allergy; atopic condition;
 KW hepatitis; human immunodeficiency virus; HIV; malaria; Francisella;
 KW lupus erythematosus; rheumatoid arthritis; multiple sclerosis;
 KW schistosomiasis; tuberculosis; acquired immunodeficiency syndrome; AIDS;
 KW Leishmania; Ebola; Anthrax; Listeria; ss.
 XX
 OS Synthetic.
 XX
 PN WO200151500-A1.
 XX
 PD 19-JUL-2001.
 XX
 PF 12-JAN-2001; 2001WO-US001122.
 XX
 PR 14-JAN-2000; 2000US-0176115P.
 XX
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX
 PI Klinman D, Ishii K, Verthelyi D;
 XX
 DR WPI; 2001-442129/47.
 XX
 PT Oligodeoxynucleotides for inducing an immune response to treat and
 PT prevent an allergic reaction, cancer, an autoimmune disorder and symptoms
 PT resulting from exposure to bio-warfare agents, comprise multiple CpG
 sequences.
 XX
 PS Claim 5; Page 32; 48pp; English.
 XX
 CC AAS09551-AAS09662 represent oligodeoxynucleotides (ODN) of at least 10
 CC nucleotides comprising multiple CpG sequences, where one of the CpG
 CC sequences is different from another of the multiple CpG sequences. The

CC ODN are useful for inducing an immune response, preferably a cell-
 CC mediated immune response, involving non-B cell activation, interferon
 CC gamma (IFN-gamma) production or a humoral immune response involving B
 CC cell activation, antibody and interleukin-6 production in a host, for
 CC treating, preventing or ameliorating an allergic reaction, e.g. asthma,
 CC cancer, e.g. solid tumor cancer, a disease associated with the immune
 CC system e.g. autoimmune disorder or an immune system deficiency, infection
 CC or a symptom resulting from exposure to bio-warfare agent in a human. The
 CC induction of immune response improves the efficacy of a vaccine and is
 CC used in antisense therapy. The ODN are useful for treating, preventing or
 CC ameliorating allergic reactions, including eczema, allergic rhinitis or
 CC coryza, hay fever, bronchial asthma, urticaria (hives), food allergies
 CC and other atopic conditions, for improving the efficacy of vaccines
 CC against hepatitis A, B and C, human immunodeficiency virus (HIV) and
 CC malaria, for treating immune system deficiencies, e.g. lupus
 CC erythematous and autoimmune diseases such as rheumatoid arthritis and
 CC multiple sclerosis, infections including Francisella, schistosomiasis,
 CC tuberculosis, acquired immunodeficiency syndrome (AIDS), Leishmania and
 CC symptoms resulting from exposure of bio-warfare agent, including Ebola,
 CC Anthrax and Listeria

XX Sequence 20 BP; 3 A; 3 C; 11 G; 3 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 4; Length 20;
 Best Local Similarity 100.0%; Pred. No. 3;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTGATCGATCGAGGGGG 20
 |||||
 Db 1 GGTGATCGATCGAGGGGG 20

RESULT 12

AAS09588
 ID AAS09588 standard; DNA; 20 BP.

XX AAS09588;

26-SEP-2001 (first entry)

DE Immunoreactive CpG sequence-containing oligonucleotide #38.

XX CpG sequence; immune response; non-B cell activation; interferon gamma;
 KW IFN-gamma; humoral; antibody production; interleukin-6 production;
 KW therapeutic; allergy; asthma; cancer; autoimmune disorder; infection;
 KW bio-warfare; vaccine; antisense therapy; eczema; allergic rhinitis;
 KW coryza; hay fever; urticaria; hives; food allergy; atopic condition;
 KW hepatitis; human immunodeficiency virus; HIV; malaria; Francisella;
 KW lupus erythematous; rheumatoid arthritis; multiple sclerosis;
 KW schistosomiasis; tuberculosis; acquired immunodeficiency syndrome; AIDS;
 KW Leishmania; Ebola; Anthrax; Listeria; ss.

XX Synthetic.

XX WO200151500-A1.

XX 19-JUL-2001.

XX 12-JAN-2001; 2001WO-US001122.

XX 14-JAN-2000; 2000US-0176115P.

XX (USSH) US DEPT HEALTH & HUMAN SERVICES.

XX Klinman D, Ishii K, Verthelyi D;

XX WPI; 2001-442129/47.

XX Oligodeoxynucleotides for inducing an immune response to treat and
 PT prevent an allergic reaction, cancer, an autoimmune disorder and symptoms
 PT resulting from exposure to bio-warfare agents, comprise multiple CpG
 PT sequences.

XX

PS Claim 5; Page 33; 48pp; English.

XX AAS09551-AAS09662 represent oligodeoxynucleotides (ODN) of at least 10
 CC nucleotides comprising multiple CpG sequences, where one of the CpG
 CC sequences is different from another of the multiple CpG sequences. The
 CC ODN are useful for inducing an immune response, preferably a cell-
 CC mediated immune response, involving non-B cell activation, interferon
 CC gamma (IFN-gamma) production or a humoral immune response involving B
 CC cell activation, antibody and interleukin-6 production in a host, for
 CC treating, preventing or ameliorating an allergic reaction, e.g. asthma,
 CC cancer, e.g. solid tumor cancer, a disease associated with the immune
 CC system e.g. autoimmune disorder or an immune system deficiency, infection
 CC or a symptom resulting from exposure to bio-warfare agent in a human. The
 CC induction of immune response improves the efficacy of a vaccine and is
 CC used in antisense therapy. The ODN are useful for treating, preventing or
 CC ameliorating allergic reactions, including eczema, allergic rhinitis or
 CC coryza, hay fever, bronchial asthma, urticaria (hives), food allergies
 CC and other atopic conditions, for improving the efficacy of vaccines
 CC against hepatitis A, B and C, human immunodeficiency virus (HIV) and
 CC malaria, for treating immune system deficiencies, e.g. lupus
 CC erythematous and autoimmune diseases such as rheumatoid arthritis and
 CC multiple sclerosis, infections including Francisella, schistosomiasis,
 CC tuberculosis, acquired immunodeficiency syndrome (AIDS), Leishmania and
 CC symptoms resulting from exposure of bio-warfare agent, including Ebola,
 CC Anthrax and Listeria

XX Sequence 20 BP; 3 A; 3 C; 11 G; 3 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 4; Length 20;

Best Local Similarity 100.0%; Pred. No. 3;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTGATCGATCGAGGGGG 20

|||||

Db 1 GGTGATCGATCGAGGGGG 20

RESULT 13

ABL35568

ID ABL35568 standard; DNA; 20 BP.

XX ABL35568;

04-APR-2002 (first entry)

DE Immunostimulatory oligonucleotide SEQ ID NO: 494.

XX DNA/RNA hybrid; phosphorothioate backbone; immunostimulatory; vaccine;
 KW infection; allergy; cancer; hypersensitivity; bio-warfare;
 KW immunostimulant; antiallergic; cytostatic; antimicrobial; anti-HIV;
 KW immunosuppressive; protozoicide; virucide; hepatotropic; gene therapy;
 KW antiinflammatory; antibacterial; ss.

XX Synthetic.

XX Key Location/Qualifiers

FT misc_RNA 1..20

FT /*tag= a

FT /note= "optionally thymidine is replaced by uracil to
 form RNA or DNA/RNA hybrids. Thymidine is linked to at
 least one other base through a ribose sugar"

XX WO200193902-A2.

XX 13-DEC-2001.

XX 07-JUN-2001; 2001WO-US018276.

XX 07-JUN-2000; 2000US-0209797P.

XX (BIOS-) BIOSYNEXUS INC.

XX Mond JJ, Flora M, Klinman DM;

PT oligonucleotides, useful for enhancing an immune response or inducing
PT cytokines, particularly for treating diseases, e.g. cancer, allergy or
PT HIV infection.
XX

PS Example 11; Page 61; 68pp; English.

XX The present invention relates to an immunostimulatory composition, which
CC comprises at least one oligonucleotide comprising both an RNA region and
CC a DNA region. The composition is useful for enhancing an immune response
CC or inducing cytokines. It can be used as a vaccine adjuvant and in
CC treating diseases, including pathogenic infection, (non-)malignant
CC tumours (e.g. cancers of the brain, lung, ovary, breast, prostate or
CC colon, or carcinomas and sarcomas), autoimmune diseases or allergies
CC (e.g. allergic rhinitis, hay fever or food allergies), Lyme disease,
CC hepatitis, HIV or malaria. The composition is also useful for treating,
CC preventing or ameliorating the symptoms resulting from exposure to a bio-
CC warfare agent, e.g. Ebola, Anthrax or Listeria. The present sequence is
CC an immunostimulatory oligonucleotide described in the exemplification of
CC the invention

XX Sequence 20 BP; 3 A; 3 C; 11 G; 3 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTCATCGATGCGAGGGGG 20
|||||
Db 1 GGTCATCGATGCGAGGGGG 20

Search completed: July 2, 2004, 08:31:32
Job time : 151.878 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 2, 2004, 08:09:30 ; Search time 31.3415 Seconds
(without alignments)
354.132 Million cell updates/sec

Title: US-10-068-160-1

Perfect score: 20

Sequence: 1 ggtgcacgacgagggggg 20

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Issued Patents_NA:*
- 1: /cgm2_6/ptodata/2/ina/5A_COMB.seq:**
 - 2: /cgm2_6/ptodata/2/ina/5B_COMB.seq:**
 - 3: /cgm2_6/ptodata/2/ina/6A_COMB.seq:**
 - 4: /cgm2_6/ptodata/2/ina/6B_COMB.seq:**
 - 5: /cgm2_6/ptodata/2/ina/PTCUS_COMB.seq:**
 - 6: /cgm2_6/ptodata/2/ina/backfiles.seq:**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	15.8	79.0	3358	3	US-09-248-571-2
2	15.8	79.0	3358	4	US-09-553-736-2
3	15.2	76.0	1584	4	US-09-252-981A-7138
4	15.2	76.0	1794	4	US-09-252-981A-7259
5	15.2	76.0	1872	4	US-09-252-991A-7359
6	14.8	74.0	622	3	US-09-125-030-45
7	14.4	72.0	759	4	US-09-252-991A-1486
8	14.4	72.0	1086	4	US-09-252-991A-13644
9	14.4	72.0	1092	4	US-09-252-991A-13444
10	14.4	72.0	1194	4	US-09-252-991A-13697
11	14.4	72.0	1308	4	US-09-252-991A-1592
12	14.4	72.0	1356	4	US-09-252-991A-1425
13	14.4	72.0	3591	4	US-09-252-991A-1690
14	14.4	72.0	4280	4	US-09-079-592-1
15	14.4	72.0	5496	4	US-09-462-284-1
16	14.4	72.0	32654	4	US-09-801-191A-3
17	14.4	72.0	1664976	4	US-08-916-421B-1
18	14.4	72.0	4403765	3	US-09-103-840A-2
19	14.4	72.0	4411529	3	US-09-103-840A-1
20	14.2	71.0	236	4	US-09-621-976-18710
21	14.2	71.0	339	4	US-09-107-532A-3414
22	14.2	71.0	589	1	US-08-454-196-3
23	14.2	71.0	589	3	US-09-064-033-3
24	14.2	71.0	589	4	US-09-291-046-3
25	14.2	71.0	1020	4	US-09-107-532A-1250
26	14.2	71.0	1029	2	US-08-743-637B-191
27	14.2	71.0	1128	4	US-09-107-532A-210

28	14.2	71.0	1140	1	US-08-454-196-1
29	14.2	71.0	1140	3	US-09-064-033-1
30	14.2	71.0	1140	4	US-09-291-046-1
31	14.2	71.0	1392	4	US-09-489-039A-4664
32	14.2	71.0	1607	4	US-09-328-857A-1
33	14.2	71.0	1627	1	US-08-615-170-2
34	14.2	71.0	1666	1	US-08-615-170-4
35	14.2	71.0	2728	3	US-09-188-930-213
36	14.2	71.0	2728	4	US-09-312-283C-213
37	14.2	71.0	2820	5	PCT-US93-11725-1
38	14.2	71.0	3842	4	US-09-976-594-279
39	14.2	71.0	4389	4	US-09-023-655-991
40	14.2	71.0	4726	4	US-09-598-401C-96
41	14.2	71.0	5581	4	US-09-023-655-966
42	14.2	71.0	28958	1	US-08-258-361B-6
43	14.2	71.0	28958	1	US-08-456-837-6
44	14.2	71.0	28958	1	US-08-457-342-6
45	14.2	71.0	28958	1	US-08-457-646A-6

ALIGNMENTS

RESULT 1
US-09-248-571-2
; Sequence 2, Application US/09248571
; Patent No. 6136539
; GENERAL INFORMATION:
; APPLICANT: BASBAUM, CAROL
; APPLICANT: GALLUP, MARIANNE
; APPLICANT: DAIZONG, LI
; APPLICANT: GEBREMICHAEL, ASSEFA
; APPLICANT: GENSCH, ERIN
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR INHIBITION OF MUC-5 MUCIN
; TITLE OF INVENTION: GENE EXPRESSION
; FILE REFERENCE: UCSF12/02
; CURRENT APPLICATION NUMBER: US/09/248,571
; EARLIER FILING DATE: 1999-02-11
; EARLIER APPLICATION NUMBER: 60/074,398
; EARLIER FILING DATE: 1998-02-11
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 3358
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-248-571-2

Query Match 79.0%; Score 15.8; DB 3; Length 3358;
Best Local Similarity 89.3%; Pred. No. 71;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 2 GTGCATCGATCGACGGGGG 20
Db 998 GTGCACCCATCGACGGGGG 1016

RESULT 2
US-09-553-736-2
; Sequence 2, Application US/09553736
; Patent No. 6440672
; GENERAL INFORMATION:
; APPLICANT: BASBAUM, CAROL
; APPLICANT: GALLUP, MARIANNE
; APPLICANT: DAIZONG, LI
; APPLICANT: GEBREMICHAEL, ASSEFA
; APPLICANT: GENSCH, ERIN
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE INHIBITION OF MUC-5
; TITLE OF INVENTION: MUCIN GENE EXPRESSION
; FILE REFERENCE: UCSF-012/03US
; CURRENT APPLICATION NUMBER: US/09/553,736
; CURRENT FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 09/248,571

Query Match 79.0%; Score 15.8; DB 4; Length 3358;
Best Local Similarity 89.5%; Pred. No. 71;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2 GTGCATCGATCGAGGGGG 20
DB 998 GTGCACCCATCGAGGGGG 1016
RESULT 3
US-09-252-991A-7138/c
Sequence 7138, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 7138
TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-7138

Query Match 76.0%; Score 15.2; DB 4; Length 1584;
Best Local Similarity 85.0%; Pred. No. 1.3e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 GTGCATCGATCGAGGGGG 20
DB 1521 GGCGACGCGATCGAGGGTGG 1502
RESULT 4
US-09-252-991A-7259/c
Sequence 7259, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 7259
LENGTH: 1794
TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-7259

Query Match 76.0%; Score 15.2; DB 4; Length 1794;
Best Local Similarity 85.0%; Pred. No. 1.3e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 GTGCATCGATCGAGGGGG 20
DB 208 GGCGACGCGATCGAGGGTGG 189

RESULT 5
US-09-252-991A-7359
Sequence 7359, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 7359
LENGTH: 1872
TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-7359

Query Match 76.0%; Score 15.2; DB 4; Length 1872;
Best Local Similarity 85.0%; Pred. No. 1.3e+02;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 GTGCATCGATCGAGGGGG 20
DB 271 GGCGACGCGATCGAGGGTGG 290

RESULT 6
US-09-129-030-46
Sequence 46, Application US/09129030A
Patent No. 6242221
GENERAL INFORMATION:
APPLICANT: COMMONWEALTH SCIENTIFIC AND INDUSTRIAL RESEARCH ORGANISATION
TITLE OF INVENTION: GENOMIC PPO CLONES
FILE REFERENCE: 57072-PCT-US
CURRENT APPLICATION NUMBER: US/09/129,030A
CURRENT FILING DATE: 1998-08-04
EARLIER APPLICATION NUMBER: AU PN7856
EARLIER FILING DATE: 1996-02-05
EARLIER APPLICATION NUMBER: AU P02361
EARLIER FILING DATE: 1996-09-16
EARLIER APPLICATION NUMBER: PCT/AU97/00041
EARLIER FILING DATE: 1997-01-24
NUMBER OF SEQ ID NOS: 66
SOFTWARE: Patent in Ver. 2.0
SEQ ID NO 46
LENGTH: 622
TYPE: DNA
ORGANISM: RICE
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(300)
FEATURE:
NAME/KEY: CDS
LOCATION: (303)..(620)
US-09-129-030-46

Query Match 74.0%; Score 14.8; DB 3; Length 622;
Best Local Similarity 88.9%; Pred. No. 1.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GTGTCGATGCAGGGG 19
 Db 217 GTGTCGATGCAGCGC 234

RESULT 7

US-09-252-991A-1486/c
 ; Sequence 1486, Application US/09252991A
 ; Patent No. 6551795
 ; GENERAL INFORMATION:
 ; APPLICANT: Marc J. Rubenfield et al.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 ; FILE REFERENCE: 107196.136
 ; CURRENT APPLICATION NUMBER: US/09/252,991A
 ; CURRENT FILING DATE: 1999-02-18
 ; PRIOR APPLICATION NUMBER: US 60/074,788
 ; PRIOR FILING DATE: 1998-02-18
 ; PRIOR APPLICATION NUMBER: US 60/094,190
 ; PRIOR FILING DATE: 1998-07-27
 ; NUMBER OF SEQ ID NOS: 33142
 ; SEQ ID NO 1486
 ; LENGTH: 759
 ; TYPE: DNA
 ; ORGANISM: Pseudomonas aeruginosa
 US-09-252-991A-1486

Query Match 72.0%; Score 14.4; DB 4; Length 759;
 Best Local Similarity 93.8%; Pred. No. 3.1e+02;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTGTCATGCAGCAGG 16
 Db 374 GGTGTCGTCATGCAGG 359

RESULT 8

US-09-252-991A-13644/c
 ; Sequence 13644, Application US/09252991A
 ; Patent No. 6551795
 ; GENERAL INFORMATION:
 ; APPLICANT: Marc J. Rubenfield et al.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 ; FILE REFERENCE: 107196.136
 ; CURRENT APPLICATION NUMBER: US/09/252,991A
 ; CURRENT FILING DATE: 1999-02-18
 ; PRIOR APPLICATION NUMBER: US 60/074,788
 ; PRIOR FILING DATE: 1998-02-18
 ; PRIOR APPLICATION NUMBER: US 60/094,190
 ; PRIOR FILING DATE: 1998-07-27
 ; NUMBER OF SEQ ID NOS: 33142
 ; SEQ ID NO 13644
 ; LENGTH: 1086
 ; TYPE: DNA
 ; ORGANISM: Pseudomonas aeruginosa
 US-09-252-991A-13644

Query Match 72.0%; Score 14.4; DB 4; Length 1086;
 Best Local Similarity 93.8%; Pred. No. 3.2e+02;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 GCATCGATGCAGGGG 19
 Db 264 GCATCGATGCCGGGG 249

RESULT 9

US-09-252-991A-13444/c
 ; Sequence 13444, Application US/09252991A
 ; Patent No. 6551795
 ; GENERAL INFORMATION:

; APPLICANT: Marc J. Rubenfield et al.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 ; FILE REFERENCE: 107196.136
 ; CURRENT APPLICATION NUMBER: US/09/252,991A
 ; CURRENT FILING DATE: 1999-02-18
 ; PRIOR APPLICATION NUMBER: US 60/074,788
 ; PRIOR FILING DATE: 1998-02-18
 ; PRIOR APPLICATION NUMBER: US 60/094,190
 ; PRIOR FILING DATE: 1998-07-27
 ; NUMBER OF SEQ ID NOS: 33142
 ; SEQ ID NO 13444
 ; LENGTH: 1092
 ; TYPE: DNA
 ; ORGANISM: Pseudomonas aeruginosa
 US-09-252-991A-13444

Query Match 72.0%; Score 14.4; DB 4; Length 1092;
 Best Local Similarity 93.8%; Pred. No. 3.2e+02;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 GCATCGATGCAGGGG 19
 Db 305 GCATCGATGCCGGGG 290

RESULT 10

US-09-252-991A-13697
 ; Sequence 13697, Application US/09252991A
 ; Patent No. 6551795
 ; GENERAL INFORMATION:
 ; APPLICANT: Marc J. Rubenfield et al.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 ; FILE REFERENCE: 107196.136
 ; CURRENT APPLICATION NUMBER: US/09/252,991A
 ; CURRENT FILING DATE: 1999-02-18
 ; PRIOR APPLICATION NUMBER: US 60/074,788
 ; PRIOR FILING DATE: 1998-02-18
 ; PRIOR APPLICATION NUMBER: US 60/094,190
 ; PRIOR FILING DATE: 1998-07-27
 ; NUMBER OF SEQ ID NOS: 33142
 ; SEQ ID NO 13697
 ; LENGTH: 1194
 ; TYPE: DNA
 ; ORGANISM: Pseudomonas aeruginosa
 US-09-252-991A-13697

Query Match 72.0%; Score 14.4; DB 4; Length 1194;
 Best Local Similarity 93.8%; Pred. No. 3.2e+02;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 GCATCGATGCAGGGG 19
 Db 971 GCATCGATGCCGGGG 986

RESULT 11

US-09-252-991A-1592
 ; Sequence 1592, Application US/09252991A
 ; Patent No. 6551795
 ; GENERAL INFORMATION:
 ; APPLICANT: Marc J. Rubenfield et al.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 ; FILE REFERENCE: 107196.136
 ; CURRENT APPLICATION NUMBER: US/09/252,991A
 ; CURRENT FILING DATE: 1999-02-18
 ; PRIOR APPLICATION NUMBER: US 60/074,788
 ; PRIOR FILING DATE: 1998-02-18
 ; PRIOR APPLICATION NUMBER: US 60/094,190
 ; PRIOR FILING DATE: 1998-07-27
 ; NUMBER OF SEQ ID NOS: 33142

```
; SEQ ID NO 1592
; LENGTH: 1308
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-1592

Query Match 72.0%; Score 14.4; DB 4; Length 1308;
Best Local Similarity 93.8%; Pred. No. 3.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTGCGTCGATGCAGG 16
    |||||
Db 367 GGTGCGTCGATGCAGG 382

RESULT 12
US-09-252-991A-1425/c
; Sequence 1425, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 1425
; TYPE: DNA
; LENGTH: 1356
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-1425

Query Match 72.0%; Score 14.4; DB 4; Length 1356;
Best Local Similarity 93.8%; Pred. No. 3.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTGCGTCGATGCAGG 16
    |||||
Db 981 GGTGCGTCGATGCAGG 966

RESULT 13
US-09-252-991A-1690
; Sequence 1690, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 1690
; TYPE: DNA
; LENGTH: 3591
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-1690

Query Match 72.0%; Score 14.4; DB 4; Length 3591;
Best Local Similarity 93.8%; Pred. No. 3.5e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTGCGTCGATGCAGG 16
    |||||
Db 981 GGTGCGTCGATGCAGG 966

RESULT 14
US-09-079-592-1/c
; Sequence 1, Application US/09079592B
; Patent No. 6664092
; GENERAL INFORMATION:
; APPLICANT: Alexander Blinkovsky
; APPLICANT: Kimberly Brown
; APPLICANT: Michael W. Rey
; APPLICANT: Alan Klotz
; APPLICANT: Tony Byun
; TITLE OF INVENTION: Polypeptides Having Dipeptidyl
; TITLE OF INVENTION: Aminopeptidase Activity And Nucleic Acids Encoding Same
; FILE REFERENCE: 5254.200-US
; CURRENT APPLICATION NUMBER: US/09/079,592B
; CURRENT FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 08/857,884
; PRIOR FILING DATE: 1997-05-16
; PRIOR APPLICATION NUMBER: 60/062,892
; PRIOR FILING DATE: 1997-10-20
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; TYPE: DNA
; LENGTH: 4280
; ORGANISM: Aspergillus
US-09-079-592-1

Query Match 72.0%; Score 14.4; DB 4; Length 4280;
Best Local Similarity 93.8%; Pred. No. 3.6e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 TGCATCGATCCAGGG 18
    |||||
Db 3367 TGCATCGATCCAGGG 3352

RESULT 15
US-09-462-284-1/c
; Sequence 1, Application US/09462284
; Patent No. 6309868
; GENERAL INFORMATION:
; APPLICANT: Nestec S.A.
; APPLICANT: Monod, Michel
; APPLICANT: Dumas, Agnes
; APPLICANT: Affolter, Micheal
; APPLICANT: Van Den Broek, Peter
; TITLE OF INVENTION: CLONING OF THE
; TITLE OF INVENTION: PROLYL-DIPEPTIDYL-PEPTIDASE FROM
; TITLE OF INVENTION: ASPERGILLUS ORYZAE
; FILE REFERENCE: 8265-298
; CURRENT APPLICATION NUMBER: US/09/462,284
; CURRENT FILING DATE: 2000-01-03
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; TYPE: DNA
; LENGTH: 5496
; ORGANISM: Fungus
US-09-462-284-1

Query Match 72.0%; Score 14.4; DB 4; Length 5496;
Best Local Similarity 93.8%; Pred. No. 3.6e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 TGCATCGATCCAGGG 18
    |||||
Db 3745 TGCATCGATCCAGGG 3730
```

Fri Jul 2 14:53:26 2004

Search completed: July 2, 2004, 13:37:17
Job time : 38.3415 secs

us-10-068-160-1.rni

Page 5

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 2, 2004, 08:11:05 ; Search time 154.146 Seconds
(without alignments)
625.926 Million cell updates/sec

Title: US-10-068-160-1

Perfect score: 20

Sequence: 1 ggtgcacgacgacggggg 20

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3163042 seqs, 2412103800 residues

Total number of hits satisfying chosen parameters: 6326084

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:
1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:
2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:
3: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:
4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:
5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:
6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:
7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:
8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:
9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:
10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:
11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:
12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:
13: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:
14: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:
15: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:
16: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:
17: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:
18: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:
19: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	20	13	US-09-874-991C-494
2	20	100.0	20	13	US-09-874-991C-505
3	20	100.0	20	13	US-09-874-991C-538
4	20	100.0	20	15	US-10-068-160-1
5	20	100.0	20	15	US-10-068-160-54
6	20	100.0	20	15	US-10-194-035-32
7	20	100.0	20	15	US-10-194-035-34
8	20	100.0	20	15	US-10-194-035-37
9	20	100.0	20	15	US-10-194-035-38
10	20	100.0	20	15	US-10-194-035-43
11	20	100.0	20	15	US-10-194-035-72
12	20	100.0	20	17	US-10-666-022-176
13	20	100.0	20	17	US-10-666-022-177
14	20	100.0	22	13	US-09-874-991C-500

15	20	100.0	22	13	US-09-874-991C-544	Sequence 544, App
16	20	100.0	22	13	US-09-874-991C-515	Sequence 515, App
17	20	100.0	28	13	US-09-874-991C-527	Sequence 527, App
18	20	100.0	29	13	US-09-874-991C-533	Sequence 533, App
19	20	100.0	30	13	US-09-874-991C-521	Sequence 521, App
20	20	100.0	30	13	US-09-874-991C-526	Sequence 526, App
21	20	100.0	32	13	US-09-874-991C-463	Sequence 463, App
22	19	95.0	19	15	US-10-194-035-53	Sequence 53, Appl
23	19	95.0	19	15	US-10-194-035-73	Sequence 73, Appl
24	18.4	92.0	20	13	US-09-874-991C-498	Sequence 498, App
25	18.4	92.0	20	13	US-09-874-991C-499	Sequence 499, App
26	18.4	92.0	20	13	US-09-874-991C-509	Sequence 509, App
27	18.4	92.0	20	13	US-09-874-991C-510	Sequence 510, App
28	18.4	92.0	20	13	US-09-874-991C-542	Sequence 542, App
29	18.4	92.0	20	13	US-09-874-991C-543	Sequence 543, App
30	18.4	92.0	20	15	US-10-068-160-7	Sequence 7, Appl
31	18.4	92.0	20	15	US-10-068-160-11	Sequence 11, Appl
32	18.4	92.0	20	15	US-10-068-160-21	Sequence 21, Appl
33	18.4	92.0	20	15	US-10-068-160-30	Sequence 30, Appl
34	18.4	92.0	20	15	US-10-068-160-35	Sequence 35, Appl
35	18.4	92.0	20	15	US-10-068-160-37	Sequence 37, Appl
36	18.4	92.0	20	15	US-10-068-160-52	Sequence 52, Appl
37	18.4	92.0	20	15	US-10-068-160-53	Sequence 53, Appl
38	18.4	92.0	20	15	US-10-068-160-64	Sequence 64, Appl
39	18.4	92.0	20	15	US-10-068-160-65	Sequence 65, Appl
40	18.4	92.0	20	15	US-10-194-035-40	Sequence 40, Appl
41	18.4	92.0	20	15	US-10-194-035-81	Sequence 81, Appl
42	18.4	92.0	20	15	US-10-194-035-82	Sequence 82, Appl
43	18.4	92.0	20	15	US-10-194-035-100	Sequence 100, App
44	18.4	92.0	20	15	US-10-194-035-101	Sequence 101, App
45	18.4	92.0	20	15	US-10-194-035-104	Sequence 104, App

ALIGNMENTS

RESULT 1
US-09-874-991C-494
; Sequence 494, Application US/09874991C
; Publication No. US20040052763A1
; GENERAL INFORMATION:
; APPLICANT: MOND, JAMES J.
; APPLICANT: FLORA, MICHAEL
; APPLICANT: KLINMAN, DENNIS M.
; TITLE OF INVENTION: IMMUNOSTIMULATORY RNA/DNA HYBRID MOLECULES
; FILE REFERENCE: 07787.0042-0
; CURRENT APPLICATION NUMBER: US/09/874.991C
; CURRENT FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: 60/209,797
; PRIOR FILING DATE: 2000-06-07
; NUMBER OF SEQ ID NOS: 620
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 494
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic HDR
US-09-874-991C-494

Query Match 100.0%; Score 20; DB 13; Length 20;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 GGTGCATCGATCGAGGGGG 20
|||
Db 1 GGTGCATCGATCGAGGGGG 20

RESULT 2

US-09-874-991C-505
; Sequence 505, Application US/09874991C
; Publication No. US20040052763A1

```
; GENERAL INFORMATION:
; APPLICANT: MOND, JAMES J.
; APPLICANT: FLORA, MICHAEL
; APPLICANT: KLINMAN, DENNIS M.
; TITLE OF INVENTION: IMMUNOSTIMULATORY RNA/DNA HYBRID MOLECULES
; FILE REFERENCE: 07787.0042-0
; CURRENT APPLICATION NUMBER: US/09/874,991C
; CURRENT FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: 60/209,797
; PRIOR FILING DATE: 2000-06-07
; NUMBER OF SEQ ID NOS: 620
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 505
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic HDR
US-09-874-991C-505

Query Match          100.0%; Score 20; DB 13; Length 20;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTGCATCGATCGAGGGGG 20
   |||||
Db 1 GGTGCATCGATCGAGGGGG 20

RESULT 3
US-09-874-991C-538
; Sequence 538, Application US/09874991C
; Publication No. US20040052763A1
; GENERAL INFORMATION:
; APPLICANT: MOND, JAMES J.
; APPLICANT: FLORA, MICHAEL
; APPLICANT: KLINMAN, DENNIS M.
; TITLE OF INVENTION: IMMUNOSTIMULATORY RNA/DNA HYBRID MOLECULES
; FILE REFERENCE: 07787.0042-0
; CURRENT APPLICATION NUMBER: US/09/874,991C
; CURRENT FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: 60/209,797
; PRIOR FILING DATE: 2000-06-07
; NUMBER OF SEQ ID NOS: 620
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 538
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic HDR
US-09-874-991C-538

Query Match          100.0%; Score 20; DB 13; Length 20;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTGCATCGATCGAGGGGG 20
   |||||
Db 1 GGTGCATCGATCGAGGGGG 20

RESULT 4
US-10-068-160-1
; Sequence 1, Application US/10068160
; Publication No. US20030060440A1
; GENERAL INFORMATION:
; APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA, REPRESENTED BY THE
; APPLICANT: SECRETARY, DEPARTMENT OF HEALTH AND HUMAN SERVICES
; APPLICANT: KLINMAN, DENNIS
; APPLICANT: ISHII, Ken
; APPLICANT: VERTHELYI, Daniela
; TITLE OF INVENTION: OLIGODEOXYNUCLEOTIDE AND ITS USE TO INDUCE AN IMMUNE RESPONSE
; FILE REFERENCE: 4239-63317
; CURRENT APPLICATION NUMBER: US/10/194,035
; CURRENT FILING DATE: 2002-07-12
```

```
; FILE REFERENCE: 4239-61999
; CURRENT APPLICATION NUMBER: US/10/068,160
; CURRENT FILING DATE: 2002-02-06
; PRIOR APPLICATION NUMBER: 60/128,898
; PRIOR FILING DATE: 1999-04-12
; NUMBER OF SEQ ID NOS: 120
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide
US-10-068-160-1

Query Match          100.0%; Score 20; DB 15; Length 20;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTGCATCGATCGAGGGGG 20
   |||||
Db 1 GGTGCATCGATCGAGGGGG 20

RESULT 5
US-10-068-160-54
; Sequence 54, Application US/10068160
; Publication No. US20030060440A1
; GENERAL INFORMATION:
; APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA, REPRESENTED BY THE
; APPLICANT: SECRETARY, DEPARTMENT OF HEALTH AND HUMAN SERVICES
; APPLICANT: KLINMAN, DENNIS
; APPLICANT: ISHII, Ken
; APPLICANT: VERTHELYI, Daniela
; TITLE OF INVENTION: OLIGODEOXYNUCLEOTIDE AND ITS USE TO INDUCE AN IMMUNE RESPONSE
; FILE REFERENCE: 4239-61999
; CURRENT APPLICATION NUMBER: US/10/068,160
; CURRENT FILING DATE: 2002-02-06
; PRIOR APPLICATION NUMBER: 60/128,898
; PRIOR FILING DATE: 1999-04-12
; NUMBER OF SEQ ID NOS: 120
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 54
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide
US-10-068-160-54

Query Match          100.0%; Score 20; DB 15; Length 20;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTGCATCGATCGAGGGGG 20
   |||||
Db 1 GGTGCATCGATCGAGGGGG 20

RESULT 6
US-10-194-035-32
; Sequence 32, Application US/10194035
; Publication No. US20030144229A1
; GENERAL INFORMATION:
; APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS REPRESENTED BY THE
; APPLICANT: SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES
; APPLICANT: KLINMAN, DENNIS
; APPLICANT: ISHII, Ken
; APPLICANT: VERTHELYI, Daniela
; TITLE OF INVENTION: OLIGODEOXYNUCLEOTIDE AND ITS USE TO INDUCE AN IMMUNE RESPONSE
; FILE REFERENCE: 4239-63317
; CURRENT APPLICATION NUMBER: US/10/194,035
; CURRENT FILING DATE: 2002-07-12
```

; PRIOR APPLICATION NUMBER: PCT/US01/01122
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: US 60/176,115
; PRIOR FILING DATE: 2000-01-14
; NUMBER OF SEQ ID NOS: 119
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 32
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
US-10-194-035-32

Query Match 100.0%; Score 20; DB 15; Length 20;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTGCATCGATCGAGGGGG 20
|||||
DB 1 GGTGCATCGATCGAGGGGG 20

RESULT 7
US-10-194-035-34
; Sequence 34, Application US/10194035
; Publication No. US20030144229A1
; GENERAL INFORMATION:
; APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS REPRESENTED BY THE
; APPLICANT: SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES
; APPLICANT: KLINMAN, Dennis
; APPLICANT: ISHII, Ken
; APPLICANT: VERTHELYI, Daniela
; TITLE OF INVENTION: OLIGODEOXYNUCLEOTIDE AND ITS USE TO INDUCE AN IMMUNE RESPONSE
; FILE REFERENCE: 4239-63317
; CURRENT APPLICATION NUMBER: US/10/194,035
; CURRENT FILING DATE: 2002-07-12
; PRIOR APPLICATION NUMBER: PCT/US01/01122
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: US 60/176,115
; PRIOR FILING DATE: 2000-01-14
; NUMBER OF SEQ ID NOS: 119
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 34
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
US-10-194-035-34

Query Match 100.0%; Score 20; DB 15; Length 20;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTGCATCGATCGAGGGGG 20
|||||
DB 1 GGTGCATCGATCGAGGGGG 20

RESULT 8
US-10-194-035-37
; Sequence 37, Application US/10194035
; Publication No. US20030144229A1
; GENERAL INFORMATION:
; APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS REPRESENTED BY THE
; APPLICANT: SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES
; APPLICANT: KLINMAN, Dennis
; APPLICANT: ISHII, Ken
; APPLICANT: VERTHELYI, Daniela
; TITLE OF INVENTION: OLIGODEOXYNUCLEOTIDE AND ITS USE TO INDUCE AN IMMUNE RESPONSE
; FILE REFERENCE: 4239-63317
; CURRENT APPLICATION NUMBER: US/10/194,035

; CURRENT FILING DATE: 2002-07-12
; PRIOR APPLICATION NUMBER: PCT/US01/01122
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: US 60/176,115
; PRIOR FILING DATE: 2000-01-14
; NUMBER OF SEQ ID NOS: 119
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 37
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
US-10-194-035-37

Query Match 100.0%; Score 20; DB 15; Length 20;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTGCATCGATCGAGGGGG 20
|||||
DB 1 GGTGCATCGATCGAGGGGG 20

RESULT 9
US-10-194-035-38
; Sequence 38, Application US/10194035
; Publication No. US20030144229A1
; GENERAL INFORMATION:
; APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS REPRESENTED BY THE
; APPLICANT: SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES
; APPLICANT: KLINMAN, Dennis
; APPLICANT: ISHII, Ken
; APPLICANT: VERTHELYI, Daniela
; TITLE OF INVENTION: OLIGODEOXYNUCLEOTIDE AND ITS USE TO INDUCE AN IMMUNE RESPONSE
; FILE REFERENCE: 4239-63317
; CURRENT APPLICATION NUMBER: US/10/194,035
; CURRENT FILING DATE: 2002-07-12
; PRIOR APPLICATION NUMBER: PCT/US01/01122
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: US 60/176,115
; PRIOR FILING DATE: 2000-01-14
; NUMBER OF SEQ ID NOS: 119
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 38
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
US-10-194-035-38

Query Match 100.0%; Score 20; DB 15; Length 20;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTGCATCGATCGAGGGGG 20
|||||
DB 1 GGTGCATCGATCGAGGGGG 20

RESULT 10
US-10-194-035-43
; Sequence 43, Application US/10194035
; Publication No. US20030144229A1
; GENERAL INFORMATION:
; APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS REPRESENTED BY THE
; APPLICANT: SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES
; APPLICANT: KLINMAN, Dennis
; APPLICANT: ISHII, Ken
; APPLICANT: VERTHELYI, Daniela
; TITLE OF INVENTION: OLIGODEOXYNUCLEOTIDE AND ITS USE TO INDUCE AN IMMUNE RESPONSE
; FILE REFERENCE: 4239-63317

; CURRENT APPLICATION NUMBER: US/10/194,035
; CURRENT FILING DATE: 2002-07-12
; PRIOR APPLICATION NUMBER: PCT/US01/01122
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: US 60/176,115
; PRIOR FILING DATE: 2000-01-14
; NUMBER OF SEQ ID NOS: 119
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 43
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
US-10-194-035-43

Query Match 100.0%; Score 20; DB 15; Length 20;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTGCATCGATCGAGGGGG 20
|||||
Db 1 GGTGCATCGATCGAGGGGG 20

RESULT 11
US-10-194-035-72
; Sequence 72, Application US/10194035
; Publication No. US2003014429A1
; GENERAL INFORMATION:
; APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS REPRESENTED BY THE
; APPLICANT: SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES
; APPLICANT: KLINMAN, Dennis
; APPLICANT: VERTHELYI, Daniela
; TITLE OF INVENTION: OLIGODEOXYNUCLEOTIDE AND ITS USE TO INDUCE AN IMMUNE RESPONSE
; FILE REFERENCE: 4239-63317
; CURRENT APPLICATION NUMBER: US/10/194,035
; CURRENT FILING DATE: 2002-07-12
; PRIOR APPLICATION NUMBER: PCT/US01/01122
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: US 60/176,115
; PRIOR FILING DATE: 2000-01-14
; NUMBER OF SEQ ID NOS: 119
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 72
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
US-10-194-035-72

Query Match 100.0%; Score 20; DB 15; Length 20;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTGCATCGATCGAGGGGG 20
|||||
Db 1 GGTGCATCGATCGAGGGGG 20

RESULT 12
US-10-666-022-176
; Sequence 176, Application US/10666022
; Publication No. US2004010587A1
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America, as represented by the
; APPLICANT: Secretary of the Department of Health and Human Services
; APPLICANT: KLINMAN, Dennis M.
; APPLICANT: Vertheilyi, Daniela
; TITLE OF INVENTION: METHOD OF TREATING AND PREVENTING INFECTIONS IN IMMUNOCOMPROMISED
; TITLE OF INVENTION: SUBJECTS WITH IMMUNOSTIMULATORY CPG

; FILE REFERENCE: 4239-66899
; CURRENT APPLICATION NUMBER: US/10/666,022
; CURRENT FILING DATE: 2003-09-17
; PRIOR APPLICATION NUMBER: US 60/411,944
; PRIOR FILING DATE: 2002-09-18
; NUMBER OF SEQ ID NOS: 181
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 176
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic
US-10-666-022-176

Query Match 100.0%; Score 20; DB 17; Length 20;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTGCATCGATCGAGGGGG 20
|||||
Db 1 GGTGCATCGATCGAGGGGG 20

RESULT 13
US-10-666-022-177
; Sequence 177, Application US/10666022
; Publication No. US2004010587A1
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America, as represented by the
; APPLICANT: Secretary of the Department of Health and Human Services
; APPLICANT: KLINMAN, Dennis M.
; APPLICANT: Vertheilyi, Daniela
; TITLE OF INVENTION: METHOD OF TREATING AND PREVENTING INFECTIONS IN IMMUNOCOMPROMISED
; FILE REFERENCE: 4239-66899
; CURRENT APPLICATION NUMBER: US/10/666,022
; CURRENT FILING DATE: 2003-09-17
; PRIOR APPLICATION NUMBER: US 60/411,944
; PRIOR FILING DATE: 2002-09-18
; NUMBER OF SEQ ID NOS: 181
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 177
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic
US-10-666-022-177

Query Match 100.0%; Score 20; DB 17; Length 20;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTGCATCGATCGAGGGGG 20
|||||
Db 1 GGTGCATCGATCGAGGGGG 20

RESULT 14
US-09-874-991C-500
; Sequence 500, Application US/09874991C
; Publication No. US20040052763A1
; GENERAL INFORMATION:
; APPLICANT: FLORA, MICHAEL
; APPLICANT: MOND, JAMES J.
; APPLICANT: KLINMAN, DENNIS M.
; TITLE OF INVENTION: IMMUNOSTIMULATORY RNA/DNA HYBRID MOLECULES
; FILE REFERENCE: 07787.0042-0
; CURRENT APPLICATION NUMBER: US/09/874,991C
; CURRENT FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: 60/209,797
; PRIOR FILING DATE: 2000-06-07

; NUMBER OF SEQ ID NOS: 620
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 500
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic HDR
US-09-874-991C-500

Query Match 100.0%; Score 20; DB 13; Length 22;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTGCATCGATCGAGGGGG 20
|||
Db 3 GGTGCATCGATCGAGGGGG 22

RESULT 15
US-09-874-991C-544
; Sequence 544, Application US/09874991C
; Publication No. US20040052763A1
; GENERAL INFORMATION:
; APPLICANT: MOND, JAMES J.
; APPLICANT: FLORA, MICHAEL
; APPLICANT: KLINMAN, DENNIS M.
; TITLE OF INVENTION: IMMUNOSTIMULATORY RNA/DNA HYBRID MOLECULES
; FILE REFERENCE: 07787.0042-0
; CURRENT APPLICATION NUMBER: US/09/874,991C
; CURRENT FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: 60/209,797
; PRIOR FILING DATE: 2000-06-07
; NUMBER OF SEQ ID NOS: 620
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 544
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic HDR
US-09-874-991C-544

Query Match 100.0%; Score 20; DB 13; Length 22;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTGCATCGATCGAGGGGG 20
|||
Db 3 GGTGCATCGATCGAGGGGG 22

Search completed: July 2, 2004, 13:58:23
Job time : 155.146 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

QM nucleic - nucleic search, using sw model

Run on: July 2, 2004, 07:38:45 ; Search time 1497.8 Seconds
(without alignments)
398.746 Million cell updates/sec

Title: US-10-068-160-1

Perfect score: 20

Sequence: 1 ggtgcacgatcagggggg 20

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: em_estba:*

2: em_esthum:*

3: em_estin:*

4: em_estmu:*

5: em_estov:*

6: em_estpl:*

7: em_estro:*

8: em_estc:*

9: gb_est1:*

10: gb_est2:*

11: gb_est3:*

12: gb_est4:*

13: gb_est5:*

14: gb_est6:*

15: em_estfun:*

16: em_estom:*

17: em_esthum:*

18: em_estinv:*

19: em_estpln:*

20: em_estvrt:*

21: em_estfun:*

22: em_estmam:*

23: em_estmus:*

24: em_estpro:*

25: em_estrod:*

26: em_estphg:*

27: em_estvrl:*

28: gb_ges1:*

29: gb_ges2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	18.4	92.0	257	9	AV268287
2	17.4	87.0	240	9	AV281636
3	17.4	87.0	303	9	AV269637
4	17.4	87.0	473	12	BI507147

C 5	17.4	87.0	1214	13	BQ898390
C 6	17	85.0	541	28	B01614
C 7	17	85.0	807	13	CA101677
C 8	17	85.0	839	29	CG066914
C 9	16.8	84.0	272	13	EX639713
C 10	16.8	84.0	597	9	AV028453
C 11	16.8	84.0	631	12	BJ244833
C 12	16.8	84.0	638	9	AL692509
C 13	16.8	84.0	648	14	CB065500
C 14	16.8	84.0	671	12	BJ229325
C 15	16.8	84.0	671	14	CA920724
C 16	16.8	84.0	685	12	BJ634520
C 17	16.8	84.0	697	12	BJ250701
C 18	16.8	84.0	740	12	BJ617983
C 19	16.8	84.0	868	29	CG675673
C 20	16.8	84.0	927	12	BI733127
C 21	16.8	84.0	979	13	CA157988
C 22	16.8	84.0	1206	29	CG747404
C 23	16.4	82.0	245	10	AW325275
C 24	16.4	82.0	259	10	BB422123
C 25	16.4	82.0	277	28	AQ444154
C 26	16.4	82.0	374	14	CB966250
C 27	16.4	82.0	553	28	BH374854
C 28	16.4	82.0	584	13	BQ875411
C 29	16.4	82.0	621	28	BH450526
C 30	16.4	82.0	670	28	BH936954
C 31	16.4	82.0	679	28	BH577346
C 32	16.4	82.0	700	28	BH685253
C 33	16.4	82.0	702	28	BH471235
C 34	16.4	82.0	705	29	CE730492
C 35	16.4	82.0	712	13	BQ860936
C 36	16.4	82.0	738	28	BZ063097
C 37	16.4	82.0	747	28	BZ449138
C 38	16.4	82.0	815	14	CA766588
C 39	16.4	82.0	853	28	BZ449800
C 40	16.4	82.0	866	28	BH128747
C 41	16.4	82.0	915	29	CC588288
C 42	16.4	82.0	960	29	AG073881
C 43	16.4	82.0	1014	29	AG056417
C 44	16.4	82.0	1055	29	CNS05E18
C 45	16.4	82.0	1096	29	CNS05CPL

ALIGNMENTS

RESULT 1
AV268287

LOCUS
DEFINITION

musculus

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

AV268287 257 bp mRNA linear EST 05-NOV-1999
musculus full-length enriched, adult male testis (DH10B) Mus
musculus CDNA clone 4930534F16 3', mRNA sequence.

AV268287.1 GI:6256324

EST.

Mus musculus (house mouse)

Mus musculus

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (bases 1 to 257)

Konno, H., Aizawa, K., Akabira, S., Akiyama, J., Carninci, P., Endo, T.,

Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N., Hirozane, T., Hori, F.,

Ishii, Y., Ishikawa, I., Itoh, M., Izawa, M., Kadota, K., Kagawa, I.,

Kai, C., Kawai, J., Kikuchi, N., Kojima, Y., Koya, S., Kusakabe, M.,

Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y.,

Owa, C., Ozawa, Y., Saito, H., Sano, M., Sato, K., Shibata, K.,

Shibata, Y., Shigemoto, Y., Shiraki, T., Sogabe, Y., Sugahara, Y.,

Suzuki, H., Suzuki, H., Takahashi, F., Tateo, M., Tomimaga, N.,

Tsunoda, Y., Watahiki, A., Watanabe, S., Yamamura, T., Yasunishi, A.,

Yokota, I., Yoshiki, A., Yoshino, M., Muramatsu, M., and Hayashizaki, Y.

RIKEN Mouse ESTs (Konno, H., et al. 1999)

Unpublished (1999)

Contact: Yoshihide Hayashizaki

Laboratory for Genome Exploration Research Group, RIKEN Genomic

Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration
Sciences Center (GSC) Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
tel: 81-45-503-9222
fax: 81-45-503-9216

Email: genome-res@sc.riken.go.jp,
URL: <http://genome.gsc.riken.go.jp/>
Sasaki, N., Izawa, M., Watahiki, M., Ozawa, K., Tanaka, T., Yoneda, Y.,
Watsutsuma, S., Carninci, P., Muramatsu, M., Okazaki, Y. and
Hayashizaki, Y.
Transcriptional sequencing: A method for DNA sequencing using RNA
polymerase. *Proc. Natl. Acad. Sci. U.S.A.* 95 (7), 3455-3460 (1998)
Itoh, M., Kitsuai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J.,
Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M.,
Okazaki, Y. and Hayashizaki, Y.
Automated filtration-based high-throughput plasmid preparation
system. *Genome Res.* 9 (5), 463-470 (1999)
Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning. *Methods Enzymol.* 303,
9-44 (1999)
Please visit our web site (<http://genome.rtc.riken.go.jp/>) for
further details.

(DH10B) *
[note=Site 1: SalI; Site 2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN, Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5',
GAGGAGAGAGAGATCCAGAGCTCTTTTTTTTTTTTTTNN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence [5',
GAGGAGAGAGATTCGAGTTCATTAATTAATCCCCCCCCC 3']. cDNA was cloned into the XhoI and BamHI sites. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLX I. Cloning sites, 5' end: SalI; 3' end: BamHI.]

ORIGIN

Query Match 87.0%; Score 17.4; DB 9; Length 240;
Best Local Similarity 94.7%; Pred. NO. 2e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

QY      2 GTGCATCGAGCGGGGG 20
      |||||
      84 GTGCATCGAGCGGGGG 102

RESULT 3
AV269637
LOCUS      303 bp mRNA linear EST 05-NOV-1999
DEFINITION RIKEN full-length enriched, adult male testis (DH10B) Mus
            musculus cDNA clone 4930544G09 3', mRNA sequence.
ACCESSION  AV269637
VERSION     AV269637.1 GI:6257674
KEYWORDS   Mus musculus (house mouse)
SOURCE     Mus musculus
ORGANISM   Mus musculus

REFERENCE
AUTHORS    Konno,H., Aizawa,K., Akahira,S., Akiyama,J., Carninci,P., Endo,T.,
            Fukuda,S., Fukunishi,Y., Hara,A., Hayatsu,N., Hirozane,T., Hori,P.,
            Ishii,Y., Ishikawa,T., Itoh,M., Izawa,M., Kadota,K., Kagawa,I.,
            Kai,C., Kawai,J., Kikuchi,N., Kojima,Y., Koya,S., Kusakabe,M.,
            Matsuyama,T., Miki,R., Mizuno,Y., Nakamura,M., Oda,H., Okazaki,Y.,
            Owa,C., Ozawa,Y., Saito,H., Sano,M., Sato,K., Shibata,K.,
            Shibata,Y., Shigenoto,Y., Shiraki,T., Sogabe,Y., Sugahara,Y.,
            Suzuki,H., Suzuki,H., Takahashi,F., Tateno,M., Tominaga,N.,
            Tsunoda,Y., Watahiki,A., Watanabe,S., Yamamura,T., Yasunishi,A.,
            Yokota,T., Yoshiki,A., Yoshino,M., Muramatsu,M. and Hayashizaki,Y.
            RIKEN Mouse ESTs (Konno,H., et al. 1999)
            Unpublished (1999)
            Contact: Yoshinide Hayashizaki
            Laboratory for Genome Exploration Research Group, RIKEN Genomic
            Sciences Center (GSC), Yokohama Institute
            The Institute of Physical and Chemical Research (RIKEN)
            1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
            Tel: 81-45-503-9222
            Fax: 81-45-503-9216
            Email: genome-resgsc.riken.go.jp,
            URL: http://genome.gsc.riken.go.jp/
            Sasaki,N., Izawa,M., Watahiki,M., Ozawa,K., Tanaka,T., Yoneda,Y.,
            Matsuura,S., Carninci,P., Muramatsu,M., Okazaki,Y. and
            Hayashizaki,Y.
            Transcriptional sequencing: A method for DNA sequencing using RNA
            polymerase. Proc. Natl. Acad. Sci. U.S.A. 95 (7), 3455-3460 (1998)
            Toh,M., Kikunishi,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J.,
            Tozaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M.,
            Okazaki,Y. and Hayashizaki,Y.
            Automated filtration-based high-throughput plasmid preparation
            system. Genome Res. 9 (5), 463-470 (1999)
            Carninci,P. and Hayashizaki,Y.
            High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
            19-44 (1999)
            Please visit our web site (http://genome.rtc.riken.go.jp) for
            further details.

FEATURES
source
1. 303
   /organism="Mus musculus"
   /mol_type="mRNA"
   /strain="CS7BL/6J"
   /db_xref="taxon:10090"
   /clone="4930544G09"
   /sex="male"
   /tissue_type="testis"
   /dev_stage="adult"
   /lab_host="DH10B"
   /note="Site 1: Sali; Site 2: BamHI; cDNA library was
   prepared and sequenced in Mouse Genome Encyclopedia
   Project of Genome Exploration Research Group in Riken
   Genomic Sciences Center and Genome Science Laboratory in
   RIKEN. Division of Experimental Animal Research in Riken
   contributed to prepare mouse tissues. 1st strand cDNA was

```

```

primed with a primer [5',
GAGAGAGAGAGAGAGAGAGAGCTTTTITTTTTTITVN 3'], cDNA was
prepared by using trehalose thermo-activated reverse
transcriptase and subsequently enriched for full-length by
cap-trapper. Second strand cDNA was prepared with the
primer adapter of sequence [5'
GAGAGAGAGAGAGAGAGAGTAAATTAATTCCTCCCCCCCC 3']. cDNA
was cloned into the XhoI and BamHI sites. Vector: a
modified paluescript KS(+) after bulk excision from Lambda
FLC I. Cloning sites, 5' end: Sali; 3' end: BamHI."

ORIGIN
Query Match      87.0%; Score 17.4; DB 9; Length 303;
Best Local Similarity 94.7%; Pred. No. 2.1e+03;
Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 GTGCATCGAGCGGGGG 20
      |||||
      142 GTGCATCGAGCGGGGG 160

RESULT 4
BIS07147/c
LOCUS      473 bp mRNA linear EST 08-APR-2002
DEFINITION BBI70025B20H07.5 Bee Brain Normalized/Subtracted Library, BBI7 Apis
            mellifera cDNA clone BBI70025B20H07 5', mRNA sequence.
ACCESSION  BIS07147
VERSION     BIS07147.1 GI:15357521
KEYWORDS   EST.
SOURCE     Apis mellifera (honeybee)
ORGANISM   Apis mellifera

REFERENCE
AUTHORS    Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Apoidea;
            Apidae; Apis.
            1 (bases 1 to 473)
            Whitfield,C.W., Band,M.R., Donald,M.F., Kumar,C.G., Liu,L.,
            Pardinas,J., Robertson,H.M., Soares,B. and Robinson,G.E.
            Annotated expressed sequence tags and cDNA microarrays for studies
            of brain and behavior in the honey bee
            Genome Res. 12 (4), 555-566 (2002)
            21929762
            11932240
            Contact: Gene E. Robinson
            Department of Entomology
            University of Illinois
            505 S. Goodwin Ave., Urbana, IL 61801, USA
            Tel: 217 265 0309
            Fax: 217 244 3499
            Email: generobi@life.uiuc.edu
            This research was funded by the University of Illinois Critical
            Research Initiatives Fund and a Burroughs-Wellcome Trust Innovation
            Award in Functional Genomics to G.E. Robinson and an NSF
            Postdoctoral Fellowship in Bioinformatics to C.W. Whitfield.
            REPEAT IN THE SEQUENCE
            Simple repeat STRAND (+) ELEMENT (A)n LOCATION (449,468).
            PCR Primers
            FORWARD: TAATACGACTCACTATAGG
            BACKWARD: ATTAACCTCTACTAAG
            Plate: BBI70025B20 row: H column: 07
            Seq primer: AGGGGTAACAATTCACACGGA
            High quality sequence stop: 473.

FEATURES
source
1. 473
   /organism="Apis mellifera"
   /mol_type="mRNA"
   /strain="mixed strains of European bees, predominantly
   A.m. ligustica"
   /db_xref="taxon:7460"
   /clone="BBI70025B20H07"
   /sex="female"
   /tissue_type="brain"
   /dev_stage="adult worker honey bee"
   /lab_host="DH10B"

```

/clone lib="Bee Brain Normalized/Subtracted Library, BB17"
 /note="Organ: Brain; Vector: pMT3-Pac; Site: 1; EcoRI;
 Site: 2; NotI; This BB17 cDNA library was generated by
 subtraction of the BB16 library with 4000 previously
 sequenced clones. The BB16 library was contributed by the
 Soares laboratory and it was constructed and normalized
 as described by Bonaldo, M.F., Lennon, G. and Soares,
 M.B. (1996). Genome Research 6(9): 791-806. RNA was
 prepared from dissected brains of adult worker bees of
 various ages and various behavioral groups. "

ORIGIN

Query Match 87.0%; Score 17.4; DB 12; Length 473;
 Best Local Similarity 94.7%; Pred. No. 2.4e+03;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGTGATCGATCGAGGGG 19
 |||||
 Db 336 GGTGATCGAGCGGGG 318

RESULT 5

BQ898390/c 1214 bp mRNA linear EST 16-AUG-2002
 LOCUS AGENCOURT_8712137 NIH_MGC_112 Homo sapiens cDNA clone IMAGE:6295181
 DEFINITION 5', mRNA sequence.

ACCESSION BQ898390
 VERSION BQ898390.1 GI:22290404
 KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 1214)

NIH-MGC http://mgi.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

COMMENT

Contact: Robert Strausberg, Ph.D.
 Email: cgabbs@mail.nih.gov
 Tissue Procurement: DCTD/DTF
 cDNA Library Preparation: Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov

Plate: LLCM2501 row: a column: 06

High quality sequence stop: 150.

Location/Qualifiers

FEATURES

source

1..1214
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:6295181"
 /tissue_type="melanotic melanoma, cell line"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH MGC 112"
 /note="Organ: Skin; Vector: pOT37; Site 1: XhoI; Site 2:
 EcoRI; cDNA made by oligo-dT priming. Directionally cloned
 into EcoRI/XhoI sites using the following 5' adaptor:
 GCCACGAG(G). Library constructed by Ling Hong in the
 laboratory of Gerald M. Rubin (University of California,
 Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
 Superscript II RT (Life Technologies). Note: this is a
 NIH_MGC Library."

ORIGIN

Query Match 87.0%; Score 17.4; DB 13; Length 1214;
 Best Local Similarity 94.7%; Pred. No. 3.2e+03;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGTGATCGATCGAGGGG 19
 |||||
 Db 336 GGTGATCGAGCGGGG 318

Db 301 GGTGACCGATCGAGGGG 283

RESULT 6

B01614/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Unpublished (1996)

Contact: Evans CA, Shane Probst

McDermott Center for Human Growth and Development

University of Texas Southwestern Medical Center At Dallas

5323 Harry Hines Blvd, Dallas TX 75235-8591

Tel: 214-648-1600

Fax: 214-648-1666

Email: gevaus@utsw.swmed.edu, shane@mcdermott.swmed.edu

PCR Primers

FORWARD: TACTAAGCGAGCTAGCTG

BACKWARD: TTTGGACGATTAGCTCAG

Seq primer: T7

Class: cosmid ends

High quality sequence stop: 541.

Location/Qualifiers

1..541

/organism="Homo sapiens"

/mol_type="genomic DNA"

/db_xref="taxon:9606"

/clones="CSRL-134g10"

/sex="female"

/cell_type="chimeric hamster somatic cell hybrid"

/clone_lib="CSRL flow sorted Chromosome 11 specific

cosmid"

/note="vector: sCos-1; Human Chromosome 11 specific cosmid

library prepared from flow sorted human Chromosome 11

derived from Chinese Hamster Ovary (CHO) monochromosomal

somatic cell hybrid, J1"

Query Match 85.0%; Score 17; DB 28; Length 541;

Best Local Similarity 100.0%; Pred. No. 3.9e+03;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTGATCGATCGAGGG 17

|||||

Db 181 GGTGATCGATCGAGGG 165

|||||

RESULT 7

CA101677/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

EST.

Saccharum officinarum

Saccharum officinarum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACAD

clade; Panicoideae; Andropogoneae; Saccharum.

Query Match 807 bp mRNA linear EST 23-SEP-2003

Best Local Similarity 100.0%; Pred. No. 3.9e+03;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTGATCGATCGAGGG 17

|||||

Db 181 GGTGATCGATCGAGGG 165

|||||

```

REFERENCE 1 (bases 1 to 807)
AUTHORS Vettore,A.L., da Silva,F.R., Kemper,E.L. and Arruda,P.
TITLE The libraries that made SUCEST
JOURNAL Genet. Mol. Biol. 24 (1-4), 1-7 (2001)
COMMENT Centro de Biologia Molecular e Engenharia Genetica
Universidade Estadual de Campinas
Caixa Postal 6010, 13083-970, Campinas SP, Brazil
Tel: 55 19 3788 1137
Fax: 55 19 3788 1089
Email: parruda@unicamp.br
Clone distribution: clone distribution information can be found
through the Brazilian Clone Collection Center (BCCC) at
http://www.bcccenter.fcav.unesp.br
Plate: 040 row: C column: 03
Seq primer: T7 Promoter Primer.
FEATURES             source
    1..807
        /organism="Saccharum officinarum"
        /mol_type="mRNA"
        /db_xref="taxon:4547"
        /clone="SCACHRI040C03"
        /lab_host="DH10B"
        /clone_lib="HRI"
    Note="Organ: seedlings inoculated with Herbaspirillum
    rubrisubalbicans; Vector: pSport1; Site 1: SalI; Site 2:
    NotI; An unidirectional cDNA library generated from
    [seedlings inoculated with Herbaspirillum
    rubrisubalbicans]. cDNA was prepared from poly(A+ mRNA
    using SuperScript Plasmid System Kit (Invitrogen). The
    double-strand cDNAs were fractionated in a sepharose
    CL-2B 40cm-columns and fragments sizing between 0.8 and
    1.5 Kb were directionally cloned into the vector. Details
    of each source of RNA and library construction can be
    obtained at http://succest.lad.ic.unicamp.br/public"
ORIGIN
Query Match      85.0%; Score 17; DB 13; Length 807;
Best Local Similarity 100.0%; Pred. No. 4.2e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GCATCGATGCAGGGGG 20
    |||||
Db 32 GCATCGATGCAGGGGG 16

RESULT 8
CG066914/c
LOCUS PUBJ87TD_ZM_0.6_1.0_KB_Zea_mays_genomic_clone_ZMWBTa0544P06,
DEFINITION genomic survey sequence.
ACCESSION CG066914
VERSION CG066914.1. GI:33939094
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 839)
AUTHORS Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
Reinick,A., Fraser,C.M., Yuan,Y., San Miguel,P., Ma,J. and
Bennetzen,J.
TITLE Maize Genomics Consortium
JOURNAL Unpublished (2003)
COMMENT Other GSSs: PUBJ87TB
Contact: Cathy Whitelaw
TIGR 9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: TP

```

```

FEATURES             source
    Class: sheared ends.
    Location/Qualifiers
        1..839
            /organism="Zea mays"
            /mol_type="genomic DNA"
            /strain="B73"
            /db_xref="taxon:4577"
            /clone="ZMWBTa0544P06"
            /clone_lib="ZM 0.6 1.0 KB"
            /notes="Vector: PCR4-TOPO; Site 1: EcoRI; 0.6-1.0 kb high
            COT selected genomic DNA library"
ORIGIN
Query Match      85.0%; Score 17; DB 29; Length 839;
Best Local Similarity 100.0%; Pred. No. 4.3e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GTGCATCGATGCAGGGG 18
    |||||
Db 124 GTGCATCGATGCAGGGG 108

RESULT 9
BX639713/c
LOCUS BX639713 pBluescript Lion Mus musculus cDNA clone LIONP462H0719 3',
DEFINITION mRNA sequence.
ACCESSION BX639713
VERSION BX639713.1 GI:33619588
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 272)
AUTHORS Henrich,J., Hermanns,J., Kranz,H., Loebbert,R., Schluerer,T.,
Schuette,D., Weirde,M., Heil,O., Ebert,L., Neubert,P., Peters,M.,
Radelof,U., Schneider,D. and Korn,B.
TITLE Mouse ArrayTAG cDNA (LION)
JOURNAL Unpublished (2003)
COMMENT Contact: Ina Rolfs
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany
RZPD: LIONP462H0719.
RZPDLIB:
http://www.rzpd.de/cgi-bin/products/showlib.pl.cgi/response?libNo=4
G2 Contact: Ina Rolfs
RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Heubnerweg 6, D-14059 Berlin, Germany
Tel: +49 30 32639 101
Fax: +49 30 32639 111
www.rzpd.de
This clone is available royalty-free from RZPD;
Contact RZPD (clone@rzpd.de) for further information. Seq primer:
RP: CAGGAACAGCTATGAC.
FEATURES             source
    1..272
        /organism="Mus musculus"
        /mol_type="mRNA"
        /db_xref="taxon:10090"
        /clone="LIONP462H0719"
        /lab_host="DH10B"
        /clone_lib="pBluescript Lion"
ORIGIN
Query Match      84.0%; Score 16.8; DB 13; Length 272;
Best Local Similarity 90.0%; Pred. No. 3.8e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGTCATCGATGCAGGGGG 20
    |||||
Db 168 GGTCCTCGAGGCAGGGGG 149

```

```

RESULT 10
AV028453
LOCUS
DEFINITION
  AV028453 Mus musculus adult C57BL/6J brain Mus musculus cDNA clone
  1432000GLJ3, mRNA sequence.
ACCESSION
  AV028453
VERSION
  AV028453.1 GI:4783418
KEYWORDS
  EST.
SOURCE
  Mus musculus (house mouse)
ORGANISM
  Mus musculus
REFERENCE
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
  1 (bases 1 to 597)
AUTHORS
  Carninci, P., Shibata, K., Ozawa, Y., Konno, H., Itoh, M., Aizawa, K.,
  Akahira, S., Akiyama, J., Fukuda, S., Fukunishi, Y., Funayama, T.,
  Hara, A., Hayatsu, N., Hori, F., Ishikawa, T., Itoh, M., Izawa, M.,
  Kawai, J., Kikuchi, N., Kojima, Y., Matsuyama, T., Niitsuma, H., Oda, H.,
  Owa, C., Sato, K., Shibata, Y., Shigenoto, Y., Shiraki, T., Sogabe, Y.,
  Sugahara, Y., Suzuki, H., Suzuki, H., Tateo, M., Tomaru, Y.,
  Tomimaga, N., Watanabe, S., Yagane, M., Yamamura, T., Yokota, T.,
  Yoshino, M., Muramatsu, M., Okazaki, Y. and Hayashizaki, Y.
  RIKEN Mouse ESTs
  Unpublished (1999)
  Contact: Chie Owa
  Genome Science Laboratory
  RIKEN
  3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
  Tel: 81-298-36-9145
  Fax: 81-298-36-9098
  Email: genome-resortc.riken.go.jp
  Thermostabilization and thermoactivation of thermolabile enzymes by
  trehalose and its application for the synthesis of full length cDNA
  (Proc. Natl. Acad. Sci. U.S.A. 95(2):520-524 (1998))
  Transcriptional sequencing: A method for DNA sequencing using RNA
  polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998))
  Please visit our web site (http://genome.rtc.riken.go.jp) for
  further details.
FEATURES
  source
  1..597
  /organism="Mus musculus"
  /mol_type="mRNA"
  /strain="C57BL/6J"
  /db_xref="taxon:10090"
  /clone="1432000GLJ3"
  /sex="male"
  /tissue_type="brain"
  /dev_stage="adult"
  /clone_lib="Mus musculus adult C57BL/6J brain"
ORIGIN
  Query Match 84.0%; Score 16.8; DB 9; Length 597;
  Best Local Similarity 90.0%; Pred. No. 4.7e+03;
  Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
  QY 1 GTGTCATCGATCGAGGGGG 20
  |||||
  DB 64 GTGTCATCGATCGAGGGGG 83
  |||||
RESULT 11
BJ244833/c
LOCUS
DEFINITION
  BJ244833 Y. Ogihara unpublished cDNA library, Wh_f Triticum
  aestivum cDNA clone whf16m07 5', mRNA sequence.
ACCESSION
  BJ244833
VERSION
  BJ244833.1 GI:20057113
KEYWORDS
  EST.
SOURCE
  Triticum aestivum (bread wheat)
ORGANISM
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

```

```

Poolidae; Triticeae; Triticum.
REFERENCE
  1 (bases 1 to 631)
AUTHORS
  Ogihara, Y. and Murai, K.
  Expressed genes in Triticum aestivum
  Unpublished (2002)
  Contact: Tadasi Shin-i
  Center For Genetic Resource Information
  National Institute of Genetics
  1111 Yata, Mishima, Shizuoka 411-8540, Japan
  Tel: 81-559-81-6856
  Fax: 81-559-81-6855
  Email: tshini@genes.nig.ac.jp.
  Location/Qualifiers
  1..631
  /organism="Triticum aestivum"
  /mol_type="mRNA"
  /cultivar="Chinese Spring"
  /db_xref="taxon:4565"
  /clone="whf16m07"
  /tissue_type="spike at flowering date"
  /dev_stage="Peekes" scale 10.5.1"
  /clone_lib="Y. Ogihara unpublished cDNA library, Wh_f"
ORIGIN
  Query Match 84.0%; Score 16.8; DB 12; Length 631;
  Best Local Similarity 90.0%; Pred. No. 4.8e+03;
  Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
  QY 1 GTGTCATCGATCGAGGGGG 20
  |||||
  DB 559 GTGTCATCGAGAGGGGG 540
  |||||
RESULT 12
AL692509
LOCUS
DEFINITION
  AL692509 NAH Anopheles gambiae cDNA clone NAH-P05-H-10-5, mRNA
  sequence.
ACCESSION
  AL692509
VERSION
  AL692509.1 GI:19612418
KEYWORDS
  EST.
SOURCE
  Anopheles gambiae (African malaria mosquito)
  Anopheles gambiae
  Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
  Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae;
  Anopheles.
REFERENCE
  1 (bases 1 to 638)
  Christophides, G.K., Blass, K., Zdobnov, E.M., Carmouch, R., Benes, V.
  and Karatos, F.C.
  Anopheles gambiae EST, European Molecular Biology Laboratory
  Unpublished (2002)
  Contact: Christophides GK
  Fotis C. Kafatos Laboratory
  European Molecular Biology Laboratory
  Meyerhofstrasse 1, 69117 Heidelberg, Germany
  Tel: +49 6221 387-440
  Fax: +49 6221 387-306
  Email: christop@embl-heidelberg.de
  Plate: P05 row: H column: 10.
  Location/Qualifiers
  1..638
  /organism="Anopheles gambiae"
  /mol_type="mRNA"
  /db_xref="taxon:7165"
  /clone="NAH-P05-H-10-5"
  /lab_host="E. coli DH10B"
  /clone_lib="NAH"
  /note="Vector: pT73D-Pac (Pharmacia); Site 1: NotI;
  Site 2: EcoRI; ESTs sequenced from the 77 priming site
  that reads from the 5' end of cDNA. The NAH1 is a
  directionally cloned and normalized, oligo-r primed cDNA
  library constructed from heads of Anopheles gambiae
  according to: Bonaldo, Lennon & Soares (1996);

```


Qy 1 GGTGCATCGATCAGGGGG 20
|||||
Db 445 GGTGCATCGTTGCAGTGGG 426

TITLE	JOURNAL	COMMENT
1. The Role of the Teacher in the Classroom	Journal of Educational Research	1965, Vol. 68, No. 1, pp. 1-10
2. The Impact of Technology on Education	Journal of Educational Technology	1970, Vol. 1, No. 2, pp. 1-10
3. The Role of the Teacher in the Classroom	Journal of Educational Research	1975, Vol. 78, No. 1, pp. 1-10
4. The Impact of Technology on Education	Journal of Educational Technology	1980, Vol. 2, No. 2, pp. 1-10
5. The Role of the Teacher in the Classroom	Journal of Educational Research	1985, Vol. 88, No. 1, pp. 1-10
6. The Impact of Technology on Education	Journal of Educational Technology	1990, Vol. 3, No. 2, pp. 1-10
7. The Role of the Teacher in the Classroom	Journal of Educational Research	1995, Vol. 98, No. 1, pp. 1-10
8. The Impact of Technology on Education	Journal of Educational Technology	2000, Vol. 4, No. 2, pp. 1-10
9. The Role of the Teacher in the Classroom	Journal of Educational Research	2005, Vol. 108, No. 1, pp. 1-10
10. The Impact of Technology on Education	Journal of Educational Technology	2010, Vol. 5, No. 2, pp. 1-10

University of Minnesota
220 BioSci Center, 1445 Gortner Ave., St. Paul, MN 55108, USA
Tel: 612 524 2755
Fax: 612 525 1738
Email: kvandenb@chs.umn.edu

TV plate 31 rotated 180 degrees at TIGR
TIGR sequence name: MTUS63TV
More information is available at: www.medicago.org
Seq primer: (gtA ATA CgA Ctc ACT ATA 999 C).
Location/Qualifiers
1. .671
/organism="Medicago truncatula"
/mol_type="mRNA"
/cultivar="Al7"
/db_xref="taxon:3880"
/clone="MTUS-31C10"
/tissue_type="mixed tissues"
/dev_stage="various stages"
/lab_host="XLOLA"
/clone_lib="MTUS"
/notes="Vector: pBluescript SK-; Site 1: EcoRI; Site 2: XhoI; cDNA was prepared from polyA+ enriched RNA. The cDNA was directionally ligated into the Unizap XR vector from Stratagene and packaged using Gigapack III Gold packaging extracts. Plasmids containing cDNA inserts were excised from the recombinant Lambda-Zap phage using Ex-assist helper phage and propagated in XLOLR cells."

ORIGIN

Query Match 84.0%; Score 16.8; DB 14; Length 671;
Best Local Similarity 90.0%; Pred. No. 4.9e+03;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGTGCATCGATCGAGGGGG 20
|||
Db 376 GGTGCATCGTTGCGTGGGG 357

Search completed: July 2, 2004, 13:32:50
Job time : 1502.92 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model
Run on: July 2, 2004, 07:36:05 ; Search time 704.146 Seconds
(without alignments)
1231.080 Million cell updates/sec

Title: US-10-068-160-2
Perfect score: 20
Sequence: 1 ggtgacccggtagcagggggg 20

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues
Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl :
1: gb_ba :
2: gb_hgt :
3: gb_in :
4: gb_om :
5: gb_ov :
6: gb_pat :
7: gb_pi :
8: gb_pr :
9: gb_re :
10: gb_ri :
11: gb_sy :
12: gb_un :
13: gb_vl :
14: gb_vl :
15: em_ba :
16: em_fun :
17: em_hum :
18: em_in :
19: em_mu :
20: em_om :
21: em_or :
22: em_ov :
23: em_pat :
24: em_ph :
25: em_pl :
26: em_ro :
27: em_sts :
28: em_un :
29: em_vi :
30: em_hgt_hum :
31: em_hgt_inv :
32: em_hgt_other :
33: em_hgt_mus :
34: em_hgt_pin :
35: em_hgt_rod :
36: em_hgt_man :
37: em_hgt_vrt :
38: em_sv :
39: em_hgtgo_hum :
40: em_hgtgo_mus :
41: em_hgtgo_other :

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	20	6	AX194442 Sequence
2	20	100.0	20	6	AX352200 Sequence
3	20	100.0	20	6	AX352208 Sequence
4	20	100.0	20	6	AX352211 Sequence
5	20	100.0	20	6	AX352218 Sequence
6	20	100.0	20	6	AX352244 Sequence
7	20	100.0	20	6	AX465392 Sequence
8	20	100.0	28	6	AX352221 Sequence
9	20	100.0	28	6	AX352229 Sequence
10	20	100.0	28	6	AX352233 Sequence
11	20	100.0	28	6	AX352241 Sequence
12	20	100.0	40	6	AX352252 Sequence
13	18.4	92.0	20	6	AX194501 Sequence
14	18.4	92.0	20	6	AX352199 Sequence
15	18.4	92.0	20	6	AX352203 Sequence
16	18.4	92.0	20	6	AX352210 Sequence
17	18.4	92.0	20	6	AX352214 Sequence
18	18.4	92.0	20	6	AX352247 Sequence
19	18.4	92.0	28	6	AX352220 Sequence
20	18.4	92.0	28	6	AX352224 Sequence
21	18.4	92.0	28	6	AX352232 Sequence
22	18.4	92.0	28	6	AX352236 Sequence
23	17.4	87.0	19	6	AX194422 Sequence
24	17.4	87.0	19	6	AX465372 Sequence
25	17.4	87.0	155724	4	AC091316 Sus. scro.
26	17.4	87.0	170523	9	AP002387 Homo sap.
27	17.4	87.0	187364	10	AC012295 Mus muscu.
28	17.4	87.0	238358	10	AL592465 Mouse DN.
29	17.4	87.0	260424	2	AC131745 Mus muscu.
30	17.4	87.0	307820	2	AC130831 Mus muscu.
31	17	85.0	10782	1	AE001002 Archaeogl.
32	17	85.0	138859	9	AL359076 Human DN.
33	16.8	84.0	20	6	AX194432 Sequence
34	16.8	84.0	20	6	AX194434 Sequence
35	16.8	84.0	20	6	AX194437 Sequence
36	16.8	84.0	20	6	AX194438 Sequence
37	16.8	84.0	20	6	AX194443 Sequence
38	16.8	84.0	20	6	AX194472 Sequence
39	16.8	84.0	20	6	AX194503 Sequence
40	16.8	84.0	20	6	AX194504 Sequence
41	16.8	84.0	20	6	AX352198 Sequence
42	16.8	84.0	20	6	AX352209 Sequence
43	16.8	84.0	20	6	AX352242 Sequence
44	16.8	84.0	20	6	AX465382 Sequence
45	16.8	84.0	20	5	AX465384 Sequence

ALIGNMENTS

RESULT 1
AX194442
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL

AX194442
Sequence 42 from Patent WO0151500.
AX194442
AX194442.1 GI:15385098

synthetic construct
synthetic construct
artificial sequences.

1
Klinman,D., Ishii,K. and Verthelyi,D.
Oligodeoxynucleotide and its use to induce an immune response
Patent: WO 0151500-A 42 19-JUL-2001;
Secretary of the Department of Health and Human Services (US)

Pred. No. is the number of results predicted by chance to have a

```
FEATURES
  source
    Location/Qualifiers
      1..20
      /organism="synthetic construct"
      /mol_type="unassigned DNA"
      /db_xref="taxon:32630"
      /note="Synthetic DNA"

ORIGIN
Query Match
Best Local Similarity 100.0%; Score 20; DB 6; Length 20;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTGACCCGGTGCAGGGGG 20
    |||||
Db 1 GGTGACCCGGTGCAGGGGG 20

RESULT 2
AX352200
LOCUS AX352200 20 bp DNA linear PAT 06-FEB-2002
DEFINITION Sequence 496 from Patent WO0193902.
ACCESSION AX352200
VERSION AX352200.1 GI:18617483
KEYWORDS
SOURCE
  synthetic construct
  synthetic construct
  artificial sequences.
ORGANISM
REFERENCE
  1
AUTHORS Mond, J.J., Flora, M. and Klinman, D.M.
TITLE Immunostimulatory rna/dna hybrid molecules
JOURNAL Patent: WO 0193902-A 496 13-DEC-2001;
Biosynexus Incorporated (US)
FEATURES
  source
    Location/Qualifiers
      1..20
      /organism="synthetic construct"
      /mol_type="unassigned DNA"
      /db_xref="taxon:32630"
      /note="Synthetic HDR"

ORIGIN
Query Match
Best Local Similarity 100.0%; Score 20; DB 6; Length 20;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTGACCCGGTGCAGGGGG 20
    |||||
Db 1 GGTGACCCGGTGCAGGGGG 20

RESULT 3
AX352208
LOCUS AX352208 20 bp DNA linear PAT 06-FEB-2002
DEFINITION Sequence 504 from Patent WO0193902.
ACCESSION AX352208
VERSION AX352208.1 GI:18617491
KEYWORDS
SOURCE
  synthetic construct
  synthetic construct
  artificial sequences.
ORGANISM
REFERENCE
  1
AUTHORS Mond, J.J., Flora, M. and Klinman, D.M.
TITLE Immunostimulatory rna/dna hybrid molecules
JOURNAL Patent: WO 0193902-A 504 13-DEC-2001;
Biosynexus Incorporated (US)
FEATURES
  source
    Location/Qualifiers
      1..20
      /organism="synthetic construct"
      /mol_type="unassigned DNA"
      /db_xref="taxon:32630"
      /note="Synthetic HDR"

ORIGIN
Query Match
Best Local Similarity 100.0%; Score 20; DB 6; Length 20;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTGACCCGGTGCAGGGGG 20
    |||||
Db 1 GGTGACCCGGTGCAGGGGG 20

RESULT 4
AX352211
LOCUS AX352211 20 bp DNA linear PAT 06-FEB-2002
DEFINITION Sequence 507 from Patent WO0193902.
ACCESSION AX352211
VERSION AX352211.1 GI:18617494
KEYWORDS
SOURCE
  synthetic construct
  synthetic construct
  artificial sequences.
ORGANISM
REFERENCE
  1
AUTHORS Mond, J.J., Flora, M. and Klinman, D.M.
TITLE Immunostimulatory rna/dna hybrid molecules
JOURNAL Patent: WO 0193902-A 507 13-DEC-2001;
Biosynexus Incorporated (US)
FEATURES
  source
    Location/Qualifiers
      1..20
      /organism="synthetic construct"
      /mol_type="unassigned DNA"
      /db_xref="taxon:32630"
      /note="Synthetic HDR"

ORIGIN
Query Match
Best Local Similarity 100.0%; Score 20; DB 6; Length 20;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTGACCCGGTGCAGGGGG 20
    |||||
Db 1 GGTGACCCGGTGCAGGGGG 20

RESULT 5
AX352218
LOCUS AX352218 20 bp DNA linear PAT 06-FEB-2002
DEFINITION Sequence 514 from Patent WO0193902.
ACCESSION AX352218
VERSION AX352218.1 GI:18617501
KEYWORDS
SOURCE
  synthetic construct
  synthetic construct
  artificial sequences.
ORGANISM
REFERENCE
  1
AUTHORS Mond, J.J., Flora, M. and Klinman, D.M.
TITLE Immunostimulatory rna/dna hybrid molecules
JOURNAL Patent: WO 0193902-A 514 13-DEC-2001;
Biosynexus Incorporated (US)
FEATURES
  source
    Location/Qualifiers
      1..20
      /organism="synthetic construct"
      /mol_type="unassigned DNA"
      /db_xref="taxon:32630"
      /note="Synthetic HDR"

ORIGIN
Query Match
Best Local Similarity 100.0%; Score 20; DB 6; Length 20;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTGACCCGGTGCAGGGGG 20
    |||||
Db 1 GGTGACCCGGTGCAGGGGG 20

RESULT 6
AX352218
LOCUS AX352218 20 bp DNA linear PAT 06-FEB-2002
DEFINITION Sequence 514 from Patent WO0193902.
ACCESSION AX352218
VERSION AX352218.1 GI:18617501
KEYWORDS
SOURCE
  synthetic construct
  synthetic construct
  artificial sequences.
ORGANISM
REFERENCE
  1
AUTHORS Mond, J.J., Flora, M. and Klinman, D.M.
TITLE Immunostimulatory rna/dna hybrid molecules
JOURNAL Patent: WO 0193902-A 514 13-DEC-2001;
Biosynexus Incorporated (US)
FEATURES
  source
    Location/Qualifiers
      1..20
      /organism="synthetic construct"
      /mol_type="unassigned DNA"
      /db_xref="taxon:32630"
      /note="Synthetic HDR"

ORIGIN
Query Match
Best Local Similarity 100.0%; Score 20; DB 6; Length 20;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTGACCCGGTGCAGGGGG 20
    |||||
Db 1 GGTGACCCGGTGCAGGGGG 20
```

```
AX352244      AX352244      20 bp      DNA      linear      PAT 06-FEB-2002
DEFINITION    Sequence 540 from Patent WO0193902.
ACCESSION     AX352244
VERSION       AX352244.1  GI:18617527
KEYWORDS      synthetic construct
SOURCE        synthetic construct
ORGANISM      artificial sequences.
REFERENCE     1
AUTHORS       Mond, J.J., Flora, M. and Klinman, D.M.
TITLE         Immunostimulatory rna/dna hybrid molecules
JOURNAL       Patent: WO 0193902-A 540 13-DEC-2001;
              Biosynexus Incorporated (US)
FEATURES      Location/Qualifiers
               1..20
               /organism="synthetic construct"
               /mol_type="unassigned DNA"
               /db_xref="taxon:32630"
               /note="Synthetic HDR"
ORIGIN
Query Match   100.0%; Score 20; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTGCACCGGTGCAGGGGGG 20
    |||||
DB 1 GGTGCACCGGTGCAGGGGGG 20

RESULT 7
AX465392
LOCUS         AX465392      20 bp      DNA      linear      PAT 16-JUL-2002
DEFINITION    Sequence 60 from Patent WO0211761.
ACCESSION     AX465392
VERSION       AX465392.1  GI:21899755
KEYWORDS      synthetic construct
SOURCE        synthetic construct
ORGANISM      artificial sequences.
REFERENCE     1
AUTHORS       Mond, J.J., Prince, G. and Klinman, D.M.
TITLE         Vaccine against RSV
JOURNAL       Patent: WO 0211761-A 60 14-FEB-2002;
              HENRY M. JACKSON FOUNDATION FOR THE ADVANCEMENT OF MILITARY
              MEDICINE (US)
FEATURES      Location/Qualifiers
               1..20
               /organism="synthetic construct"
               /mol_type="unassigned DNA"
               /db_xref="taxon:32630"
               /note="Synthetic oligonucleotide"
ORIGIN
Query Match   100.0%; Score 20; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTGCACCGGTGCAGGGGGG 20
    |||||
DB 1 GGTGCACCGGTGCAGGGGGG 20

RESULT 8
AX352221
LOCUS         AX352221      28 bp      DNA      linear      PAT 06-FEB-2002
DEFINITION    Sequence 517 from Patent WO0193902.
ACCESSION     AX352221
VERSION       AX352221.1  GI:18617504
KEYWORDS      synthetic construct
SOURCE        synthetic construct
ORGANISM      artificial sequences.
REFERENCE     1
AUTHORS       Mond, J.J., Flora, M. and Klinman, D.M.
TITLE         Immunostimulatory rna/dna hybrid molecules
JOURNAL       Patent: WO 0193902-A 529 13-DEC-2001;
              Biosynexus Incorporated (US)
FEATURES      Location/Qualifiers
               1..28
               /organism="synthetic construct"
               /mol_type="unassigned DNA"
               /db_xref="taxon:32630"
               /note="Synthetic HDR"
ORIGIN
Query Match   100.0%; Score 20; DB 6; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTGCACCGGTGCAGGGGGG 20
    |||||
DB 1 GGTGCACCGGTGCAGGGGGG 20

RESULT 10
AX352233
LOCUS         AX352233      28 bp      DNA      linear      PAT 06-FEB-2002
DEFINITION    Sequence 529 from Patent WO0193902.
ACCESSION     AX352233
VERSION       AX352233.1  GI:18617516
KEYWORDS      synthetic construct
SOURCE        synthetic construct
ORGANISM      artificial sequences.
REFERENCE     1
AUTHORS       Mond, J.J., Flora, M. and Klinman, D.M.
TITLE         Immunostimulatory rna/dna hybrid molecules
JOURNAL       Patent: WO 0193902-A 529 13-DEC-2001;
              Biosynexus Incorporated (US)
FEATURES      Location/Qualifiers
               1..28
               /organism="synthetic construct"
               /mol_type="unassigned DNA"
               /db_xref="taxon:32630"
               /note="Synthetic HDR"
ORIGIN
Query Match   100.0%; Score 20; DB 6; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTGCACCGGTGCAGGGGGG 20
    |||||
DB 1 GGTGCACCGGTGCAGGGGGG 20

RESULT 9
AX352229
LOCUS         AX352229      28 bp      DNA      linear      PAT 06-FEB-2002
DEFINITION    Sequence 525 from Patent WO0193902.
ACCESSION     AX352229
VERSION       AX352229.1  GI:18617512
KEYWORDS      synthetic construct
SOURCE        synthetic construct
ORGANISM      artificial sequences.
REFERENCE     1
AUTHORS       Mond, J.J., Flora, M. and Klinman, D.M.
TITLE         Immunostimulatory rna/dna hybrid molecules
JOURNAL       Patent: WO 0193902-A 525 13-DEC-2001;
              Biosynexus Incorporated (US)
FEATURES      Location/Qualifiers
               1..28
               /organism="synthetic construct"
               /mol_type="unassigned DNA"
               /db_xref="taxon:32630"
               /note="Synthetic HDR"
ORIGIN
Query Match   100.0%; Score 20; DB 6; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTGCACCGGTGCAGGGGGG 20
    |||||
DB 1 GGTGCACCGGTGCAGGGGGG 20
```

ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 28;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTGCACCGGTGCAGGGGG 20
 |||||
 Db 9 GGTGCACCGGTGCAGGGGG 28

RESULT 11

AX352241
 LOCUS AX352241 28 bp DNA linear PAT 06-FEB-2002
 DEFINITION Sequence 537 from Patent WO0193902.
 ACCESSION AX352241
 VERSION AX352241.1 GI:18617524
 KEYWORDS
 SOURCE synthetic construct
 ORGANISM synthetic construct
 artificial sequences.
 REFERENCE
 AUTHORS Mond, J.J., Flora, M. and Klimman, D.M.
 TITLE Immunostimulatory rna/dna hybrid molecules
 JOURNAL Patent: WO 0193902-A 537 13-DEC-2001;
 Biosynexus Incorporated (US)
 FEATURES
 source
 1..28
 /organism="synthetic construct"
 /mol_type="unassigned DNA"
 /db_xref="taxon:32630"
 /note="Synthetic HDR"

ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 28;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTGCACCGGTGCAGGGGG 20
 |||||
 Db 9 GGTGCACCGGTGCAGGGGG 28

RESULT 12

AX352252
 LOCUS AX352252 40 bp DNA linear PAT 06-FEB-2002
 DEFINITION Sequence 548 from Patent WO0193902.
 ACCESSION AX352252
 VERSION AX352252.1 GI:18617535
 KEYWORDS
 SOURCE synthetic construct
 ORGANISM synthetic construct
 artificial sequences.
 REFERENCE
 AUTHORS Mond, J.J., Flora, M. and Klimman, D.M.
 TITLE Immunostimulatory rna/dna hybrid molecules
 JOURNAL Patent: WO 0193902-A 548 13-DEC-2001;
 Biosynexus Incorporated (US)
 FEATURES
 source
 1..40
 /organism="synthetic construct"
 /mol_type="unassigned DNA"
 /db_xref="taxon:32630"
 /note="Synthetic HDR"

ORIGIN

Query Match 100.0%; Score 20; DB 6; Length 40;
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTGCACCGGTGCAGGGGG 20
 |||||
 Db 14 GGTGCACCGGTGCAGGGGG 33

RESULT 13

AX194501
 LOCUS AX194501 20 bp DNA linear PAT 28-AUG-2001
 DEFINITION Sequence 101 from Patent WO0151500.
 ACCESSION AX194501
 VERSION AX194501.1 GI:15385157
 KEYWORDS
 SOURCE synthetic construct
 ORGANISM synthetic construct
 artificial sequences.
 REFERENCE
 AUTHORS Klinman, D., Ishii, K. and Verthelyi, D.
 TITLE Oligodeoxynucleotide and its use to induce an immune response
 JOURNAL Patent: WO 0151500-A 101 19-JUL-2001;
 Secretary of the Department of Health and Human Services (US)
 FEATURES
 Location/Qualifiers
 1..20
 /organism="synthetic construct"
 /mol_type="unassigned DNA"
 /db_xref="taxon:32630"
 /note="Synthetic DNA"

ORIGIN

Query Match 92.0%; Score 18.4; DB 6; Length 20;
 Best Local Similarity 95.0%; Pred. No. 7.6e+02;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTGCACCGGTGCAGGGGG 20
 |||||
 Db 1 GGTGCACCGGTGCAGGGGG 20

RESULT 14

AX352199
 LOCUS AX352199 20 bp DNA linear PAT 06-FEB-2002
 DEFINITION Sequence 495 from Patent WO0193902.
 ACCESSION AX352199
 VERSION AX352199.1 GI:18617482
 KEYWORDS
 SOURCE synthetic construct
 ORGANISM synthetic construct
 artificial sequences.
 REFERENCE
 AUTHORS Mond, J.J., Flora, M. and Klimman, D.M.
 TITLE Immunostimulatory rna/dna hybrid molecules
 JOURNAL Patent: WO 0193902-A 495 13-DEC-2001;
 Biosynexus Incorporated (US)
 FEATURES
 Location/Qualifiers
 1..20
 /organism="synthetic construct"
 /mol_type="unassigned DNA"
 /db_xref="taxon:32630"
 /note="Synthetic HDR"

ORIGIN

Query Match 92.0%; Score 18.4; DB 6; Length 20;
 Best Local Similarity 95.0%; Pred. No. 7.6e+02;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTGCACCGGTGCAGGGGG 20
 |||||
 Db 1 GGTGCACCGGTGCAGGGGG 20

RESULT 15

AX352203
 LOCUS AX352203 20 bp DNA linear PAT 06-FEB-2002
 DEFINITION Sequence 499 from Patent WO0193902.

```

ACCESSION  AX352203
VERSION    AX352203.1  GI:18617486
KEYWORDS   .
SOURCE     synthetic construct
ORGANISM   synthetic construct
           artificial sequences.
REFERENCE  1
AUTHORS    Mond, J.J., Flora, M. and Klinman, D.M.
TITLE      Immunostimulatory rna/dna hybrid molecules
JOURNAL    Patent: WO 0193902-A 499 13-DEC-2001;
           Biosynexus Incorporated (US)
FEATURES   Location/Qualifiers
           1..20
           source
           /organism="synthetic construct"
           /mol_type="unassigned DNA"
           /db_xref="taxon:32830"
           /note="Synthetic HDR"

ORIGIN
Query Match      92.0%;  Score 18.4;  DB 6;  Length 20;
Best Local Similarity 95.0%;  Pred. No. 7.6e+02;
Matches 19;  Conservative 0;  Mismatches 1;  Indels 0;  Gaps 0;

QY      1  GGTGCACCGGTCACGGGGG 20
        |||||
        |||||
Db       1  GGTGCACCGGTCACGGGGG 20

Search completed: July 2, 2004, 10:07:55
Job time : 705.146 secs

```

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 2, 2004, 06:05:50 ; Search time 149.878 Seconds

(without alignments)
566.887 Million cell updates/sec

Title: US-10-068-160-2

Perfect score: 20

Sequence: 1 ggtgaccggtcagggggg 20

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 212409041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_29Jan04:*

1: Geneseq1980s:*

2: Geneseq1990s:*

3: Geneseq2000s:*

4: Geneseq2001as:*

5: Geneseq2001bs:*

6: Geneseq2002e:*

7: Geneseq2003as:*

8: Geneseq2003bs:*

9: Geneseq2003cs:*

10: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	100.0	20	4	AAC80622 Immunogen
2	20	100.0	20	4	AAS09592 Immunorea
3	20	100.0	20	6	ABL35614 Immunosti
4	20	100.0	20	6	ABL35578 Immunosti
5	20	100.0	20	6	ABL35581 Immunosti
6	20	100.0	20	6	ABL35570 Immunosti
7	20	100.0	20	6	ABL35588 Immunosti
8	20	100.0	20	6	ABK46470 Immunosti
9	20	100.0	20	7	ACC48296 CpG oligo
10	20	100.0	20	7	ACC48313 CpG oligo
11	20	100.0	20	8	ACC83118 D class C
12	20	100.0	20	8	ACC83152 D class C
13	20	100.0	20	9	ADD01049 CpG D oli
14	20	100.0	20	6	ABL35599 Immunosti
15	20	100.0	20	6	ABL35603 Immunosti
16	20	100.0	20	6	ABL35591 Immunosti
17	20	100.0	20	6	ABL35611 Immunosti
18	20	100.0	20	6	ABL35622 Immunosti
19	18.4	92.0	20	4	AAS09651 Immunorea
20	18.4	92.0	20	6	ABL35573 Immunosti
21	18.4	92.0	20	6	ABL35584 Immunosti
22	18.4	92.0	20	6	ABL35569 Immunosti
23	18.4	92.0	20	6	ABL35617 Immunosti

24	18.4	92.0	20	6	ABL35580	ABL35580 Immunosti
25	18.4	92.0	20	7	ACC48311	Acc48311 CpG oligo
26	18.4	92.0	20	7	ACC48320	Acc48320 CpG oligo
27	18.4	92.0	20	7	ACC48321	Acc48321 CpG oligo
28	18.4	92.0	20	8	ACC83125	Acc83125 D class C
29	18.4	92.0	20	8	ACC83116	Acc83116 D class C
30	18.4	92.0	20	8	ACC83126	Acc83126 D class C
31	18.4	92.0	20	9	ADD01076	Add01076 CpG D oli
32	18.4	92.0	20	9	ADD01059	Add01059 CpG D oli
33	18.4	92.0	20	6	ABL35590	ABL35590 Immunosti
34	18.4	92.0	20	6	ABL35594	ABL35594 Immunosti
35	18.4	92.0	20	6	ABL35606	ABL35606 Immunosti
36	18.4	92.0	20	6	ABL35602	ABL35602 Immunosti
37	18.4	92.0	20	7	ACC48300	Acc48300 CpG oligo
38	17.4	87.0	19	4	AAC80602	AAC80602 Immunogen
39	17.4	87.0	19	4	AAS09572	Aas09572 Immunorea
40	17.4	87.0	19	6	ABK46450	Abk46450 Immunosti
41	16.8	84.0	20	4	AAC80652	AAC80652 Immunogen
42	16.8	84.0	20	4	AAC80722	AAC80722 Immunogen
43	16.8	84.0	20	4	AAC80614	AAC80614 Immunogen
44	16.8	84.0	20	4	AAC80612	AAC80612 Immunogen
45	16.8	84.0	20	4	AAC80617	AAC80617 Immunogen

ALIGNMENTS

RESULT 1
AAC80622
ID AAC80622 standard; DNA; 20 BP.
XX
AC AAC80622;
XX
DF 14-FEB-2001 (first entry)
XX
DE Immunogenic CpG oligodeoxynucleotide, SEQ ID NO:42.

XX CpG oligodeoxynucleotide; unmethylated; antigen-presenting cell;
KW immunogenic; cytokine release; natural killer cell; NK cell activation;
KW cell-mediated immune response; T-cell response; humoral response; vaccine;
KW B-cell response; antibody production; immune response induction; bacterial;
KW allergy; asthma; infection; viral; fungal; protozoal;
KW parasitic; tuberculosis; AIDS; autoimmune disease; lupus erythematosus;
KW rheumatoid arthritis; multiple sclerosis; solid tumour; cancer;
KW immune deficiency; biological warfare agent; cytostatic; antiarthritic;
KW antimicrobial; antiallergic; protozoacide; tuberculostatic;
KW antiasthmatic; dermatological; phosphorothioate; ss.
XX Synthetic.

XX WO200061151-A2.
XX
XX 19-OCT-2000.
XX
XX 12-APR-2000; 2000WO-US009839.
XX
XX 12-APR-1999; 99US-0128898P.

XX (KLIN)/ KLINMAN D.
XX (ISHI)/ ISHII K.
XX (VERT)/ VERTHELYI D.

XX Klinman D, Ishii K, Verthelyi D;
XX WPI; 2001-006880/01.

XX Novel oligonucleotides useful for the prevention and treatment of
PT allergies, cancer, and autoimmune disorders and for ameliorating symptoms
PT resulting from exposure to a bio-warfare agent.

XX Claim 4; Page 30; 46pp; English.

XX The invention relates to novel immunogenic CpG oligodeoxynucleotides

CC (AAC80581-C80723). The oligonucleotide are at least 10 bases long and
 CC comprise one of the generic sequences 5'-NNNT-CpG-WNNN-3' or 5'-RY-CpG-RY
 CC -3'. The central CpG motif is unmetlylated, and the oligonucleotides
 CC optionally have phosphorothioate linkages which make them more resistant
 CC to degradation. The invention also relates to an oligonucleotide delivery
 CC complex comprising an oligonucleotide of the invention and a targeting
 CC agent, and a pharmaceutical composition comprising the oligonucleotide
 CC delivery complex. The oligonucleotides are able to induce either a cell-
 CC mediated (n-cell) response or a humoral (B-cell, antibody) response, with
 CC oligonucleotides of the sequence 5'-RY-CpG-RY-3', being able to induce a
 CC cell-mediated response, and those of the sequence 5'-NNNT-CpG-WNNN-3',
 CC being able to induce a humoral response. It is thought that after
 CC administration, the oligonucleotide acts on antigen-presenting cells
 CC (e.g., macrophages and dendritic cells), which then release cytokines,
 CC leading to activation of natural killer (NK) cells. A cell-mediated or
 CC humoral response can then occur by activation of T- or B-cells. The
 CC induction of an immune response is useful for treating, preventing or
 CC ameliorating an allergic reaction (preferably asthma), or an infection,
 CC where an immunogenic CpG oligonucleotide is administered either alone or
 CC in combination with an anti-allergenic agent or anti-infectious agent.
 CC The allergic conditions which may be treated include eczema, allergic
 CC rhinitis, hayfever, urticaria, food allergies and other atopic
 CC conditions, and the infections which may be treated include viral,
 CC bacterial, fungal and protozoal infections such as tuberculosis, AIDS,
 CC leishmania and schistosomiasis. Immune response induction may also be
 CC used in the treatment of an autoimmune disorder (e.g., lupus
 CC erythematosus, rheumatoid arthritis and multiple sclerosis), a disease
 CC associated with immune system deficiency, and symptoms resulting from
 CC exposure to an agent of biological warfare. An immunogenic CpG
 CC oligonucleotide, either alone or in combination with an anti-cancer
 CC agent, is useful for treating solid tumour cancer. The induction of an
 CC immune response is used in antisense therapy and to improve the efficacy
 CC of a vaccine. The oligonucleotide is preferably administered to
 CC lymphocytes ex vivo, producing activated lymphocytes which are then
 CC administered to the host. The present sequence represents an immunogenic
 CC CpG oligodeoxynucleotide of the invention
 XX
 SQ Sequence 20 BP; 2 A; 4 C; 12 G; 2 T; 0 U; 0 Other;
 Query Match 100.0%; Score 20; DB 4; Length 20;
 Best Local Similarity 100.0%; Pred. No. 21;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GGTGCACCGGTGCAGGGGG 20
 Db 1 GGTGCACCGGTGCAGGGGG 20
 RESULT 2
 AAS09592
 ID AAS09592 standard; DNA; 20 BP.
 XX
 AC AAS09592;
 XX
 DT 26-SEP-2001 (first entry)
 XX
 DE Immunoreactive CpG sequence-containing oligonucleotide #42.
 XX
 KW CpG sequence; immune response; non-B cell activation; interferon gamma;
 KW IFN-gamma; humoral; antibody production; interleukin-6 production;
 KW therapeutic; allergy; asthma; cancer; autoimmune disorder; infection;
 KW bio-warfare; vaccine; antisense therapy; eczema; allergic rhinitis;
 KW coryza; hay fever; urticaria; hives; food allergy; atopic condition;
 KW hepatitis; human immunodeficiency virus; HIV; malaria; Francisella;
 KW lupus erythematosus; rheumatoid arthritis; multiple sclerosis;
 KW schistosomiasis; tuberculosis; acquired immunodeficiency syndrome; AIDS;
 KW Leishmania; Ebola; Anthrax; Listeria; ss.
 XX
 OS Synthetic.
 XX
 PN WO200151500-A1.
 XX
 XX 19-JUL-2001.

XX 12-JAN-2001; 2001WO-US001122.
 XX
 PR 14-JAN-2000; 2000US-0176115P.
 XX
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX
 PI Klinman D, Ishii K, Verthelyi D;
 XX
 XX WPI; 2001-442129/47.
 XX
 PS Oligodeoxynucleotides for inducing an immune response to treat and
 XX prevent an allergic reaction, cancer, an autoimmune disorder and symptoms
 XX resulting from exposure to bio-warfare agents, comprise multiple CpG
 XX sequences.
 XX
 XX Claim 5; Page 34; 48pp; English.
 XX
 CC AAS09551-AAS09662 represent oligodeoxynucleotides (ODN) of at least 10
 CC nucleotides comprising multiple CpG sequences, where one of the CpG
 CC sequences is different from another of the multiple CpG sequences. The
 CC ODN are useful for inducing an immune response, preferably a cell-
 CC mediated immune response, involving non-B cell activation, interferon B
 CC gamma (IFN-gamma) production or a humoral immune response involving B
 CC cell activation, antibody and interleukin-6 production in a host, for
 CC treating, preventing or ameliorating an allergic reaction, e.g. asthma,
 CC cancer, e.g. solid tumour cancer, a disease associated with the immune
 CC system e.g. autoimmune disorder or an immune system deficiency, infection
 CC or a symptom resulting from exposure to bio-warfare agent in a human. The
 CC induction of immune response improves the efficacy of a vaccine and is
 CC used in antisense therapy. The ODN are useful for treating, preventing or
 CC ameliorating allergic reactions, including eczema, allergic rhinitis or
 CC coryza, hay fever, bronchial asthma, urticaria (hives), food allergies
 CC and other atopic conditions, for improving the efficacy of vaccines
 CC against hepatitis A, B and C, human immunodeficiency virus (HIV) and
 CC malaria, for treating immune system deficiencies, e.g. lupus
 CC erythematosus and autoimmune diseases such as rheumatoid arthritis and
 CC multiple sclerosis, infections including Francisella, schistosomiasis,
 CC tuberculosis, acquired immunodeficiency syndrome (AIDS), Leishmania and
 CC symptoms resulting from exposure of bio-warfare agent, including Ebola,
 CC Anthrax and Listeria
 XX
 SQ Sequence 20 BP; 2 A; 4 C; 12 G; 2 T; 0 U; 0 Other;
 Query Match 100.0%; Score 20; DB 4; Length 20;
 Best Local Similarity 100.0%; Pred. No. 21;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GGTGCACCGGTGCAGGGGG 20
 Db 1 GGTGCACCGGTGCAGGGGG 20
 RESULT 3
 ABL35614
 ID ABL35614 standard; DNA; 20 BP.
 XX
 AC ABL35614;
 XX
 DT 04-APR-2002 (first entry)
 XX
 DE Immunostimulatory oligonucleotide SEQ ID NO: 540.
 XX
 KW DNA/RNA hybrid; phosphorothioate backbone; immunostimulatory; vaccine;
 KW infection; allergy; cancer; hypersensitivity; bio-warfare;
 KW immunostimulant; antiallergic; cytostatic; antimicrobial; anti-HIV;
 KW immunosuppressive; protozoacide; virucide; hepatotropic; gene therapy;
 KW antiinflammatory; antibacterial; ss.
 XX
 OS Synthetic.
 XX
 XX Key Location/Qualifiers
 XX misc_RNA 1. .20
 FT

```

FT      /*tag= a
FT      /note= "optionally thymidine is replaced by uracil to
FT      form RNA or DNA/RNA hybrids. Thymidine is linked to at
FT      least one other base through a ribose sugar"
XX
XX
XX      WO200193902-A2.
XX
XX      13-DEC-2001.
XX
XX      07-JUN-2001; 2001WO-US018276.
XX
XX      07-JUN-2000; 2000US-0209797P.
XX
XX      (BIOS-) BIOSYNEXUS INC.
XX
XX      Mond JJ, Flora M, Kliman DM;
XX      WPI; 2002-130570/17.
XX
XX      New immunostimulatory compositions comprising RNA/DNA hybrid
XX      oligonucleotides, useful for enhancing an immune response or inducing
XX      cytokines, particularly for treating diseases, e.g. cancer, allergy or
XX      HIV infection.
XX
XX      Example 11; Page 62; 68pp; English.
XX
XX      The present invention relates to an immunostimulatory composition, which
XX      comprises at least one oligonucleotide comprising both an RNA region and
XX      a DNA region. The composition is useful for enhancing an immune response
XX      or inducing cytokines. It can be used as a vaccine adjuvant and in
XX      treating diseases, including pathogenic infection, (non-)malignant
XX      tumours (e.g. cancers of the brain, lung, ovary, breast, prostate or
XX      colon, or carcinomas and sarcomas), autoimmune diseases or allergies
XX      (e.g. allergic rhinitis, hay fever or food allergies), Lyme disease,
XX      hepatitis, HIV or malaria. The composition is also useful for treating,
XX      preventing or ameliorating the symptoms resulting from exposure to a bio-
XX      warfare agent, e.g. Ebola, Anthrax or Listeria. The present sequence is
XX      an immunostimulatory oligonucleotide described in the exemplification of
XX      the invention
XX
XX      Sequence 20 BP; 2 A; 4 C; 12 G; 2 T; 0 U; 0 Other;
XX
XX      Query Match      100.0%; Score 20; DB 6; Length 20;
XX      Best Local Similarity 100.0%; Pred. No. 21;
XX      Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX      QY      1 GGTGACCGGTGTCAGGGGGG 20
XX      |||||
XX      Db      1 GGTGACCGGTGTCAGGGGGG 20
XX
XX      RESULT 4
XX      ABL35578
XX      ID ABL35578 standard; DNA; 20 BP.
XX
XX      AC ABL35578;
XX
XX      DT 04-APR-2002 (first entry)
XX
XX      DE Immunostimulatory oligonucleotide SEQ ID NO: 504.
XX
XX      DNA/RNA hybrid; phosphorothioate backbone; immunostimulatory; vaccine;
XX      infection; allergy; cancer; hypersensitivity; bio-warfare;
XX      immunostimulant; antiallergic; cytostatic; antimicrobial; anti-HIV;
XX      immunosuppressive; protozoacide; virucide; hepatotropic; gene therapy;
XX      antiinflammatory; antibacterial; ss.
XX
XX      Synthetic.
XX
XX      Key      Location/Qualifiers
XX      misc_RNA      1..20
XX      /tag= a
XX      /note= "optionally thymidine is replaced by uracil to
FT      form RNA or DNA/RNA hybrids. Thymidine is linked to at
FT      least one other base through a ribose sugar"
FT

```

```

FT      form RNA or DNA/RNA hybrids. Thymidine is linked to at
FT      least one other base through a ribose sugar"
XX
XX      WO200193902-A2.
XX
XX      13-DEC-2001.
XX
XX      07-JUN-2001; 2001WO-US018276.
XX
XX      07-JUN-2000; 2000US-0209797P.
XX
XX      (BIOS-) BIOSYNEXUS INC.
XX
XX      Mond JJ, Flora M, Kliman DM;
XX      WPI; 2002-130570/17.
XX
XX      New immunostimulatory compositions comprising RNA/DNA hybrid
XX      oligonucleotides, useful for enhancing an immune response or inducing
XX      cytokines, particularly for treating diseases, e.g. cancer, allergy or
XX      HIV infection.
XX
XX      Example 11; Page 61; 68pp; English.
XX
XX      The present invention relates to an immunostimulatory composition, which
XX      comprises at least one oligonucleotide comprising both an RNA region and
XX      a DNA region. The composition is useful for enhancing an immune response
XX      or inducing cytokines. It can be used as a vaccine adjuvant and in
XX      treating diseases, including pathogenic infection, (non-)malignant
XX      tumours (e.g. cancers of the brain, lung, ovary, breast, prostate or
XX      colon, or carcinomas and sarcomas), autoimmune diseases or allergies
XX      (e.g. allergic rhinitis, hay fever or food allergies), Lyme disease,
XX      hepatitis, HIV or malaria. The composition is also useful for treating,
XX      preventing or ameliorating the symptoms resulting from exposure to a bio-
XX      warfare agent, e.g. Ebola, Anthrax or Listeria. The present sequence is
XX      an immunostimulatory oligonucleotide described in the exemplification of
XX      the invention
XX
XX      Sequence 20 BP; 2 A; 4 C; 12 G; 2 T; 0 U; 0 Other;
XX
XX      Query Match      100.0%; Score 20; DB 6; Length 20;
XX      Best Local Similarity 100.0%; Pred. No. 21;
XX      Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX      QY      1 GGTGACCGGTGTCAGGGGGG 20
XX      |||||
XX      Db      1 GGTGACCGGTGTCAGGGGGG 20
XX
XX      RESULT 5
XX      ABL35581
XX      ID ABL35581 standard; DNA; 20 BP.
XX
XX      AC ABL35581;
XX
XX      DT 04-APR-2002 (first entry)
XX
XX      DE Immunostimulatory oligonucleotide SEQ ID NO: 507.
XX
XX      DNA/RNA hybrid; phosphorothioate backbone; immunostimulatory; vaccine;
XX      infection; allergy; cancer; hypersensitivity; bio-warfare;
XX      immunostimulant; antiallergic; cytostatic; antimicrobial; anti-HIV;
XX      immunosuppressive; protozoacide; virucide; hepatotropic; gene therapy;
XX      antiinflammatory; antibacterial; ss.
XX
XX      Synthetic.
XX
XX      Key      Location/Qualifiers
XX      misc_RNA      1..20
XX      /tag= a
XX      /note= "optionally thymidine is replaced by uracil to
FT      form RNA or DNA/RNA hybrids. Thymidine is linked to at
FT      least one other base through a ribose sugar"
FT

```

```

XX WO200193902-A2.
XX 13-DEC-2001.
XX 07-JUN-2001; 2001WO-US018276.
XX 07-JUN-2000; 2000US-0209797P.
XX (BIOS-) BIOSYNEXUS INC.
XX Mond JJ, Flora M, Klinman DM;
XX WPI; 2002-130570/17.
XX New immunostimulatory compositions comprising RNA/DNA hybrid
XX oligonucleotides, useful for enhancing an immune response or inducing
XX cytokines, particularly for treating diseases, e.g. cancer, allergy or
XX HIV infection.
XX Example 11; Page 61; 68pp; English.
XX The present invention relates to an immunostimulatory composition, which
XX comprises at least one oligonucleotide comprising both an RNA region and
XX a DNA region. The composition is useful for enhancing an immune response
XX or inducing cytokines. It can be used as a vaccine adjuvant and in
XX treating diseases, including pathogenic infection, (non-)malignant
XX tumours (e.g. cancers of the brain, lung, ovary, breast, prostate or
XX colon, or carcinomas and sarcomas), autoimmune diseases or allergies
XX (e.g. allergic rhinitis, hay fever or food allergies), Lyme disease,
XX hepatitis, HIV or malaria. The composition is also useful for treating,
XX preventing or ameliorating the symptoms resulting from exposure to a bio-
XX warfare agent, e.g. Ebola, Anthrax or Listeria. The present sequence is
XX an immunostimulatory oligonucleotide described in the exemplification of
XX the invention
XX
XX Sequence 20 BP; 2 A; 4 C; 12 G; 2 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 20; DB 6; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 21;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 GGTGCACCGGTGCAGGGGGG 20
XX |||||
XX Db 1 GGTGCACCGGTGCAGGGGGG 20
XX
XX RESULT 6
XX ABL35570
XX ID ABL35570 standard; DNA; 20 BP.
XX AC ABL35570;
XX DT 04-APR-2002 (first entry)
XX DE Immunostimulatory oligonucleotide SEQ ID NO: 496.
XX KW DNA/RNA hybrid; phosphorothioate backbone; immunostimulatory; vaccine;
XX infection; allergy; cancer; hypersensitivity; bio-warfare;
XX immunostimulant; antiallergic; cytostatic; antimicrobial; anti-HIV;
XX immunosuppressive; protozoacide; virucide; hepatotropic; gene therapy;
XX antiinflammatory; antibacterial; ss.
XX OS Synthetic.
XX
XX Key Location/Qualifiers
XX misc_RNA 1..20
XX /tag= a
XX /note= "optionally thymidine is replaced by uracil to
XX form RNA or DNA/RNA hybrids. Thymidine is linked to at
XX least one other base through a ribose sugar"
XX
XX WO200193902-A2.
XX 13-DEC-2001.

```

```

XX 13-DEC-2001.
XX 07-JUN-2001; 2001WO-US018276.
XX 07-JUN-2000; 2000US-0209797P.
XX (BIOS-) BIOSYNEXUS INC.
XX Mond JJ, Flora M, Klinman DM;
XX WPI; 2002-130570/17.
XX New immunostimulatory compositions comprising RNA/DNA hybrid
XX oligonucleotides, useful for enhancing an immune response or inducing
XX cytokines, particularly for treating diseases, e.g. cancer, allergy or
XX HIV infection.
XX Example 11; Page 61; 68pp; English.
XX The present invention relates to an immunostimulatory composition, which
XX comprises at least one oligonucleotide comprising both an RNA region and
XX a DNA region. The composition is useful for enhancing an immune response
XX or inducing cytokines. It can be used as a vaccine adjuvant and in
XX treating diseases, including pathogenic infection, (non-)malignant
XX tumours (e.g. cancers of the brain, lung, ovary, breast, prostate or
XX colon, or carcinomas and sarcomas), autoimmune diseases or allergies
XX (e.g. allergic rhinitis, hay fever or food allergies), Lyme disease,
XX hepatitis, HIV or malaria. The composition is also useful for treating,
XX preventing or ameliorating the symptoms resulting from exposure to a bio-
XX warfare agent, e.g. Ebola, Anthrax or Listeria. The present sequence is
XX an immunostimulatory oligonucleotide described in the exemplification of
XX the invention
XX
XX Sequence 20 BP; 2 A; 4 C; 12 G; 2 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 20; DB 6; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 21;
XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 GGTGCACCGGTGCAGGGGGG 20
XX |||||
XX Db 1 GGTGCACCGGTGCAGGGGGG 20
XX
XX RESULT 7
XX ABL35588
XX ID ABL35588 standard; DNA; 20 BP.
XX AC ABL35588;
XX DT 04-APR-2002 (first entry)
XX DE Immunostimulatory oligonucleotide SEQ ID NO: 514.
XX KW DNA/RNA hybrid; phosphorothioate backbone; immunostimulatory; vaccine;
XX infection; allergy; cancer; hypersensitivity; bio-warfare;
XX immunostimulant; antiallergic; cytostatic; antimicrobial; anti-HIV;
XX immunosuppressive; protozoacide; virucide; hepatotropic; gene therapy;
XX antiinflammatory; antibacterial; ss.
XX OS Synthetic.
XX
XX Key Location/Qualifiers
XX misc_RNA 1..20
XX /tag= a
XX /note= "optionally thymidine is replaced by uracil to
XX form RNA or DNA/RNA hybrids. Thymidine is linked to at
XX least one other base through a ribose sugar"
XX
XX WO200193902-A2.
XX 13-DEC-2001.

```

```

XX PF 07-JUN-2001; 2001WO-US018276.
XX PR 07-JUN-2000; 2000US-0209797F.
XX PA (BIOS-) BIOSYNEXUS INC.
XX PI Mond JJ, Flora M, Klinman DM;
XX WI WPI; 2002-130570/17.
XX PT New immunostimulatory compositions comprising RNA/DNA hybrid
XX PT oligonucleotides, useful for enhancing an immune response or inducing
XX PT cytokines, particularly for treating diseases, e.g. cancer, allergy or
XX PT HIV infection.
XX PS Example 11; Page 61; 68pp; English.
XX CC The present invention relates to an immunostimulatory composition, which
XX CC comprises at least one oligonucleotide comprising both an RNA region and
XX CC a DNA region. The composition is useful for enhancing an immune response
XX CC or inducing cytokines. It can be used as a vaccine adjuvant and in
XX CC treating diseases, including pathogenic infection, (non-)malignant
XX CC tumours (e.g. cancers of the brain, lung, ovary, breast, prostate or
XX CC colon, or carcinomas and sarcomas), autoimmune diseases or allergies
XX CC (e.g. allergic rhinitis, hay fever or food allergies), Lyme disease,
XX CC hepatitis, HIV or malaria. The composition is also useful for treating,
XX CC preventing or ameliorating the symptoms resulting from exposure to a bio-
XX CC warfare agent, e.g. Ebola, Anthrax or Listeria. The present sequence is
XX CC an immunostimulatory oligonucleotide described in the exemplification of
XX CC the invention
XX SQ Sequence 20 BP; 2 A; 4 C; 12 G; 2 T; 0 U; 0 Other;

  Query Match      100.0%; Score 20; DB 6; Length 20;
  Best Local Similarity 100.0%; Pred. No. 21;
  Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTGCACCGGTGCAGGGGG 20
Db 1 GGTGCACCGGTGCAGGGGG 20

RESULT 8
ID ABK46470 standard; DNA; 20 BP.
AC ABK46470;
XX 05-JUN-2002 (first entry)
XX Immunostimulatory unmethylated CpG oligodeoxynucleotide #60.
XX unmethylated CpG; oligodeoxynucleotide; ODN; virucide; vaccine;
XX Paramyxoviridae; F protein; respiratory syncytial virus; RSV;
XX viral bronchiolitis; pneumonia; infectious pulmonary disease;
XX bronchopulmonary dysplasia; congenital heart condition; ss.
XX Synthetic.
XX WO200211761-A2.
XX 14-FEB-2002.
XX 09-AUG-2001; 2001WO-US041633.
XX 10-AUG-2000; 2000US-0224011P.
XX 01-SEP-2000; 2000US-0229307P.
XX (JACK-) JACKSON FOUND ADVANCEMENT MILITARY MED.
XX Mond JJ, Prince G, Klinman DM;

```

```

DR WPI; 2002-227118/28.
XX Vaccine for immunizing patient against respiratory syncytial virus, has
XX PT epitopes of Paramyxoviridae F protein, and cytosine followed by guanine
XX PT linked by phosphate bond-oligodeoxynucleotides.
XX PS Claim 4; Page 8; 30pp; English.
XX CC The invention describes a vaccine comprising one or more epitopes of a
XX CC Paramyxoviridae F protein, and one or more CpG (cytosine followed by
XX CC guanine linked by phosphate bond)-oligodeoxynucleotides (ODNs). The
XX CC vaccine is useful for vaccinating a patient especially against viruses of
XX CC the Paramyxoviridae family e.g. respiratory syncytial virus (RSV), the
XX CC primary cause of viral bronchiolitis and pneumonia in infants and
XX CC children, and infectious pulmonary disease in infants. RSV has been
XX CC particularly implicated in death of infants that are premature, have
XX CC bronchopulmonary dysplasia, or congenital heart conditions. This sequence
XX CC represents an oligodeoxynucleotide that can be used in the creation of
XX CC the vaccine
XX SQ Sequence 20 BP; 2 A; 4 C; 12 G; 2 T; 0 U; 0 Other;

  Query Match      100.0%; Score 20; DB 6; Length 20;
  Best Local Similarity 100.0%; Pred. No. 21;
  Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTGCACCGGTGCAGGGGG 20
Db 1 GGTGCACCGGTGCAGGGGG 20

RESULT 9
ID ACC48296 standard; DNA; 20 BP.
XX ACC48296;
XX 11-AUG-2003 (first entry)
XX CpG oligodeoxynucleotide D29 used for dendritic cell maturation.
XX CpG oligodeoxynucleotide; dendritic cell; tumour; immunotherapy; vaccine;
XX cytostatic; immunostimulant; gene therapy; ss.
XX Synthetic.
XX Key Location/Qualifiers
XX modified_base 1..20
XX /*tag= a
XX /mod_base= OTHER
XX /note= "OTHER= phosphorothioate nucleotides"
XX modified_base 1
XX /*tag= a
XX /mod_base= OTHER
XX /note= "OTHER= phosphorothioate nucleotide"
XX WO2003020884-A2.
XX 13-MAR-2003.
XX 13-AUG-2002; 2002WO-US025732.
XX 14-AUG-2001; 2001US-0312190P.
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX Klinman DM, Gursel M, Verthelyi D;
XX WPI; 2003-300874/29.
XX Generating mature dendritic cells for tumor immunotherapy or as vaccines
XX for activating the immune system to treat diseases such as cancer,
XX comprises contacting a dendritic cell precursor with a D type

```

PT oligodeoxynucleotide.
 PS Claim 11; Page 44; 69pp; English.
 XX
 CC The present sequence is that of D type CpG oligodeoxynucleotide D29,
 CC which is used in a claimed method for generating a mature dendritic cell.
 CC The method involves contacting a dendritic cell precursor, especially a
 CC monocyte, with the oligonucleotide. The method is useful for generating
 CC mature dendritic cells and enhancing T cell responses, thus enhancing
 CC antigen presentation. Mature dendritic cells are useful for tumour
 CC immunotherapy, for augmenting an immune response to an infectious agent
 CC or to a vaccine, and as vaccines to prevent future infection or to
 CC activate the immune system to treat diseases such as cancer. Mature
 CC dendritic cells may also be used to produce activated T lymphocytes
 XX
 SQ Sequence 20 BP; 2 A; 4 C; 12 G; 2 T; 0 U; 0 Other;
 Query Match 100.0%; Score 20; DB 7; Length 20;
 Best Local Similarity 100.0%; Pred. No. 21;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GGTGACCGGTGAGGGGG 20
 Db 1 GGTGACCGGTGAGGGGG 20
 RESULT 10
 ACC48313
 ID ACC48313 standard; DNA; 20 BP.
 AC ACC48313;
 XX
 DT 11-AUG-2003 (first entry)
 DE CpG oligodeoxynucleotide.
 XX
 KW CpG oligodeoxynucleotide; dendritic cell; tumour; immunotherapy; vaccine;
 KW cytostatic; immunostimulant; gene therapy; ss.
 XX
 OS Synthetic.
 XX
 PN WO2003020884-A2.
 XX
 PD 13-MAR-2003.
 XX
 PF 13-AUG-2002; 2002WO-US025732.
 XX
 PR 14-AUG-2001; 2001US-0312190P.
 XX
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX
 PI Klinman DM, Gursel M, Verthelyi D;
 XX
 DR WPI; 2003-300874/29.
 XX
 CC Generating mature dendritic cells for tumor immunotherapy or as vaccines
 CC for activating the immune system to treat diseases such as cancer.
 CC comprises contacting a dendritic cell precursor with a D type
 CC oligodeoxynucleotide.
 XX
 PS Disclosure; Page 61; 69pp; English.
 XX
 CC The present sequence is that of a CpG oligodeoxynucleotide of the
 CC invention. A claimed method for generating dendritic cells involves
 CC contacting a dendritic cell precursor, especially a monocyte, with a D
 CC type oligodeoxynucleotide (see ACC48294) containing a central
 CC unmethylated CpG motif. The method is useful for generating mature
 CC dendritic cells and enhancing T cell responses, thus enhancing antigen
 CC presentation. Mature dendritic cells are useful for tumour immunotherapy,
 CC for augmenting an immune response to an infectious agent or to a vaccine,
 CC and as vaccines to prevent future infection or to activate the immune
 CC system to treat diseases such as cancer. Mature dendritic cells may also
 CC be used to produce activated T lymphocytes

XX
 SQ Sequence 20 BP; 2 A; 4 C; 12 G; 2 T; 0 U; 0 Other;
 Query Match 100.0%; Score 20; DB 7; Length 20;
 Best Local Similarity 100.0%; Pred. No. 21;
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GGTGACCGGTGAGGGGG 20
 Db 1 GGTGACCGGTGAGGGGG 20
 RESULT 11
 ACC83118
 ID ACC83118 standard; DNA; 20 BP.
 AC ACC83118;
 XX
 DT 27-AUG-2003 (first entry)
 DE D class CpG ODN sequence useful for encapsulating in SSCL, DV29.
 XX
 KW Sterically stabilised cationic liposome; SSCL; ODN; oligodeoxynucleotide;
 KW tuberculosis; cytokine; leishmaniasis; AIDS-associated Kaposi's tumour;
 KW thyroid; cancer; allergy; eczema; allergic rhinitis; coryza; hay fever;
 KW schistosomiasis; interferon gamma; lupus erythematosus; antimicrobial;
 KW asthma; urticaria; autoimmune disease; diabetes; rheumatoid arthritis;
 KW CpG motif; interleukin-13; cytostatic; tularemia; malaria; psoriasis;
 KW multiple sclerosis; infection; tumour; ss.
 XX
 OS Unidentified.
 XX
 PN WO2003040308-A2.
 XX
 PD 15-MAY-2003.
 XX
 PF 29-JUL-2002; 2002WO-US024235.
 XX
 PR 27-JUL-2001; 2001US-0308283P.
 PR 25-JUL-2002; 2002US-00206407.
 XX
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX
 PI Klinman DM, Gursel I, Ishii KJ, Kawakami K, Joshi BH, Puri RK;
 XX
 DR WPI; 2003-482260/45.
 XX
 CC Cationic liposome composition for delivering oligodeoxynucleotides
 CC including a CpG motif in clinical applications, comprises a cationic
 CC lipid, a co-lipid, stabilizing agent and an encapsulated oligonucleotide.
 XX
 PS Disclosure; Fig 10C; 110pp; English.
 XX
 CC The invention relates to sterically stabilised cationic liposomes (SSCL)
 CC which comprises a cationic lipid, a co-lipid, stabilising agent and
 CC encapsulating a K type oligodeoxynucleotide (ODN) including a CpG motif.
 CC The invention is useful in pharmaceutical composition for impairing
 CC growth of a solid tumour cell (e.g. human tumour cell) bearing an
 CC interleukin-13 receptor in a subject; for stimulating an immune response,
 CC which is expression of a cytokine (e.g. interferon gamma), particularly
 CC immunotherapeutic response against tumours or stimulating an in vivo or
 CC an in vitro immune cell, and for inducing an immune response against an
 CC infectious agent e.g. virus, bacteria and fungus. It is also useful for
 CC delivering oligodeoxynucleotides including a CpG motif in clinical
 CC applications; for treating infectious diseases (e.g. tularemia, malaria,
 CC francisella, schistosomiasis, tuberculosis and leishmaniasis), cancer
 CC (e.g. solid tumours, AIDS-associated Kaposi's tumour, thyroid cancer
 CC etc), allergy (e.g. eczema, allergic rhinitis or coryza), hay fever,
 CC bronchial or allergic asthma, urticaria, food allergies, autoimmune
 CC diseases (e.g. diabetes, rheumatoid arthritis, lupus erythematosus and
 CC multiple sclerosis) and psoriasis. The present sequence is a D class CpG
 CC ODN potentially useful for encapsulating in SSCL

```

SQ Sequence 20 BP; 2 A; 4 C; 12 G; 2 T; 0 U; 0 Other;
Query Match 100.0%; Score 20; DB 8; Length 20;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTGCACCGGTGCAGGGGG 20
DB 1 GGTGCACCGGTGCAGGGGG 20

RESULT 12
ACC83152
ID ACC83152 standard; DNA; 20 BP.
XX ACC83152;
XX
XX
XX 27-AUG-2003 (first entry)
XX
XX D class ODN sequence useful for encapsulating in SSCL, D29.
XX
XX Sterically stabilised cationic liposome; SSCL; ODN; oligodeoxynucleotide;
KW tuberculosis; cytokine; leishmaniasis; AIDS-associated Kaposi's tumour;
KW thyroid; cancer; eczema; allergic rhinitis; coryza; hay fever;
KW schistosomiasis; interferon gamma; lupus erythematosus; antimicrobial;
KW asthma; urticaria; autoimmune disease; diabetes; rheumatoid arthritis;
KW CpG motif; interleukin-13; cytostatic; tularemia; malaria; psoriasis;
KW multiple sclerosis; infection; tumour; phosphorothioate backbone; ss.
XX
XX Unidentified.
XX
XX Key Location/Qualifiers
FH modified_base 16..20
FT /*tag= a
FT /*mod_base= OTHER
FT /*note= "Phosphorothioate backbone"
XX
XX WO2003040308-A2.
XX
XX 15-MAY-2003.
XX
XX 29-JUL-2002; 2002WO-US024235.
XX
XX 27-JUL-2001; 2001US-0308283P.
XX
XX 25-JUL-2002; 2002US-00206407.
XX
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
XX Klinman DM, Gursel I, Ishii KJ, Kawakami K, Joshi BH, Puri RK;
XX WPI; 2003-482260/45.
XX
XX Cationic liposome composition for delivering oligodeoxynucleotides
XX including a CpG motif in clinical applications, comprises a cationic
XX lipid, a co-lipid, stabilising agent and an encapsulated oligonucleotide.
XX
XX Example 8; Page 52; 110pp; English.
XX
XX The invention relates to sterically stabilised cationic liposomes (SSCL)
XX which comprises a cationic lipid, a co-lipid, stabilising agent and
XX encapsulating a K type oligodeoxynucleotide (ODN) including a CpG motif.
XX The invention is useful in pharmaceutical composition for impairing
XX growth of a solid tumour cell (e.g. human tumour cell) bearing an
XX interleukin-13 receptor in a subject; for stimulating an immune response,
XX which is expression of a cytokine (e.g. interferon gamma), particularly
XX immunotherapeutic response against tumours or stimulating an in vivo or
XX an in vitro immune cell, and for inducing an immune response against an
XX infectious agent e.g. virus, bacteria and fungus. It is also useful for
XX delivering oligodeoxynucleotides including a CpG motif in clinical
XX applications; for treating infectious diseases (e.g. tularemia, malaria,
XX francisella, schistosomiasis, tuberculosis and leishmaniasis), cancer
XX (e.g. solid tumours, AIDS-associated Kaposi's tumour, thyroid cancer
XX etc), allergy (e.g. eczema, allergic rhinitis or coryza, hay fever,

```

```

CC bronchial or allergic asthma, urticaria, food allergies), autoimmune
CC diseases (e.g. diabetes, rheumatoid arthritis, lupus erythematosus and
CC multiple sclerosis) and psoriasis. The present sequence is a D class ODN
CC potentially useful for encapsulating in SSCL
XX
XX Sequence 20 BP; 2 A; 4 C; 12 G; 2 T; 0 U; 0 Other;
Query Match 100.0%; Score 20; DB 8; Length 20;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTGCACCGGTGCAGGGGG 20
DB 1 GGTGCACCGGTGCAGGGGG 20

RESULT 13
ADD01049
ID ADD01049 standard; DNA; 20 BP.
XX ADD01049;
XX
XX 01-JAN-2004 (first entry)
XX
XX CpG D oligonucleotide SEQ ID NO:13.
XX
XX vascular endothelial growth factor; VEGF; CpG oligonucleotide;
KW neovascularisation; angiogenesis; vulnery; vasotropic;
KW antiarteriosclerotic; gene therapy; skin graft; male pattern baldness;
KW atherosclerosis; ischaemia; ss.
XX
XX Synthetic.
XX
XX WO2003054161-A2.
XX
XX 03-JUL-2003.
XX
XX 19-DEC-2002; 2002WO-US040955.
XX
XX 20-DEC-2001; 2001US-0343457P.
XX
XX (UYTE-) UNIV TENNESSEE RES CORP.
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
XX Klinman DM, Zheng M, Rouse BT;
XX WPI; 2003-559139/52.
XX
XX Inducing the production of vascular endothelial growth factor by a cell,
XX useful for inducing angiogenesis, comprises contacting the cell with a
XX CpG oligodeoxynucleotide.
XX
XX Example 7; SEQ ID NO 13; 37pp; English.
XX
XX The present invention describes a method for inducing the production of
XX vascular endothelial growth factor (VEGF) by a cell comprising contacting
XX the cell with a CpG oligonucleotide and therefore inducing the production
XX of VEGF by the cell. Also described: (1) inducing neovascularisation in a
XX tissue, comprising introducing a CpG oligonucleotide into an area of the
XX tissue where the formation of new blood vessels is desired, and so
XX inducing neovascularisation in the area of the tissue; (2) promoting
XX angiogenesis in an area of the subject where angiogenesis is desired,
XX comprising introducing a CpG oligonucleotide to the area, and so
XX promoting angiogenesis in the subject; and (3) screening for an agent
XX that inhibits neovascularisation, comprising administering a CpG
XX oligonucleotide to a non-human mammal and administering the agent to the
XX mammal, where inhibition of angiogenesis in the animal indicates that the
XX agent is effective in inhibiting neovascularisation. The CpG
XX oligonucleotides have vulnery, vasotropic and antiarteriosclerotic
XX activities, and can be used in gene therapy. The method and the CpG
XX oligonucleotides can be used in inducing angiogenesis or
XX neovascularisation, such as in subjects with a skin graft, subjects who
XX exhibit male pattern baldness, or subjects who have a wound or who have

```

CC atherosclerosis or ischaemia. The method may also be used in screening
CC for agents that inhibit neovascularisation. The present sequence
CC represents a Cpg oligonucleotide which is used in the exemplification of
CC the present invention.

XX
SQ Sequence 20 BP; 2 A; 4 C; 12 G; 2 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTGCACCGGTGCAGGGGG 20
|||||
Db 1 GGTGCACCGGTGCAGGGGG 20

RESULT 14
ABL35599
ID ABL35599 standard; DNA; 28 BP.

XX ABL35599;

XX 04-APR-2002 (first entry)

XX Immunostimulatory oligonucleotide SEQ ID NO: 525.

XX DNA/RNA hybrid; phosphorothioate backbone; immunostimulatory; vaccine;
XX infection; allergy; cancer; hypersensitivity; bio-warfare;
XX immunostimulant; anti-allergic; cytostatic; antimicrobial; anti-HIV;
XX immunosuppressive; protozoacide; virucide; hepatotropic; gene therapy;
XX anti-inflammatory; antibacterial; ss.

XX Synthetic.

XX Key Location/Qualifiers
FH misc_RNA 1..28
FT /tag= a

FT /note= "optionally thymidine is replaced by uracil to
FT form RNA or DNA/RNA hybrids. Thymidine is linked to at
FT least one other base through a ribose sugar"

XX WO200193902-A2.

XX 13-DEC-2001.

XX 07-JUN-2001; 2001WO-US018276.

XX 07-JUN-2000; 2000US-0209797P.

XX (BIOS-) BIOSYNEXUS INC.

XX Mond JJ, Flora M, Kliman DM;

XX WPI; 2002-130570/17.

XX New immunostimulatory compositions comprising RNA/DNA hybrid
XX oligonucleotides, useful for enhancing an immune response or inducing
XX cytokines, particularly for treating diseases, e.g. cancer, allergy or
XX HIV infection.

XX Example 11; Page 61; 68pp; English.

XX The present invention relates to an immunostimulatory composition, which
XX comprises at least one oligonucleotide comprising both an RNA region and
XX a DNA region. The composition is useful for enhancing an immune response
XX or inducing cytokines. It can be used as a vaccine adjuvant and in
XX treating diseases, including pathogenic infection, (non-)malignant
XX tumours (e.g. cancers of the brain, lung, ovary, breast, prostate or
XX colon, or carcinomas and sarcomas), autoimmune diseases or allergies
XX (e.g. allergic rhinitis, hay fever or food allergies), Lyme disease,
XX hepatitis, HIV or malaria. The composition is also useful for treating,
XX preventing or ameliorating the symptoms resulting from exposure to a bio-
XX warfare agent, e.g. Ebola, Anthrax or Listeria. The present sequence is

CC an immunostimulatory oligonucleotide described in the exemplification of
CC the invention

XX Sequence 28 BP; 10 A; 4 C; 12 G; 2 T; 0 U; 0 Other;

Query Match 100.0%; Score 20; DB 6; Length 28;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTGCACCGGTGCAGGGGG 20
|||||
Db 1 GGTGCACCGGTGCAGGGGG 20

RESULT 15
ABL35603
ID ABL35603 standard; DNA; 28 BP.

XX ABL35603;

XX 04-APR-2002 (first entry)

XX Immunostimulatory oligonucleotide SEQ ID NO: 529.

XX DNA/RNA hybrid; phosphorothioate backbone; immunostimulatory; vaccine;
XX infection; allergy; cancer; hypersensitivity; bio-warfare;
XX immunostimulant; anti-allergic; cytostatic; antimicrobial; anti-HIV;
XX immunosuppressive; protozoacide; virucide; hepatotropic; gene therapy;
XX anti-inflammatory; antibacterial; ss.

XX Synthetic.

XX Key Location/Qualifiers
FH misc_RNA 1..28
FT /tag= a

FT /note= "optionally thymidine is replaced by uracil to
FT form RNA or DNA/RNA hybrids. Thymidine is linked to at
FT least one other base through a ribose sugar"

XX WO200193902-A2.

XX 13-DEC-2001.

XX 07-JUN-2001; 2001WO-US018276.

XX 07-JUN-2000; 2000US-0209797P.

XX (BIOS-) BIOSYNEXUS INC.

XX Mond JJ, Flora M, Kliman DM;

XX WPI; 2002-130570/17.

XX New immunostimulatory compositions comprising RNA/DNA hybrid
XX oligonucleotides, useful for enhancing an immune response or inducing
XX cytokines, particularly for treating diseases, e.g. cancer, allergy or
XX HIV infection.

XX Example 11; Page 61; 68pp; English.

XX The present invention relates to an immunostimulatory composition, which
XX comprises at least one oligonucleotide comprising both an RNA region and
XX a DNA region. The composition is useful for enhancing an immune response
XX or inducing cytokines. It can be used as a vaccine adjuvant and in
XX treating diseases, including pathogenic infection, (non-)malignant
XX tumours (e.g. cancers of the brain, lung, ovary, breast, prostate or
XX colon, or carcinomas and sarcomas), autoimmune diseases or allergies
XX (e.g. allergic rhinitis, hay fever or food allergies), Lyme disease,
XX hepatitis, HIV or malaria. The composition is also useful for treating,
XX preventing or ameliorating the symptoms resulting from exposure to a bio-
XX warfare agent, e.g. Ebola, Anthrax or Listeria. The present sequence is
XX an immunostimulatory oligonucleotide described in the exemplification of
XX the invention

XX
SQ Sequence 28 BP; 4 A; 6 C; 13 G; 5 T; 0 U; 0 Other;
Query Match 100.0%; Score 20; DB 6; Length 28;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GGTGCACCGGTGCAGGGGG 20
Db 9 GGTGCACCGGTGCAGGGGG 28

Search completed: July 2, 2004, 08:31:32
Job time : 149.878 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 2, 2004, 08:09:30 ; Search time 31.3415 Seconds
(without alignments)
354.132 Million cell updates/sec

Title: US-10-068-160-2

Perfect score: 20

Sequence: 1 ggtgcacgggtgcaggggggg 20

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA.*

- 1: /cgn2_6/ptodata/2/ina/5A-COMB.seq.*
- 2: /cgn2_6/ptodata/2/ina/5B-COMB.seq.*
- 3: /cgn2_6/ptodata/2/ina/6A-COMB.seq.*
- 4: /cgn2_6/ptodata/2/ina/6B-COMB.seq.*
- 5: /cgn2_6/ptodata/2/ina/PCTUS-COMB.seq.*
- 6: /cgn2_6/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	16.8	84.0	38653	4	US-09-922-445-1
C 2	15.8	79.0	633	4	US-09-489-039A-2752
C 3	15.8	79.0	3358	3	US-09-248-571-2
C 4	15.8	79.0	3358	4	US-09-553-736-2
C 5	15.8	79.0	10827	1	US-08-060-925A-12
C 6	15.8	79.0	12222	4	US-09-328-925-42
C 7	15.4	77.0	366	4	US-09-489-039A-5836
C 8	15.2	76.0	480	4	US-09-252-991A-5639
C 9	15.2	76.0	564	4	US-09-252-991A-5555
C 10	15.2	76.0	774	4	US-09-252-991A-5590
C 11	15.2	76.0	1083	4	US-09-655-270A-20
C 12	15.2	76.0	1098	4	US-09-651-941-24
C 13	15.2	76.0	1098	4	US-09-955-597-24
C 14	15.2	76.0	12508	4	US-09-655-270A-1
C 15	15.2	76.0	12523	4	US-09-651-941-1
C 16	15.2	76.0	12523	4	US-09-955-597-1
C 17	15.2	76.0	24707	4	US-09-740-027-3
C 18	15.2	76.0	45546	4	US-09-146-053-6
C 19	15.2	76.0	4403765	3	US-09-103-840A-2
C 20	15.2	76.0	4411529	3	US-09-103-840A-1
C 21	14.8	74.0	1443	3	US-08-959-381A-3
C 22	14.8	74.0	1446	4	US-09-170-496D-81
C 23	14.8	74.0	1446	4	US-09-170-496D-207
C 24	14.8	74.0	1626	3	US-08-959-381A-4
C 25	14.8	74.0	4000	2	US-08-687-289A-2
C 26	14.8	74.0	4000	4	US-09-435-897-2
C 27	14.8	74.0	4300	1	US-08-041-538-1

C 28	14.8	74.0	4300	1	US-08-463-642-1
C 29	14.8	74.0	4300	1	US-08-455-602-1
C 30	14.8	74.0	4300	2	US-08-465-157-1
C 31	14.8	74.0	4300	5	PCT-US91-09422-1
C 32	14.8	74.0	5236	5	PCT-US91-09422-16
C 33	14.8	74.0	6836	4	US-08-976-259-73
C 34	14.4	72.0	265	4	US-09-313-294A-385
C 35	14.4	72.0	273	4	US-09-313-294A-6489
C 36	14.4	72.0	2194	4	US-09-023-655-668
C 37	14.4	72.0	2511	3	US-08-422-869-19
C 38	14.2	71.0	40	4	US-09-916-510A-18
C 39	14.2	71.0	96	4	US-09-342-681C-107
C 40	14.2	71.0	236	4	US-09-621-976-18710
C 41	14.2	71.0	339	4	US-09-016-434-714
C 42	14.2	71.0	419	4	US-09-833-381-1374
C 43	14.2	71.0	548	1	US-08-469-667-6
C 44	14.2	71.0	548	4	US-09-224-110-6
C 45	14.2	71.0	548	5	PCT-US95-07289-6

ALIGNMENTS

RESULT 1
US-09-922-445-1/c
; Sequence 1, Application US/09922445
; Patent No. 6528268
; GENERAL INFORMATION:
; APPLICANT: Andersson, Maria K.
; APPLICANT: Berglund, Lars G. T.
; APPLICANT: Reneland, Rikard H.
; APPLICANT: Adam, Gail I. R.
; TITLE OF INVENTION: REAGENTS AND METHODS FOR DETECTION OF HEART FAILURE
; FILE REFERENCE: G6126US
; CURRENT APPLICATION NUMBER: US/09/922,445
; CURRENT FILING DATE: 2001-08-03
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: Patent version 3.1
; SEQ ID NO 1
; LENGTH: 38653
; TYPE: DNA
; ORGANISM: homo sapiens
; FEATURE:
; NAME/KEY: 5'UTR
; LOCATION: (1)..(26156)
; OTHER INFORMATION:
; NAME/KEY: misc feature
; LOCATION: (24801)..(24801)
; OTHER INFORMATION: nucleotide 24801 is a single nucleotide polymorphism which can
; OTHER INFORMATION: A or G
; NAME/KEY: misc feature
; LOCATION: (24941)..(24941)
; OTHER INFORMATION: nucleotide 24941 is a single nucleotide polymorphism which can
; OTHER INFORMATION: T or C
; NAME/KEY: exon
; LOCATION: (26157)..(26252)
; OTHER INFORMATION:
; NAME/KEY: Intron
; LOCATION: (26253)..(26401)
; OTHER INFORMATION:
; NAME/KEY: exon
; LOCATION: (26402)..(26543)
; OTHER INFORMATION:
; NAME/KEY: Intron
; LOCATION: (26544)..(27024)
; OTHER INFORMATION:
; NAME/KEY: exon
; LOCATION: (27025)..(27178)
; OTHER INFORMATION:
; NAME/KEY: Intron
; LOCATION: (27179)..(30519)
; OTHER INFORMATION:
; NAME/KEY: misc feature

```

; LOCATION: (27645)..(27645)
; OTHER INFORMATION: nucleotide 27645 is a single nucleotide polymorphism which can be
; OTHER INFORMATION: C or G
; NAME/KEY: exon
; LOCATION: (30520)..(30881)
; OTHER INFORMATION:
; NAME/KEY: Intron
; LOCATION: (30682)..(30894)
; OTHER INFORMATION:
; NAME/KEY: exon
; LOCATION: (30895)..(31027)
; OTHER INFORMATION:
; NAME/KEY: Intron
; LOCATION: (31028)..(31747)
; OTHER INFORMATION:
; NAME/KEY: exon
; LOCATION: (31748)..(31841)
; OTHER INFORMATION:
; NAME/KEY: Intron
; LOCATION: (31842)..(32400)
; OTHER INFORMATION:
; NAME/KEY: misc feature
; LOCATION: (32163)..(32163)
; OTHER INFORMATION: nucleotide 32163 is a single nucleotide polymorphism which can be
; OTHER INFORMATION: A or C
; NAME/KEY: exon
; LOCATION: (32401)..(32528)
; OTHER INFORMATION:
; NAME/KEY: Intron
; LOCATION: (32529)..(33414)
; OTHER INFORMATION:
; NAME/KEY: misc feature
; LOCATION: (32614)..(32614)
; OTHER INFORMATION: nucleotide 32614 is a single nucleotide polymorphism which can be
; OTHER INFORMATION: A or G
; NAME/KEY: exon
; LOCATION: (33415)..(33597)
; OTHER INFORMATION:
; NAME/KEY: Intron
; LOCATION: (33598)..(34314)
; OTHER INFORMATION:
; NAME/KEY: exon
; LOCATION: (34315)..(34588)
; OTHER INFORMATION:
; NAME/KEY: Intron
; LOCATION: (34589)..(36404)
; OTHER INFORMATION:
; NAME/KEY: exon
; LOCATION: (36405)..(36523)
; OTHER INFORMATION:
; NAME/KEY: Intron
; LOCATION: (36524)..(38341)
; OTHER INFORMATION:
; NAME/KEY: exon
; LOCATION: (38342)..(38653)
; OTHER INFORMATION:
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: Genbank/AC004923
; DATABASE ENTRY DATE: 1999-12-21
; RELEVANT RESIDUES: (1)..(38653)
US-09-922-445-1

```

```

Query Match      84.0%; Score 16.8; DB 4; Length 38653;
Best Local Similarity 90.0%; Pred. No. 57;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

```

Qy 1 GGTGCACCGGTGCAGGGGGG 20
Db 14714 GGTGCACTGGGCGAGGGGGG 14695

```

```

RESULT 2
US-09-489-039A-2752

```

```

; Sequence 2752, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 2752
; LENGTH: 633
; TYPE: DNA
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-2752

Query Match      79.0%; Score 15.8; DB 4; Length 633;
Best Local Similarity 89.5%; Pred. No. 1.6e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GGTGCACCGGTGCAGGGGGG 19
Db 614 GGTGCGCGGTGCAGGGTG 632

RESULT 3
US-09-248-571-2
; Sequence 2, Application US/09248571
; Patent No. 6136539
; GENERAL INFORMATION:
; APPLICANT: BASBAUM, CAROL
; APPLICANT: GALLUP, MARIANNE
; APPLICANT: DAIZONG, LI
; APPLICANT: GEBREMICHAEL, ASSEFA
; APPLICANT: GENSCH, ERIN
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR INHIBITION OF MUC-5-MUCIN
; FILE REFERENCE: UCSF12/02
; CURRENT APPLICATION NUMBER: US/09/248,571
; CURRENT FILING DATE: 1999-02-11
; EARLIER APPLICATION NUMBER: 60/074,398
; EARLIER FILING DATE: 1998-02-11
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 3358
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-248-571-2

Query Match      79.0%; Score 15.8; DB 3; Length 3358;
Best Local Similarity 89.5%; Pred. No. 1.6e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GTGCACCGGTGCAGGGGGG 20
Db 998 GTGCACCATGCAGGGGGG 1016

RESULT 4
US-09-553-736-2
; Sequence 2, Application US/09553736
; Patent No. 6440672
; GENERAL INFORMATION:
; APPLICANT: BASBAUM, CAROL
; APPLICANT: GALLUP, MARIANNE
; APPLICANT: DAIZONG, LI
; APPLICANT: GEBREMICHAEL, ASSEFA
; APPLICANT: GENSCH, ERIN
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE INHIBITION OF MUC-5
; FILE REFERENCE: UCSF12/02

```

FILE REFERENCE: UCSF-012/03US
CURRENT APPLICATION NUMBER: US/09/553,736
CURRENT FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US/09/248,571
PRIOR FILING DATE: 1999-02-11
PRIOR APPLICATION NUMBER: US/09/074,398
PRIOR FILING DATE: 1998-02-11
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 3358
TYPE: DNA
ORGANISM: Homo sapiens
US-09-553-736-2

Query Match 79.0%; Score 15.8; DB 4; Length 3358;
Best Local Similarity 89.5%; Pred. No. 1.6e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GTGCACCGGTGACGGGGG 20
Db 998 GTGCACCGGTGACGGGGG 1016

RESULT 5
US-08-060-925A-12
Sequence 12, Application US/08060925A
Patent No. 5439824
GENERAL INFORMATION:
APPLICANT: Brantley, Mark
APPLICANT: Laubach, Victor
TITLE OF INVENTION: INCREASED EXPRESSION OF ALPHA-1
TITLE OF INVENTION: ANTI-TRYPsin IN EXPRESSION VECTORS THROUGH THE INCLUSION OF
TITLE OF INVENTION: INTRON II
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSES: KNOBBE, MARTENS, OLSON AND BEAR
STREET: 620 NEWPORT CENTER DRIVE SIXTEENTH FLOOR
CITY: NEWPORT BEACH
STATE: CA
COUNTRY: USA
ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/060,925A
FILING DATE: 06-MAY-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Fuller, Michael L.
REGISTRATION NUMBER: 36,516
REFERENCE/DOCKET NUMBER: NIH040,001A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-235-8550
TELEFAX: 619-235-0176
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 10627 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-060-925A-12

Query Match 79.0%; Score 15.8; DB 1; Length 10627;
Best Local Similarity 89.5%; Pred. No. 1.6e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GGTCACCGGTGACGGGGG 19
Db 10086 GGTCACCGGTGACGGGGG 10104

RESULT 6
US-09-328-925-42
Sequence 42, Application US/09328925
Patent No. 6610906
GENERAL INFORMATION:
APPLICANT: Kurachi, Kotoku
APPLICANT: Kurachi, Sumiko
TITLE OF INVENTION: Nucleotide Sequences for Gene Regulation and Methods of
TITLE OF INVENTION: Use Thereof
FILE REFERENCE: US-03603
CURRENT APPLICATION NUMBER: US/09/328,925
CURRENT FILING DATE: 1999-06-09
NUMBER OF SEQ ID NOS: 84
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 42
LENGTH: 12222
TYPE: DNA
ORGANISM: Homo sapiens
US-09-328-925-42

Query Match 79.0%; Score 15.8; DB 4; Length 12222;
Best Local Similarity 89.5%; Pred. No. 1.6e+02;
Matches 17; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GGTCACCGGTGACGGGGG 19
Db 11680 GGTCACCGGTGACGGGGG 11698

RESULT 7
US-09-489-039A-5836
Sequence 5836, Application US/09489039A
Patent No. 6610836
GENERAL INFORMATION:
APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709,2004001
CURRENT APPLICATION NUMBER: US/09/489,039A
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 5836
LENGTH: 366
TYPE: DNA
ORGANISM: Klebsiella pneumoniae
US-09-489-039A-5836

Query Match 77.0%; Score 15.4; DB 4; Length 366;
Best Local Similarity 94.1%; Pred. No. 2.5e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGTCACCGGTGACGGG 17
Db 70 GGTCACCGGTGACGGG 86

RESULT 8
US-09-252-991A-5639
Sequence 5639, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A

```

; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 5639
; LENGTH: 480
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-5639

Query Match
Best Local Similarity 76.0%; Score 15.2; DB 4; Length 480;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGTGCACCGGTGCAGGGGG 20
    ||||| ||||| ||||| |||||
DB 391 GGTGCGCGGTGCAGTGGAG 410

RESULT 9
US-09-252-991A-5555/c
; Sequence 5555, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 5555
; LENGTH: 564
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-5555

Query Match
Best Local Similarity 76.0%; Score 15.2; DB 4; Length 564;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGTGCACCGGTGCAGGGGG 20
    ||||| ||||| ||||| |||||
DB 181 GGTGCGCGGTGCAGTGGAG 162

RESULT 10
US-09-252-991A-5590/c
; Sequence 5590, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 5590
; LENGTH: 774
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-5590

```

```

Query Match
Best Local Similarity 76.0%; Score 15.2; DB 4; Length 774;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGTGCACCGGTGCAGGGGG 20
    ||||| ||||| ||||| |||||
DB 363 GGTGCGCGGTGCAGTGGAG 344

RESULT 11
US-09-655-270A-20
; Sequence 20, Application US/09655270A
; Patent No. 6329151
; GENERAL INFORMATION:
; APPLICANT: Rouviere, Pierre E.
; TITLE OF INVENTION: High Density Sampling of Differentially Expressed Prokaryotic
; FILE REFERENCE: BC1011 US NA
; CURRENT APPLICATION NUMBER: US/09/655,270A
; CURRENT FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: 60/120,702
; PRIOR FILING DATE: 1999-February-19
; PRIOR APPLICATION NUMBER: 60/152,542
; PRIOR FILING DATE: 1999-September-03
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 20
; LENGTH: 1083
; TYPE: DNA
; ORGANISM: Rhodococcus erythropolis HL PM-1
US-09-655-270A-20

Query Match
Best Local Similarity 76.0%; Score 15.2; DB 4; Length 1083;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGTGCACCGGTGCAGGGGG 20
    ||||| ||||| ||||| |||||
DB 334 GGTGCACCGGTGCAGGGGG 353

RESULT 12
US-09-651-941-24
; Sequence 24, Application US/09651941
; Patent No. 6355470
; GENERAL INFORMATION:
; APPLICANT: ROUVIER, PIERRE E
; APPLICANT: WALTERS, DANA M
; APPLICANT: RAINER, RUSS
; TITLE OF INVENTION: Genes Encoding Picric Acid Degradation
; FILE REFERENCE: BC1022 US NA
; CURRENT APPLICATION NUMBER: US/09/651,941
; CURRENT FILING DATE: 2000-08-31
; PRIOR APPLICATION NUMBER: 60/152,545
; PRIOR FILING DATE: 1999-10-03
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 24
; LENGTH: 1098
; TYPE: DNA
; ORGANISM: Rhodococcus erythropolis HL PM-1
US-09-651-941-24

Query Match
Best Local Similarity 76.0%; Score 15.2; DB 4; Length 1098;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 GGTGCACCGGTGCAGGGGG 20
    ||||| ||||| ||||| |||||
DB 334 GGTGCACCGGTGCAGGGGG 353

RESULT 13

```

US-09-955-597-24
 ; Sequence 24, Application US/09955597
 ; Patent No. 6461856
 ; GENERAL INFORMATION:
 ; APPLICANT: ROUVIER, PIERRE E
 ; APPLICANT: WALTERS, DANA M
 ; APPLICANT: RAINER, RUSS
 ; TITLE OF INVENTION: Genes Encoding Picric Acid Degradation
 ; FILE REFERENCE: BC1022 US NA
 ; CURRENT APPLICATION NUMBER: US/09/955,597
 ; CURRENT FILING DATE: 2001-09-17
 ; PRIOR APPLICATION NUMBER: 60/152,545
 ; PRIOR FILING DATE: 1999-10-03
 ; NUMBER OF SEQ ID NOS: 28
 ; SOFTWARE: Microsoft Office 97
 ; SEQ ID NO 24
 ; LENGTH: 1098
 ; TYPE: DNA
 ; ORGANISM: Rhodococcus erythropolis HL PM-1
 US-09-955-597-24

Query Match 76.0%; Score 15.2; DB 4; Length 1098;
 Best Local Similarity 85.0%; Pred. No. 3e+02;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 GGTGCACCGGTGCAGGGGG 20
 |||||
 Db 334 GGTGCACCGGTGCAGGGGG 353
 |||||

RESULT 14
 US-09-655-270A-1
 ; Sequence 1, Application US/09655270A
 ; Patent No. 6329151
 ; GENERAL INFORMATION:
 ; APPLICANT: Rouviere, Pierre E.
 ; TITLE OF INVENTION: High Density Sampling of Differentially Expressed Prokaryotic m
 ; FILE REFERENCE: BC1011 US NA
 ; CURRENT APPLICATION NUMBER: US/09/655,270A
 ; CURRENT FILING DATE: 2000-09-05
 ; PRIOR APPLICATION NUMBER: 60/120,702
 ; PRIOR FILING DATE: 1999-February-19
 ; PRIOR APPLICATION NUMBER: 60/152,542
 ; PRIOR FILING DATE: 1999-September-03
 ; NUMBER OF SEQ ID NOS: 37
 ; SOFTWARE: Microsoft Office 97
 ; SEQ ID NO 1
 ; LENGTH: 12508
 ; TYPE: DNA
 ; ORGANISM: Rhodococcus erythropolis HL PM-1
 US-09-655-270A-1

Query Match 76.0%; Score 15.2; DB 4; Length 12508;
 Best Local Similarity 85.0%; Pred. No. 2.9e+02;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 GGTGCACCGGTGCAGGGGG 20
 |||||
 Db 11759 GGTGCACCGGTGCAGGGGG 11778
 |||||

RESULT 15
 US-09-651-941-1
 ; Sequence 1, Application US/09651941
 ; Patent No. 6355470
 ; GENERAL INFORMATION:
 ; APPLICANT: ROUVIER, PIERRE E
 ; APPLICANT: WALTERS, DANA M
 ; APPLICANT: RAINER, RUSS
 ; TITLE OF INVENTION: Genes Encoding Picric Acid Degradation
 ; FILE REFERENCE: BC1022 US NA
 ; CURRENT APPLICATION NUMBER: US/09/651,941
 ; CURRENT FILING DATE: 2000-08-31

; PRIOR APPLICATION NUMBER: 60/152,545
 ; PRIOR FILING DATE: 1999-10-03
 ; NUMBER OF SEQ ID NOS: 28
 ; SOFTWARE: Microsoft Office 97
 ; SEQ ID NO 1
 ; LENGTH: 12523
 ; TYPE: DNA
 ; ORGANISM: Rhodococcus erythropolis HL PM-1
 US-09-651-941-1
 Query Match 76.0%; Score 15.2; DB 4; Length 12523;
 Best Local Similarity 85.0%; Pred. No. 2.9e+02;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 GGTGCACCGGTGCAGGGGG 20
 |||||
 Db 11759 GGTGCACCGGTGCAGGGGG 11778
 |||||
 Search completed: July 2, 2004, 13:37:22
 Job time : 36.3415 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 2, 2004, 08:11:05 ; Search time 154.146 Seconds
(without alignments)
625.926 Million cell updates/sec

Title: US-10-068-160-2

Perfect score: 20
Sequence: 1 ggtgcaccggtgcaggggg 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3163042 seqs, 2412103800 residues

Total number of hits satisfying chosen parameters: 6326084

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_NA.*
1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq.*
2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq.*
3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq.*
4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq.*
5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq.*
6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq.*
7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq.*
8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq.*
9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq.*
10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq.*
11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq.*
12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq.*
13: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq.*
14: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq.*
15: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq.*
16: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq.*
17: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq.*
18: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq.*
19: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	100.0	20	13	US-09-874-991C-496
2	20	100.0	20	13	US-09-874-991C-504
3	20	100.0	20	13	US-09-874-991C-507
4	20	100.0	20	13	US-09-874-991C-514
5	20	100.0	20	13	US-09-874-991C-540
6	20	100.0	20	15	US-10-068-160-2
7	20	100.0	20	15	US-10-194-035-42
8	20	100.0	20	17	US-10-666-022-178
9	20	100.0	28	13	US-09-874-991C-517
10	20	100.0	28	13	US-09-874-991C-525
11	20	100.0	28	13	US-09-874-991C-529
12	20	100.0	28	13	US-09-874-991C-537
13	20	100.0	40	13	US-09-874-991C-548
14	18.4	92.0	20	13	US-09-874-991C-495

Sequence 499, App
Sequence 506, App
Sequence 510, App
Sequence 543, App
Sequence 37, Appl
Sequence 58, Appl
Sequence 101, App
Sequence 516, App
Sequence 526, App
Sequence 528, App
Sequence 532, App
Sequence 13, Appl
Sequence 2, Appl
Sequence 22, Appl
Sequence 454, App
Sequence 505, App
Sequence 538, App
Sequence 1, Appl
Sequence 5, Appl
Sequence 30, Appl
Sequence 41, Appl
Sequence 54, Appl
Sequence 61, Appl
Sequence 63, Appl
Sequence 32, Appl
Sequence 34, Appl
Sequence 37, Appl
Sequence 38, Appl
Sequence 43, Appl
Sequence 72, Appl

ALIGNMENTS

RESULT 1

US-09-874-991C-496
; Sequence 496, Application US/09874991C
; Publication No. US20040052763A1
; GENERAL INFORMATION:
; APPLICANT: MOND, JAMES J.
; APPLICANT: FLORA, MICHAEL
; APPLICANT: KLINMAN, DENNIS M.
; TITLE OF INVENTION: IMMUNOSTIMULATORY RNA/DNA HYBRID MOLECULES
; FILE REFERENCE: 07787.0042-0
; CURRENT APPLICATION NUMBER: US/09/874,991C
; CURRENT FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: 60/209,797
; PRIOR FILING DATE: 2000-06-07
; NUMBER OF SEQ ID NOS: 620
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 496
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic HDR
US-09-874-991C-496

Query Match 100.0%; Score 20; DB 13; Length 20;
Best Local Similarity 100.0%; Pred. No. 9.9;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTGCACCGGTGCAGGGGG 20
DB 1 GGTGCACCGGTGCAGGGGG 20

RESULT 2

US-09-874-991C-504
; Sequence 504, Application US/09874991C
; Publication No. US20040052763A1

/ GENERAL INFORMATION:
/ APPLICANT: MOND, JAMES J.
/ APPLICANT: FLORA, MICHAEL
/ APPLICANT: KLINMAN, DENNIS M.
/ TITLE OF INVENTION: IMMUNOSTIMULATORY RNA/DNA HYBRID MOLECULES
/ CURRENT APPLICATION NUMBER: US/09/874,991C
/ PRIOR FILING DATE: 2001-06-07
/ PRIOR APPLICATION NUMBER: 60/209,797
/ NUMBER OF SEQ ID NOS: 620
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 504
/ LENGTH: 20
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Synthetic HDR
US-09-874-991C-504

Query Match 100.0%; Score 20; DB 13; Length 20;
Best Local Similarity 100.0%; Pred. No. 9.9;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTGCACCGGTGCAGGGGG 20
Db 1 GGTGCACCGGTGCAGGGGG 20

RESULT 3
US-09-874-991C-507
/ Sequence 507, Application US/09874991C
/ Publication No. US20040052763A1
/ GENERAL INFORMATION:
/ APPLICANT: MOND, JAMES J.
/ APPLICANT: FLORA, MICHAEL
/ APPLICANT: KLINMAN, DENNIS M.
/ TITLE OF INVENTION: IMMUNOSTIMULATORY RNA/DNA HYBRID MOLECULES
/ FILE REFERENCE: 07787.0042-0
/ CURRENT APPLICATION NUMBER: US/09/874,991C
/ CURRENT FILING DATE: 2001-06-07
/ PRIOR APPLICATION NUMBER: 60/209,797
/ PRIOR FILING DATE: 2000-06-07
/ NUMBER OF SEQ ID NOS: 620
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 507
/ LENGTH: 20
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Synthetic HDR
US-09-874-991C-507

Query Match 100.0%; Score 20; DB 13; Length 20;
Best Local Similarity 100.0%; Pred. No. 9.9;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTGCACCGGTGCAGGGGG 20
Db 1 GGTGCACCGGTGCAGGGGG 20

RESULT 4
US-09-874-991C-514
/ Sequence 514, Application US/09874991C
/ Publication No. US20040052763A1
/ GENERAL INFORMATION:
/ APPLICANT: MOND, JAMES J.
/ APPLICANT: FLORA, MICHAEL
/ APPLICANT: KLINMAN, DENNIS M.
/ TITLE OF INVENTION: IMMUNOSTIMULATORY RNA/DNA HYBRID MOLECULES
/ FILE REFERENCE: 07787.0042-0
/ CURRENT APPLICATION NUMBER: US/09/874,991C

/ CURRENT FILING DATE: 2001-06-07
/ PRIOR APPLICATION NUMBER: 60/209,797
/ PRIOR FILING DATE: 2000-06-07
/ NUMBER OF SEQ ID NOS: 620
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 514
/ LENGTH: 20
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Synthetic HDR
US-09-874-991C-514

Query Match 100.0%; Score 20; DB 13; Length 20;
Best Local Similarity 100.0%; Pred. No. 9.9;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTGCACCGGTGCAGGGGG 20
Db 1 GGTGCACCGGTGCAGGGGG 20

RESULT 5
US-09-874-991C-540
/ Sequence 540, Application US/09874991C
/ Publication No. US20040052763A1
/ GENERAL INFORMATION:
/ APPLICANT: MOND, JAMES J.
/ APPLICANT: FLORA, MICHAEL
/ APPLICANT: KLINMAN, DENNIS M.
/ TITLE OF INVENTION: IMMUNOSTIMULATORY RNA/DNA HYBRID MOLECULES
/ FILE REFERENCE: 07787.0042-0
/ CURRENT APPLICATION NUMBER: US/09/874,991C
/ CURRENT FILING DATE: 2001-06-07
/ PRIOR APPLICATION NUMBER: 60/209,797
/ PRIOR FILING DATE: 2000-06-07
/ NUMBER OF SEQ ID NOS: 620
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 540
/ LENGTH: 20
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Synthetic HDR
US-09-874-991C-540

Query Match 100.0%; Score 20; DB 13; Length 20;
Best Local Similarity 100.0%; Pred. No. 9.9;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTGCACCGGTGCAGGGGG 20
Db 1 GGTGCACCGGTGCAGGGGG 20

RESULT 6
US-10-068-160-2
/ Sequence 2, Application US/10068160
/ Publication No. US200306040A1
/ GENERAL INFORMATION:
/ APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA, REPRESENTED BY THE
/ APPLICANT: SECRETARY, DEPARTMENT OF HEALTH AND HUMAN SERVICES
/ APPLICANT: KLINMAN, Dennis
/ APPLICANT: ISHII, Ken
/ APPLICANT: VERTHELYI, Daniela
/ TITLE OF INVENTION: OLIGODEOXYNUCLEOTIDE AND ITS USE TO INDUCE AN IMMUNE RESPONSE
/ FILE REFERENCE: 4239-61999
/ CURRENT APPLICATION NUMBER: US/10/068,160
/ CURRENT FILING DATE: 2002-02-06
/ PRIOR APPLICATION NUMBER: 60/128,898
/ PRIOR FILING DATE: 1999-04-12
/ NUMBER OF SEQ ID NOS: 120
/ SOFTWARE: PatentIn version 3.1

; SEQ ID NO 2
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide
US-10-068-160-2

Query Match 100.0%; Score 20; DB 15; Length 20;
Best Local Similarity 100.0%; Pred. No. 9.9;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTGCACCGGTGCAGGGGG 20
|||
DB 1 GGTGCACCGGTGCAGGGGG 20

RESULT 7

US-10-194-035-42
; Sequence 42, Application US/10194035
; Publication No. US20030144229A1
; GENERAL INFORMATION:
; APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS REPRESENTED BY THE
; APPLICANT: SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES
; APPLICANT: KLIMAN, Dennis
; APPLICANT: ISHII, Ken
; APPLICANT: VERHELJI, Daniela
; TITLE OF INVENTION: OLIGODEOXYNUCLEOTIDE AND ITS USE TO INDUCE AN IMMUNE RESPONSE
; FILE REFERENCE: 4239-63317
; CURRENT APPLICATION NUMBER: US/10/194,035
; PRIOR FILING DATE: 2002-07-12
; PRIOR APPLICATION NUMBER: PCT/US01/01122
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: US 60/176,115
; PRIOR FILING DATE: 2000-01-14
; NUMBER OF SEQ ID NOS: 119
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 42
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
US-10-194-035-42

Query Match 100.0%; Score 20; DB 15; Length 20;
Best Local Similarity 100.0%; Pred. No. 9.9;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTGCACCGGTGCAGGGGG 20
|||
DB 1 GGTGCACCGGTGCAGGGGG 20

RESULT 8

US-10-666-022-178
; Sequence 178, Application US/10666022
; Publication No. US20040105872A1
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America, as represented by the
; APPLICANT: Secretary of the Department of Health and Human Services
; APPLICANT: Kliman, Dennis M.
; APPLICANT: Verchelyi, Daniela
; TITLE OF INVENTION: METHOD OF TREATING AND PREVENTING INFECTIONS IN IMMUNOCOMPROMISED
; FILE REFERENCE: 4239-66899
; CURRENT APPLICATION NUMBER: US/10/666,022
; CURRENT FILING DATE: 2003-09-17
; PRIOR APPLICATION NUMBER: US 60/411,944
; PRIOR FILING DATE: 2002-09-18
; NUMBER OF SEQ ID NOS: 181
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 178

; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic
US-10-666-022-178

Query Match 100.0%; Score 20; DB 17; Length 20;
Best Local Similarity 100.0%; Pred. No. 9.9;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTGCACCGGTGCAGGGGG 20
|||
DB 1 GGTGCACCGGTGCAGGGGG 20

RESULT 9

US-09-874-991C-517
; Sequence 517, Application US/09874991C
; Publication No. US20040052763A1
; GENERAL INFORMATION:
; APPLICANT: MOND, JAMES J.
; APPLICANT: FLORA, MICHAEL
; APPLICANT: KLINMAN, DENNIS M.
; TITLE OF INVENTION: IMMUNOSTIMULATORY RNA/DNA HYBRID MOLECULES
; FILE REFERENCE: 07787.0042-0
; CURRENT APPLICATION NUMBER: US/09/874,991C
; CURRENT FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: 60/209,797
; PRIOR FILING DATE: 2000-06-07
; NUMBER OF SEQ ID NOS: 620
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 517
; LENGTH: 28
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic HDR
US-09-874-991C-517

Query Match 100.0%; Score 20; DB 13; Length 28;
Best Local Similarity 100.0%; Pred. No. 9.5;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTGCACCGGTGCAGGGGG 20
|||
DB 1 GGTGCACCGGTGCAGGGGG 20

RESULT 10

US-09-874-991C-525
; Sequence 525, Application US/09874991C
; Publication No. US20040052763A1
; GENERAL INFORMATION:
; APPLICANT: MOND, JAMES J.
; APPLICANT: FLORA, MICHAEL
; APPLICANT: KLINMAN, DENNIS M.
; TITLE OF INVENTION: IMMUNOSTIMULATORY RNA/DNA HYBRID MOLECULES
; FILE REFERENCE: 07787.0042-0
; CURRENT APPLICATION NUMBER: US/09/874,991C
; CURRENT FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: 60/209,797
; PRIOR FILING DATE: 2000-06-07
; NUMBER OF SEQ ID NOS: 620
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 525
; LENGTH: 28
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic HDR
US-09-874-991C-525

Query Match 100.0%; Score 20; DB 13; Length 28;
Best Local Similarity 100.0%; Pred. No. 9.5;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTGCACCGGTGCAGGGGG 20
DB 1 GGTGCACCGGTGCAGGGGG 20

RESULT 11

US-09-874-991C-529
; Sequence 529, Application US/09874991C
; Publication No. US20040052763A1
; GENERAL INFORMATION:
; APPLICANT: MOND, JAMES J.
; APPLICANT: FLORA, MICHAEL
; APPLICANT: KLINMAN, DENNIS M.
; TITLE OF INVENTION: IMMUNOSTIMULATORY RNA/DNA HYBRID MOLECULES
; FILE REFERENCE: 07787.0042-0
; CURRENT APPLICATION NUMBER: US/09/874,991C
; PRIOR FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: 60/209,797
; PRIOR FILING DATE: 2000-06-07
; NUMBER OF SEQ ID NOS: 620
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 529
; LENGTH: 28
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic HDR

US-09-874-991C-529
Query Match 100.0%; Score 20; DB 13; Length 28;
Best Local Similarity 100.0%; Pred. No. 9.5;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTGCACCGGTGCAGGGGG 20
DB 9 GGTGCACCGGTGCAGGGGG 28

RESULT 12

US-09-874-991C-537
; Sequence 537, Application US/09874991C
; Publication No. US20040052763A1
; GENERAL INFORMATION:
; APPLICANT: MOND, JAMES J.
; APPLICANT: FLORA, MICHAEL
; APPLICANT: KLINMAN, DENNIS M.
; TITLE OF INVENTION: IMMUNOSTIMULATORY RNA/DNA HYBRID MOLECULES
; FILE REFERENCE: 07787.0042-0
; CURRENT APPLICATION NUMBER: US/09/874,991C
; CURRENT FILING DATE: 2001-06-07
; PRIOR FILING DATE: 2000-06-07
; NUMBER OF SEQ ID NOS: 620
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 537
; LENGTH: 28
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic HDR

US-09-874-991C-537
Query Match 100.0%; Score 20; DB 13; Length 28;
Best Local Similarity 100.0%; Pred. No. 9.5;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTGCACCGGTGCAGGGGG 20
DB 9 GGTGCACCGGTGCAGGGGG 28

Query Match 100.0%; Score 20; DB 13; Length 28;
Best Local Similarity 100.0%; Pred. No. 9.5;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTGCACCGGTGCAGGGGG 20
DB 1 GGTGCACCGGTGCAGGGGG 20

RESULT 11

US-09-874-991C-529
; Sequence 529, Application US/09874991C
; Publication No. US20040052763A1
; GENERAL INFORMATION:
; APPLICANT: MOND, JAMES J.
; APPLICANT: FLORA, MICHAEL
; APPLICANT: KLINMAN, DENNIS M.
; TITLE OF INVENTION: IMMUNOSTIMULATORY RNA/DNA HYBRID MOLECULES
; FILE REFERENCE: 07787.0042-0
; CURRENT APPLICATION NUMBER: US/09/874,991C
; PRIOR FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: 60/209,797
; PRIOR FILING DATE: 2000-06-07
; NUMBER OF SEQ ID NOS: 620
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 529
; LENGTH: 28
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic HDR

US-09-874-991C-529
Query Match 100.0%; Score 20; DB 13; Length 28;
Best Local Similarity 100.0%; Pred. No. 9.5;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTGCACCGGTGCAGGGGG 20
DB 9 GGTGCACCGGTGCAGGGGG 28

RESULT 12

US-09-874-991C-537
; Sequence 537, Application US/09874991C
; Publication No. US20040052763A1
; GENERAL INFORMATION:
; APPLICANT: MOND, JAMES J.
; APPLICANT: FLORA, MICHAEL
; APPLICANT: KLINMAN, DENNIS M.
; TITLE OF INVENTION: IMMUNOSTIMULATORY RNA/DNA HYBRID MOLECULES
; FILE REFERENCE: 07787.0042-0
; CURRENT APPLICATION NUMBER: US/09/874,991C
; CURRENT FILING DATE: 2001-06-07
; PRIOR FILING DATE: 2000-06-07
; NUMBER OF SEQ ID NOS: 620
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 537
; LENGTH: 28
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic HDR

US-09-874-991C-537
Query Match 100.0%; Score 20; DB 13; Length 28;
Best Local Similarity 100.0%; Pred. No. 9.5;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTGCACCGGTGCAGGGGG 20
DB 9 GGTGCACCGGTGCAGGGGG 28

RESULT 13

US-09-874-991C-548
; Sequence 548, Application US/09874991C
; Publication No. US20040052763A1
; GENERAL INFORMATION:
; APPLICANT: MOND, JAMES J.
; APPLICANT: FLORA, MICHAEL
; APPLICANT: KLINMAN, DENNIS M.
; TITLE OF INVENTION: IMMUNOSTIMULATORY RNA/DNA HYBRID MOLECULES
; FILE REFERENCE: 07787.0042-0
; CURRENT APPLICATION NUMBER: US/09/874,991C
; CURRENT FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: 60/209,797
; PRIOR FILING DATE: 2000-06-07
; NUMBER OF SEQ ID NOS: 620
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 548
; LENGTH: 40
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic HDR

US-09-874-991C-548
Query Match 100.0%; Score 20; DB 13; Length 40;
Best Local Similarity 100.0%; Pred. No. 9;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTGCACCGGTGCAGGGGG 20
DB 14 GGTGCACCGGTGCAGGGGG 33

RESULT 14

US-09-874-991C-495
; Sequence 495, Application US/09874991C
; Publication No. US20040052763A1
; GENERAL INFORMATION:
; APPLICANT: MOND, JAMES J.
; APPLICANT: FLORA, MICHAEL
; APPLICANT: KLINMAN, DENNIS M.
; TITLE OF INVENTION: IMMUNOSTIMULATORY RNA/DNA HYBRID MOLECULES
; FILE REFERENCE: 07787.0042-0
; CURRENT APPLICATION NUMBER: US/09/874,991C
; CURRENT FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: 60/209,797
; PRIOR FILING DATE: 2000-06-07
; NUMBER OF SEQ ID NOS: 620
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 495
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic HDR

US-09-874-991C-495
Query Match 92.0%; Score 18.4; DB 13; Length 20;
Best Local Similarity 95.0%; Pred. No. 53;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTGCACCGGTGCAGGGGG 20
DB 1 GGTGCACCGGTGCAGGGGG 20

RESULT 15

US-09-874-991C-499
; Sequence 499, Application US/09874991C
; Publication No. US20040052763A1
; GENERAL INFORMATION:

```

; APPLICANT: MOND, JAMES J.
; APPLICANT: FLORA, MICHAEL
; APPLICANT: KLINMAN, DENNIS M.
; TITLE OF INVENTION: IMMUNOSTIMULATORY RNA/DNA HYBRID MOLECULES
; FILE REFERENCE: 0787.0042-0
; CURRENT APPLICATION NUMBER: US/09/874,991C
; CURRENT FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: 60/209,797
; PRIOR FILING DATE: 2000-06-07
; NUMBER OF SEQ ID NOS: 620
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 499
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic HDR
US-09-874-991C-499

```

```

Query Match      92.0%; Score 18.4; DB 13; Length 20;
Best Local Similarity 95.0%; Pred. No. 53;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

QY      1 GGTGCACCGGTGCAGGGGG 20
        |||||
Db       1 GGTGCACCGGTGCAGGGGG 20

```

Search completed: July 2, 2004, 13:58:23
Job time : 154.146 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 2, 2004, 07:38:45 ; Search time 1497.8 Seconds
(without alignments)
398.746 Million cell updates/sec

Title: US-10-068-160-2
Perfect score: 20
Sequence: 1 ggtgaccggtgcagggggg 20

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

- EST.*
- 1: em_estbta.*
 - 2: em_esthum.*
 - 3: em_estin.*
 - 4: em_estmu.*
 - 5: em_estov.*
 - 6: em_estpl.*
 - 7: em_estro.*
 - 8: em_hrc.*
 - 9: gb_est1.*
 - 10: gb_est2.*
 - 11: gb_hrc.*
 - 12: gb_est3.*
 - 13: gb_est4.*
 - 14: gb_est5.*
 - 15: em_estfun.*
 - 16: em_estom.*
 - 17: em_gss_hum.*
 - 18: em_gss_inv.*
 - 19: em_gss_pln.*
 - 20: em_gss_vrt.*
 - 21: em_gss_fun.*
 - 22: em_gss_fam.*
 - 23: em_gss_mus.*
 - 24: em_gss_pro.*
 - 25: em_gss_rod.*
 - 26: em_gss_phg.*
 - 27: em_gss_vri.*
 - 28: gb_gss1.*
 - 29: gb_gss2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
c 1	18.4	92.0	339	14	CB076094
c 2	18.4	92.0	440	14	CB087231
c 3	18.4	92.0	509	14	CB087214
c 4	18.4	92.0	598	14	CB087525

5	18.4	92.0	340	29	CG271799
6	17.4	87.0	610	29	CG692380
7	17.4	87.0	779	28	CC109078
8	17.4	87.0	799	28	CC133230
9	17.4	87.0	1005	29	CNS04021
10	17.4	87.0	1200	13	EX426076
11	17.4	87.0	1214	13	BO898390
12	17.4	85.0	354	9	AV393217
13	16.8	84.0	432	10	BE388878
14	16.8	84.0	237	28	AZ492326
15	16.8	84.0	275	10	BB496626
16	16.8	84.0	289	9	AV219401
17	16.8	84.0	294	13	BY103614
18	16.8	84.0	323	9	AL898002
19	16.8	84.0	383	28	BZ782509
20	16.8	84.0	402	29	CE182406
21	16.8	84.0	421	9	AL897989
22	16.8	84.0	430	28	BZ422920
23	16.8	84.0	513	29	CE284352
24	16.8	84.0	562	9	AI370313
25	16.8	84.0	615	12	BJ252893
26	16.8	84.0	618	10	BE973745
27	16.8	84.0	619	14	CD771763
28	16.8	84.0	630	28	BZ335826
29	16.8	84.0	631	12	BJ244833
30	16.8	84.0	646	13	CA100132
31	16.8	84.0	646	29	CB419868
32	16.8	84.0	671	12	BJ229325
33	16.8	84.0	677	28	BE886902
34	16.8	84.0	684	12	BE624520
35	16.8	84.0	685	12	BE634520
36	16.8	84.0	692	12	BE620160
37	16.8	84.0	697	12	BZ250701
38	16.8	84.0	708	12	BE621890
39	16.8	84.0	740	12	BE617983
40	16.8	84.0	748	28	BZ863203
41	16.8	84.0	768	12	BE674536
42	16.8	84.0	769	14	CF765888
43	16.8	84.0	782	10	BF582545
44	16.8	84.0	811	29	CNS041X0
45	16.8	84.0	815	12	BI334719

ALIGNMENTS

RESULT 1	CB076094/c
LOCUS	339 bp mRNA linear EST 24-JAN-2003
DEFINITION	h37c06.g1 Hedyotis terminalis flower - Stage 2 (NYBG) Hedyotis terminalis cDNA clone h37c06, mRNA sequence.
ACCESSION	CB076094
VERSION	EST.
KEYWORDS	CB076094.1 GI:27889531
SOURCE	Hedyotis terminalis
ORGANISM	Hedyotis terminalis
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons, core eudicots; asterids; lamids; Gentianales; Rubiaceae; Rubioideae; Spermacoceae; Hedyotis.
AUTHORS	Levesque,M.P., Twigg,R.W., Motley,T., Katari,M.S., Dedhia,N.N., O'Shaughnessy,A.L., Ballija,V., Martienssen,R.A., McCombie,R.W., Benfey,P. and Stevenson,D.
TITLE	Expressed tag sequences from Hedyotis terminalis flower - Stage 2 (NYBG)
JOURNAL	Unpublished (2003)
COMMENT	Contact: W. Richard McCombie Lita Annenberg Hazen Genome Sequencing Center Cold Spring Harbor Laboratory PO Box 100, Cold Spring Harbor, NY 11724, USA Tel: 516 367 8884 Fax: 516 367 8874

Email: mccombe@cshl.org
 Plate: hf37 row: c column: 06
 Seq primer: -21M13UnivRev
 High quality sequence stop: 339.
 Location/Qualifiers

FEATURES

source
 1..339
 /organism="Hedyotis terminalis"
 /mol_type="mRNA"
 /db_xref="taxon:219667"
 /clone="hf37c06"
 /dev_stage="pre-anthesis; Stage 2"
 /clone_lib="Hedyotis terminalis flower - Stage 2 (NYBG)"
 /note="Organ: flower; Vector: pBK-CMV; Site: 1: XhoI;
 Site 2: Eco RI; Date: Completed 12/18/01. Submitted to
 CSHL 12/21/01 Library: Stratagene ZAP Express cDNA
 Synthesis Kit. The library was size-fractionated to enrich
 for large inserts. Sample: collected on the island of
 Hawaii, Hawaii; NYBG herbarium voucher TM2562"

ORIGIN

Query Match 92.0%; Score 18.4; DB 14; Length 339;
 Best Local Similarity 95.0%; Pred. No. 3.2e+03;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGTGCACCGGTGCAGGGGG 20
 |||||
 Db 99 GGTGCACCTGTCAGGGGG 80

RESULT 2

CB087291/c
 LOCUS 440 bp mRNA linear EST 27-JAN-2003
 DEFINITION hj98g11.g1 Hedyotis centranthoides flower - Stage 2 (NYBG) Hedyotis
 centranthoides cDNA clone hj98g11, mRNA sequence.

ACCESSION

CB087291
 VERSION GI:27911483

KEYWORDS

EST.

SOURCE

Hedyotis centranthoides
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 asterids; lamids; Gentianales; Rubiaceae; Rubioideae;
 Spermacoceae; Hedyotis.

REFERENCE

1 (bases 1 to 440)

AUTHORS

Levesque, M.P., Twigg, R.W., Motley, T., Katari, M.S., Dedhia, N.N.,
 O'Shaughnessy, A.L., Ballia, V., Martienssen, R.A., McCombie, R.W.,
 Benfey, P. and Stevenson, D.

TITLE

Expressed tag sequences from Hedyotis centranthoides flower - Stage
 2 (NYBG)

JOURNAL

Unpublished (2003)
 Contact: W. Richard McCombie
 Lita Annenberg Hazen Genome Sequencing Center
 Cold Spring Harbor Laboratory
 PO Box 100, Cold Spring Harbor, NY 11724, USA

COMMENT

Tel: 516 367 8884
 Fax: 516 367 8874
 Email: mccombe@cshl.org
 Plate: hf37 row: c column: 11
 Seq primer: -21M13UnivRev
 High quality sequence stop: 440.

FEATURES

source
 Location/Qualifiers
 1..440
 /organism="Hedyotis centranthoides"
 /mol_type="mRNA"
 /db_xref="taxon:219666"
 /clone="hj98g11"
 /dev_stage="pre-anthesis; Stage 2"
 /clone_lib="Hedyotis centranthoides flower - Stage 2
 (NYBG)"
 /note="Organ: flower; Vector: pBK-CMV; Site: 1: XhoI;
 Site 2: Eco RI; Date: Completed 12/18/01. Submitted to
 CSHL 12/21/01 Library: Stratagene ZAP Express cDNA
 Synthesis Kit. The library was size-fractionated to enrich
 for large inserts. Sample: collected on the island of
 Hawaii, Hawaii; NYBG herbarium voucher TM2563"

for large inserts. Sample: collected on the island of
 Hawaii, Hawaii; NYBG herbarium voucher TM2563"

ORIGIN

Query Match 92.0%; Score 18.4; DB 14; Length 440;
 Best Local Similarity 95.0%; Pred. No. 3.3e+03;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGTGCACCGGTGCAGGGGG 20
 |||||
 Db 131 GGTGCACCTGTCAGGGGG 112

RESULT 3

CB087214/c

LOCUS

DEFINITION

CB087214

ACCESSION

CB087214

VERSION

EST.

SOURCE

Hedyotis centranthoides

ORGANISM

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 asterids; lamids; Gentianales; Rubiaceae; Rubioideae;
 Spermacoceae; Hedyotis.

REFERENCE

1 (bases 1 to 509)

AUTHORS

Levesque, M.P., Twigg, R.W., Motley, T., Katari, M.S., Dedhia, N.N.,
 O'Shaughnessy, A.L., Ballia, V., Martienssen, R.A., McCombie, R.W.,
 Benfey, P. and Stevenson, D.

TITLE

Expressed tag sequences from Hedyotis centranthoides flower - Stage
 2 (NYBG)

JOURNAL

Unpublished (2003)

COMMENT

Contact: W. Richard McCombie
 Lita Annenberg Hazen Genome Sequencing Center
 Cold Spring Harbor Laboratory
 PO Box 100, Cold Spring Harbor, NY 11724, USA

KEYWORDS

Tel: 516 367 8884
 Fax: 516 367 8874
 Email: mccombe@cshl.org
 Plate: hf37 row: e column: 04
 Seq primer: -21M13UnivRev
 High quality sequence stop: 509.

FEATURES

Location/Qualifiers
 1..509
 /organism="Hedyotis centranthoides"
 /mol_type="mRNA"
 /db_xref="taxon:219666"
 /clone="hj97e04"
 /dev_stage="pre-anthesis; Stage 2"
 /clone_lib="Hedyotis centranthoides flower - Stage 2
 (NYBG)"
 /note="Organ: flower; Vector: pBK-CMV; Site: 1: XhoI;
 Site 2: Eco RI; Date: Completed 12/18/01. Submitted to
 CSHL 12/21/01 Library: Stratagene ZAP Express cDNA
 Synthesis Kit. The library was size-fractionated to enrich
 for large inserts. Sample: collected on the island of
 Hawaii, Hawaii; NYBG herbarium voucher TM2563"

ORIGIN

Query Match 92.0%; Score 18.4; DB 14; Length 509;
 Best Local Similarity 95.0%; Pred. No. 3.3e+03;
 Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGTGCACCGGTGCAGGGGG 20
 |||||
 Db 146 GGTGCACCTGTCAGGGGG 127

RESULT 4

CB087525/c

LOCUS

598 bp mRNA linear EST 27-JAN-2003

```

DEFINITION   hk03f05_g1 Hedyotis centranthoides flower - Stage 2 (NYBG) Hedyotis
              centranthoides cDNA clone hk03f05, mRNA sequence.
ACCESSION    CB087525
VERSION      CB087525.1 GI:27911717
KEYWORDS     EST.
SOURCE       Hedyotis centranthoides
              Hedyotis centranthoides
              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
              Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
              asterids; lamids; Gentianales; Rubiaceae; Rubioideae;
              Spermacoceae; Hedyotis.
REFERENCE    1 (bases 1 to 598)
AUTHORS      Levesque,M.P., Twigg,R.W., Motley,T., Katari,M.S., Dedhia,N.N.,
              O'Shaughnessy,A.L., Ballija,V., Martienssen,R.A., McCombie,R.W.,
              Benfey,P. and Stevenson,D.
              Expressed tag sequences from Hedyotis centranthoides flower - Stage
              2 (NYBG)
JOURNAL      Unpublished (2003)
COMMENT      Contact: W. Richard McCombie
              Lita Annenberg Hazen Genome Sequencing Center
              Cold Spring Harbor Laboratory
              PO Box 100, Cold Spring Harbor, NY 11724, USA
              Tel: 516 367 8884
              Fax: 516 367 8874
              Email: mcombie@cshl.org
              Plate: hk03 row: f column: 05
              Seq primer: -21M13UnivRev
              High quality sequence stop: 598.
              Location/Qualifiers
FEATURES     source
              1..598
               /organism="Hedyotis centranthoides"
               /mol_type="mRNA"
               /db_xref="taxon:219666"
               /clone="hk03f05"
               /dev_stage="pre-anthesis; Stage 2"
               /clone_lib="Hedyotis centranthoides flower - Stage 2
               (NYBG)"
               /note="Organ: flower; Vector: pSK-CMV; Site:1: XhoI;
               Site:2: Eco RI; Date: Completed 12/18/01. Submitted to
               CSHL 12/21/01 Library: Stratagene ZAP Express cDNA
               Synthesis kit. The library was size-fractionated to enrich
               for large inserts. Sample: collected on the island of
               Hawaii, Hawaii; NYBG herbarium voucher TW2563"
ORIGIN
Query Match          92.0%; Score 18.4; DB 14; Length 598;
Best Local Similarity 95.0%; Pred. No. 3.4e+03;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTGCACCGGTGCAGGGGG 20
    |||||
DB 148 GGTGCACGTGTGCAGGGGG 129

RESULT 5
CG271799
LOCUS       CG00D226TV_ZM_0.7_1.5_KB_Zea_mays_genomic_clone_ZMMBMA0696F04,
DEFINITION  genomic survey sequence.
ACCESSION   CG271799
VERSION     CG271799.1 GI:34183940
KEYWORDS    GSS.
SOURCE      Zea mays
              Zea mays
              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
              Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
              clade; Panicoideae; Andropogoneae; Zea.
REFERENCE    1 (bases 1 to 840)
AUTHORS      Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
              Resnick,A., Fraser,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T.,
              Cicek,R.W., Nurnberg,A., Robbins,D. and Lakey,N.
              Consortium for Maize Genomics
              Unpublished (2002)
              Location/Qualifiers
              1..840
               /organism="Zea mays subsp. mays"
               /mol_type="genomic DNA"
               /cultivar="B73"
               /sub_species="mays"
               /db_xref="taxon:4578"
               /clone="ZMMBMA0696F04"
               /lab_host="DH10B"
               /clone_lib="ZMMBMA0696F04"
               /note="vector: pBESK-; Site 1: HindIII; Site 2:
               methylation filtered genomic DNA library"

QY 1 GGTGCACCGGTGCAGGGGG 20
    |||||
DB 499 GGTGCACCGGTGCAGGGGG 518

RESULT 6
CG692380
LOCUS       CG692380
DEFINITION  ZMMBMA0292G11.f_ZMMBMA0292G11_5', genomic survey sequence.
ACCESSION   CG692380
VERSION     CG692380.1 GI:37656062
KEYWORDS    GSS.
SOURCE      Zea mays subsp. mays (maize)
              Zea mays subsp. mays
              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
              Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
              clade; Panicoideae; Andropogoneae; Zea.
REFERENCE    1 (bases 1 to 610)
AUTHORS      Yu,Y., Kim,H.R., Hatfield,J., Soderlund,C., Sharti,A.K., Messing,J.
              and Wing,R.
              Sequencing of the maize genome
              Unpublished (2003)
              Contact: Rod Wing
              Arizona Genomics Institute
              University of Arizona
              Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ
              85721-0088, USA
              Tel: 520 626 3967
              Fax: 520 621 9288
              Email: http://genome.arizona.edu
              PCR Primers
              FORWARD: T7
              BACKWARD: M13r
              Plate: 0292 row: G column: 11
              Seq primer: T7
              Class: BAC ends.
              Location/Qualifiers
              1..610
               /organism="Zea mays subsp. mays"
               /mol_type="genomic DNA"
               /cultivar="B73"
               /sub_species="mays"
               /db_xref="taxon:4578"
               /clone="ZMMBMA0292G11"
               /lab_host="DH10B"
               /clone_lib="ZMMBMA0292G11"
               /note="vector: pBeloBAC11; Site_1: HindIII; Site_2:

```

```

COMMENT      Other_GSSs: OG0D226TH
              TIGR
              9712 Medical Center Drive, Rockville, MD 20850, USA
              Tel: 301-838-5843
              Fax: 301-838-0208
              Email: whitelaw@tigr.org
              Seq primer: T7
              Class: sheared ends.
              Location/Qualifiers
              1..840
               /organism="Zea mays"
               /mol_type="genomic DNA"
               /strain="B73"
               /db_xref="taxon:4577"
               /clone="ZMMBMA0696F04"
               /clone_lib="ZM_0.7_1.5_KB"
               /note="vector: pBESK-; Site 1: HindIII; 0.7-1.5 kb
               methylation filtered genomic DNA library"

ORIGIN
Query Match          92.0%; Score 18.4; DB 29; Length 840;
Best Local Similarity 95.0%; Pred. No. 3.5e+03;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGTGCACCGGTGCAGGGGG 20
    |||||
DB 499 GGTGCACCGGTGCAGGGGG 518

RESULT 6
CG692380
LOCUS       CG692380
DEFINITION  ZMMBMA0292G11.f_ZMMBMA0292G11_5', genomic survey sequence.
ACCESSION   CG692380
VERSION     CG692380.1 GI:37656062
KEYWORDS    GSS.
SOURCE      Zea mays subsp. mays (maize)
              Zea mays subsp. mays
              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
              Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
              clade; Panicoideae; Andropogoneae; Zea.
REFERENCE    1 (bases 1 to 610)
AUTHORS      Yu,Y., Kim,H.R., Hatfield,J., Soderlund,C., Sharti,A.K., Messing,J.
              and Wing,R.
              Sequencing of the maize genome
              Unpublished (2003)
              Contact: Rod Wing
              Arizona Genomics Institute
              University of Arizona
              Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ
              85721-0088, USA
              Tel: 520 626 3967
              Fax: 520 621 9288
              Email: http://genome.arizona.edu
              PCR Primers
              FORWARD: T7
              BACKWARD: M13r
              Plate: 0292 row: G column: 11
              Seq primer: T7
              Class: BAC ends.
              Location/Qualifiers
              1..610
               /organism="Zea mays subsp. mays"
               /mol_type="genomic DNA"
               /cultivar="B73"
               /sub_species="mays"
               /db_xref="taxon:4578"
               /clone="ZMMBMA0292G11"
               /lab_host="DH10B"
               /clone_lib="ZMMBMA0292G11"
               /note="vector: pBeloBAC11; Site_1: HindIII; Site_2:

```

HindIII; Zea mays L. ssp. mays"

ORIGIN

Query Match 87.0%; Score 17.4; DB 29; Length 610;
 Best Local Similarity 94.7%; Pred. No. 8.3e+03;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GTGCACCGGTGCAGGGGG 20
 |||||
 Db 524 GTGCACCGGTTCAGGGGG 542

RESULT 7

CC109078/c
 LOCUS ND1.50B23.T7 Notre Dame Liverpool Aedes aegypti genomic clone linear GSS 16-APR-2003
 DEFINITION ND1.50B23, genomic survey sequence.

ACCESSION CC109078

VERSION CC109078.1 GI:29978133

KEYWORDS Aedes aegypti (yellow fever mosquito)

SOURCE Aedes aegypti

ORGANISM Aedes aegypti

REFERENCE 1 (bases 1 to 779)
 Loftus, B., Shetty, J., Knudson, D. and Severson, D.
 BAC end sequencing of Aedes aegypti

AUTHORS

TITLE

JOURNAL

COMMENT

Other GSSs: ND1.50B23.SP6

Contact: Brendan Loftus

Department of Eukaryotic Genomics

TIGR

9712 Medical Center Drive, Rockville, MD 20850, USA

Tel: 301-838-3543

Fax: 301-838-0208

Email: enta@tigr.org

Library was provided by David Severson

Seq primer: T7

Class: BAC ends.

FEATURES

source

1..779

/organism="Aedes aegypti"

/mol_type="genomic DNA"

/strain="liverpool"

/db_xref="taxon:7159"

/clone="ND1.50B23"

/clone_lib="Notre Dame Liverpool"

/notes="Vector: pECBAC1; Site_1: Hind III; The library was

prepared from whole body tissue of newly hatched L1 larvae

by David Severson at the University of Notre Dame and

Hongbin Zhang"

Query Match 87.0%; Score 17.4; DB 28; Length 779;

Best Local Similarity 94.7%; Pred. No. 8.5e+03;

Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GTGCACCGGTGCAGGGGG 20

|||||

Db 307 GTGCACCGGTTCAGGGGG 289

RESULT 8

CC133230/c

LOCUS ND1.50B22.T7 Notre Dame Liverpool Aedes aegypti genomic clone linear GSS 16-APR-2003

DEFINITION ND1.50B22, genomic survey sequence.

ACCESSION CC133230

VERSION CC133230.1 GI:30002285

KEYWORDS Aedes aegypti (yellow fever mosquito)

SOURCE Aedes aegypti

ORGANISM Aedes aegypti

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Aedes;
 Stegomyia.

REFERENCE

1 (bases 1 to 799)

AUTHORS

TITLE

JOURNAL

COMMENT

Other GSSs: ND1.50B22.SP6

Contact: Brendan Loftus

Department of Eukaryotic Genomics

TIGR

9712 Medical Center Drive, Rockville, MD 20850, USA

Tel: 301-838-3543

Fax: 301-838-0208

Email: enta@tigr.org

Library was provided by David Severson

Seq primer: T7

Class: BAC ends.

FEATURES

source

1..799

/organism="Aedes aegypti"

/mol_type="genomic DNA"

/strain="liverpool"

/db_xref="taxon:7159"

/clone="ND1.50B22"

/clone_lib="Notre Dame Liverpool"

/notes="Vector: pECBAC1; Site_1: Hind III; The library was

prepared from whole body tissue of newly hatched L1 larvae

by David Severson at the University of Notre Dame and

Hongbin Zhang"

ORIGIN

Query Match

Best Local Similarity

Matches

Conservative

Mismatches

Indels

Gaps

0;

QY 2 GTGCACCGGTGCAGGGGG 20

|||||

Db 307 GTGCACCGGTTCAGGGGG 289

RESULT 9

CNS04021

LOCUS

DEFINITION

Tetraodon nigroviridis genome survey sequence PUC-Ori end of clone

073018 of library G from Tetraodon nigroviridis, genomic survey

sequence.

ACCESSION

AL269542

VERSION

AL269542.1 GI:7991434

KEYWORDS

GSS; genome survey sequence.

SOURCE

Tetraodon nigroviridis

ORGANISM

Tetraodon nigroviridis

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;

Acanthomorpha; Acanthopterygii; Percomorphia; Tetraodontiformes;

Tetraodontidae; Tetraodontidae; Tetraodon.

REFERENCE

1

AUTHORS

Roest Crolius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C.,

Bernot, A., Fizes, C., Wincker, P., Brottier, P., Quetier, F.,

Saurin, W. and Weissenbach, J.

Estimate of human gene number provided by genome-wide analysis

using Tetraodon nigroviridis DNA sequence

Nat. Genet. 25 (2), 235-238 (2000)

20296633

10835645

2

AUTHORS

Roest Crolius, H., Jaillon, O., Dasilva, C., Ozouf-Costaz, C.,

Fizes, C., Fischer, C., Bouneau, L., Billault, A., Quetier, F.,

Saurin, W., Bernot, A. and Weissenbach, J.

Characterization and repeat analysis of the compact genome of the

freshwater pufferfish Tetraodon nigroviridis

Genome Res. 10 (7), 939-949 (2000)

20359837

PUBMED 10899143
 REFERENCE 3 (bases 1 to 1005)
 GENOSCOPE Genoscope.
 AUTHORS Direct Submission
 TITLE Submitted (12-APR-2000) Genoscope - Centre National de Sequencage :
 JOURNAL BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
 - Web : www.genoscope.cns.fr)
 COMMENT This sequence is a single read and was generated as part of a large
 scale clone-end sequencing project of the Tetraodon nigroviridis
 genome. For more information, please take a look at
 http://www.genoscope.cns.fr/tetraodon.

FEATURES

source
 Location/Qualifiers
 1..1005
 /organism="Tetraodon nigroviridis"
 /mol_type="genomic DNA"
 /db_xref="taxon:9983"
 /clone="073018"
 /clone_lib="G"
 /note="Genoscope sequence ID : COBG073BH09SP1-end :
 PUC-Ori"

ORIGIN

Query Match 87.0%; Score 17.4; DB 29; Length 1005;
 Best Local Similarity 94.7%; Pred. No. 8.7e+03;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 2 GTGCACCGGTGCAGGCGG 20
 |||||
 Db 84 GTGCTCGGTGCAGGCGG 102
 |||||

RESULT 10

EX426076 1200 bp mRNA linear EST 15-MAY-2003
 LOCUS BX426076 Homo sapiens FETAL BRAIN Homo sapiens cDNA clone
 DEFINITION CS0DF009YC20 5-PRIME, mRNA sequence.
 ACCESSION BX426076
 VERSION BX426076.1 GI:30774523
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 1200)
 AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
 JOURNAL Full-length cDNA libraries and normalization
 COMMENT Unpublished (2001)
 Contact: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 EVRY cedex - France
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
 Library was constructed by Life Technologies, a division of
 Invitrogen. This sequence belongs to sequence cluster 1373.1 For
 more information about this cluster, see
 http://www.genoscope.cns.fr/
 cgi-bin/cluster.cgi?seq=CS0AAW152A08QP1&cluster=1373.1. Contact :
 Feng Liang Email : fliang@lifetech.com URL :
 http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
 Faraday Avenue Genoscope sequence ID : CS0AAW152A08QP1.

FEATURES

source
 Location/Qualifiers
 1..1200
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="CS0DF009YC20"
 /tissue_type="FETAL BRAIN"
 /dev_stage="fetal"
 /clone_lib="Homo sapiens FETAL BRAIN"
 /note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA
 was primed with a NotI-oligo(dT) primer. Five prime end
 enriched, double-strand cDNA was digested with Not I and
 cloned into the Not I and EcoRV sites of the pCMVSPORT 6
 vector. Library was not normalized."

ORIGIN

Query Match 87.0%; Score 17.4; DB 13; Length 1200;
 Best Local Similarity 94.7%; Pred. No. 8.8e+03;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 GGTGCACCGGTGCAGGCGG 19
 |||||
 Db 1117 GGGGACCGGTGCAGGCGG 1135
 |||||

RESULT 11

BQ989390/c
 LOCUS BQ989390.1 1214 bp mRNA linear EST 16-AUG-2002
 DEFINITION AGENCOURT 8712137 NIH_MGC_112 Homo sapiens cDNA clone IMAGE:6295181
 5' mRNA sequence.
 ACCESSION BQ989390
 VERSION BQ989390.1 GI:22290404
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 1214)
 AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: DCTD/BTP
 cDNA Library Preparation: Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLCM9501 row: a column: 06
 High quality sequence stop: 150.
 Location/Qualifiers
 1..1214
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:6295181"
 /tissue_type="melanotic melanoma, cell line"
 /clone_lib="NIH_MGC_112"
 /note="Organ: skin; Vector: pOTB7; Site 1: XhoI; Site 2:
 EcoRI; cDNA made by oligo-dT priming. Directionally cloned
 into EcoRI/XhoI sites using the following 5' adaptor:
 GGCAACGAG(G). Library constructed by Ling Hong in the
 laboratory of Gerald W. Rubin (University of California,
 Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
 Superscript II RT (Life Technologies). Note: this is a
 NIH_MGC Library."

FEATURES

source
 Location/Qualifiers
 1..1214
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:6295181"
 /tissue_type="melanotic melanoma, cell line"
 /clone_lib="NIH_MGC_112"
 /note="Organ: skin; Vector: pOTB7; Site 1: XhoI; Site 2:
 EcoRI; cDNA made by oligo-dT priming. Directionally cloned
 into EcoRI/XhoI sites using the following 5' adaptor:
 GGCAACGAG(G). Library constructed by Ling Hong in the
 laboratory of Gerald W. Rubin (University of California,
 Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
 Superscript II RT (Life Technologies). Note: this is a
 NIH_MGC Library."

ORIGIN

Query Match 87.0%; Score 17.4; DB 13; Length 1214;
 Best Local Similarity 94.7%; Pred. No. 8.8e+03;
 Matches 18; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 GGTGCACCGGTGCAGGCGG 19
 |||||
 Db 301 GGTGCACCGGTGCAGGCGG 283
 |||||

RESULT 12

AV393217/c
 LOCUS AV393217 354 bp mRNA linear EST 23-APR-2002
 DEFINITION AV393217 Chlamydomonas reinhardtii C9 Chlamydomonas reinhardtii
 cDNA clone CM097f03_r 5', mRNA sequence.
 ACCESSION AV393217
 VERSION AV393217.1 GI:6547433

```

KEYWORDS
SOURCE Chlamydomonas reinhardtii
ORGANISM Chlamydomonas reinhardtii
        Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
        Chlamydomonadaceae; Chlamydomonas.
REFERENCE
1 (bases 1 to 354)
AUTHORS Asamizu,S., Nakamura,Y., Sato,S., Fukuzawa,H. and Tabata,S.
TITLE A large scale structural analysis of cDNAs in a unicellular green
        alga, Chlamydomonas reinhardtii. I. Generation of 3433
        non-redundant expressed sequence tags
JOURNAL DNA Res. 6 (6), 369-373 (1999)
MEDLINE 20152988
PUBMED 10691129
COMMENT Contact: Yasukazu Nakamura
        The First Laboratory for Plant Gene Research
        Kazusa DNA Research Institute
        Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
        Email: ynakam@kazusa.or.jp, URL: http://www.kazusa.or.jp/en/plant/.
FEATURES
        source
        1..354
        /organism="Chlamydomonas reinhardtii"
        /mol_type="mRNA"
        /strain="C9"
        /db_xref="taxon:3055"
        /clone="CM097f03 r"
        /dev_stage="photoautotrophic growth"
        /clone_lib="Chlamydomonas reinhardtii C9"
        /note="Vector: pBluescriptII SK; Site_1: EcoRI; Site_2:
        XhoI"
ORIGIN
Query Match 85.0%; Score 17; DB 9; Length 354;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGTGCACCGGTGCAGGG 17
    |||||
DB 310 GGTGCACCGGTGCAGGG 294
RESULT 13
LOCUS BE388878 142 bp mRNA linear EST 21-JUL-2000
DEFINITION 601284657f1 NIH_MGC_44 Homo sapiens cDNA clone IMAGE:3606422 5',
        mRNA sequence.
ACCESSION BE388878
VERSION BE388878.1 GI:9334243
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 NIH-MGC http://mgi.nci.nih.gov/
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE Unpublished (1999)
JOURNAL Contact: Robert Strausberg, Ph.D.
COMMENT Email: cgapbs-x@mail.nih.gov
        Tissue Procurement: ATCC
        cDNA Library Preparation: Ling Hong/Rubin Laboratory
        cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
        DNA Sequencing by: Incyte Genomics, Inc.
        Clone distribution: MGC clone distribution information can be
        found through the I.M.A.G.E. Consortium/LLNL at:
        http://image.llnl.gov
        Plate: L1CM256 row: a column: 15
        High quality sequence start: 2
        High quality sequence stop: 18.
        Location/Qualifiers
            1..142
            /organism="Homo sapiens"
            /mol_type="mRNA"
            /db_xref="taxon:9606"

```

```

/clone="IMAGE:3606422"
/tissue_type="endometrium, adenocarcinoma cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 44"
/notes="Organ: uterus; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adapter: GGCACGAG(G). Library constructed by Ling Hong
in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."
```

ORIGIN

Query Match 84.0%; Score 16.8; DB 10; Length 142;
Best Local Similarity 90.0%; Pred. No. 1.3e+04;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGTGCACCGGTGCAGGGGGG 20
 |||||
DB 109 GGTGCACCGGTGCAGGGGAG 128

RESULT 14
LOCUS AZ492326/c
DEFINITION IM0326G23F Mouse 10kb plasmid UUC1M library Mus musculus genomic
clone UUC1M0326G23 F, genomic survey sequence.

ACCESSION AZ492326
VERSION AZ492326.1 GI:10664936
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 237)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,
Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von
Niederhausern,A. and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: daune@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0326 row: G column: 23
Seq primer: CGTGTAAACGACGCGCAGT
Class: plasmid ends
High quality sequence stop: 237.
Location/Qualifiers
 1..237
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="UUC1M0326G23"
 /sex="Male"
 /lab_host="E. Coli strain XL10-Gold, Tl-resistant, F-"
 /clone_lib="Mouse 10kb plasmid UUC1M library"
 /note="Vector: pMD42mv; Purified genomic DNA from M.
 musculus C57BL/6J (male) was obtained from the Jackson
 Laboratory Mouse DNA Resource
 (http://www.jax.org/resources/documents/dnares/). The DNA
 was hydrodynamically sheared by repeated passage through a
 0.005 inch orifice at constant velocity. The sheared DNA
 was blunt end-repaired with T4 DNA polymerase and T4
 polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (G14732114|g|Ap129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent *E. coli* XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN

Query Match 84.0%; Score 16.8; DB 28; Length 237;
Best Local Similarity 90.0%; Pred. No. 1.3e+04;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GGTGCACCGGTGCAGGGGG 20
Db 100 GGTGCACCGGTGCAGGGGG 81

RESULT 15
LOCUS BB496626
DEFINITION BB496626 RIKEN full-length enriched, 0 day neonate kidney Mus musculus cDNA clone D63004A12 3' similar to X52101 Mouse mRNA for a 25kDa nuclear protein found in murine plasmacytoma, mRNA sequence.
ACCESSION BB496626
VERSION BB496626
KEYWORDS EST.
SOURCE BB496626.1 GI:9469711
ORGANISM Mus musculus (house mouse)

REFERENCE
AUTHORS Sukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 275)
Konno.H., Aizawa.K., Akahira.S., Akiyama.J., Arakawa.T., Carninci.P., Endo.T., Fukuda.S., Fukunishi.Y., Hara.A., Hayatsu.N., Hirozane.T., Hori.F., Ishii.Y., Ishikawa.J., Ishikawa.T., Itoh.M., Izawa.M., Kadota.K., Kagawa.I., Kai.C., Kawai.J., Kikuchi.N., Kiyosawa.H., Kojima.Y., Kondo.S., Koya.S., Kurihara.C., Kusakabe.M., Matsuyama.T., Miki.R., Mizuno.Y., Nakamura.M., Oda.H., Okazaki.Y., Ono.T., Owa.C., Saito.H., Sakai.C., Sato.K., Shibata.K., Shibata.Y., Shigemoto.Y., Shinagawa.A., Shiraki.T., Sogabe.Y., Sugahara.Y., Suzuki.H., Suzuki.H., Tagawa.A., Watanabe.S., Yamamura.T., Yamanaka.I., Yano.R., Yasunishi.A., Yokota.T., Yoshida.K., Yoshiki.A., Yoshino.M., Muramatsu.M. and Hayashizaki.Y.

RIKEN Mouse ESTs (Konno.H., et al.)
Unpublished (2000)
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsc.riken.go.jp
URL: http://genome.gsc.riken.go.jp/

Carninci.P., Nishiyama.Y., Westover.A., Itoh.M., Nagaoka.S., Sasaki.N., Okazaki.Y., Muramatsu.M. and Hayashizaki.Y.
Thermotabilization and thermoactivation of thermostable enzymes by trehalose and its application for the synthesis of full length cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2): 520-524 (1998)
Itoh.M., Kiteunai.T., Akiyama.J., Shibata.Y., Ozawa.Y., Muramatsu.M., Tomaru.Y., Carninci.P., Shibata.Y., Okazaki.Y. and Hayashizaki.Y.
Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5): 463-470 (1999)
Carninci.P. and Hayashizaki.Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303,

19-44 (1999)
Please visit our web site (http://genome.rtc.riken.go.jp) for further details.

FEATURES

Source
1..275
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clones="D630004A12"
/tissue_type="kidney"
/dev_stage="0 day neonate"
/lab_host="DH10B"
/clone_lib="RIKEN full-length enriched, 0 day neonate kidney"
/note="Site 1: Sali; Site 2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5', GAGAGAGAGCGCGCGACTCGAGTTTCTTTTNN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence [5', GAGAGAGAGTTCTCGAGTTTCTTTTNN 3']. cDNA was cleaved with BamHI and XhoI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda PLC I."

ORIGIN

Query Match 84.0%; Score 16.8; DB 10; Length 275;
Best Local Similarity 90.0%; Pred. No. 1.3e+04;
Matches 18; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 GGTGCACCGGTGCAGGGGG 20
Db 152 GGTGCACCGGTGCAGGGGG 171

Search completed: July 2, 2004, 13:32:53
Job time : 1500.92 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 2, 2004, 06:05:50 ; Search time 134.89 Seconds
(without alignments)

566.887 Million cell updates/sec

Title: US-10-068-160-13

Perfect score: 18
Sequence: 1 tgcaccggtgcagg9999 18

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N Geneseq 29Jan04:.*
1: geneseqm1980s:.*
2: geneseqm1990s:.*
3: geneseqm2000s:.*
4: geneseqm2001as:.*
5: geneseqm2001bs:.*
6: geneseqm2002s:.*
7: geneseqm2003as:.*
8: geneseqm2003bs:.*
9: geneseqm2003cs:.*
10: geneseqm2004s:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	18	100.0	20	4 AAC80622	Immunogen
2	18	100.0	20	4 AAS09592	Immunorea
3	18	100.0	20	6 ABL35614	Immunosti
4	18	100.0	20	6 ABL35578	Immunosti
5	18	100.0	20	6 ABL35581	Immunosti
6	18	100.0	20	6 ABL35570	Immunosti
7	18	100.0	20	6 ABL35588	Immunosti
8	18	100.0	20	6 ABK46470	Immunosti
9	18	100.0	20	7 ACC48296	CpG oligo
10	18	100.0	20	7 ACC48300	CpG oligo
11	18	100.0	20	7 ACC48313	CpG oligo
12	18	100.0	20	8 ACC83118	D class C
13	18	100.0	20	8 ACC83152	D class O
14	18	100.0	20	9 ADD01049	CpG D oli
15	18	100.0	28	6 ABL35599	Immunosti
16	18	100.0	28	6 ABL35603	Immunosti
17	18	100.0	28	6 ABL35591	Immunosti
18	18	100.0	28	6 ABL35611	Immunosti
19	18	100.0	40	6 ABL35622	Immunosti
20	16.4	91.1	20	4 AAS09651	Immunorea
21	16.4	91.1	20	6 ABL35573	Immunosti
22	16.4	91.1	20	6 ABL35584	Immunosti
23	16.4	91.1	20	6 ABL35569	Immunosti

24	16.4	91.1	20	6 ABL35617	Immunosti
25	16.4	91.1	20	6 ABL35580	Immunosti
26	16.4	91.1	20	7 ACC48311	CpG oligo
27	16.4	91.1	20	7 ACC48320	CpG oligo
28	16.4	91.1	20	7 ACC48321	CpG oligo
29	16.4	91.1	20	8 ACC83125	D class C
30	16.4	91.1	20	8 ACC83116	D class C
31	16.4	91.1	20	8 ACC83126	D class C
32	16.4	91.1	20	9 ADD01076	CpG D oli
33	16.4	91.1	20	9 ADD01059	CpG D oli
34	16.4	91.1	28	6 ABL35590	Immunosti
35	16.4	91.1	28	6 ABL35594	Immunosti
36	16.4	91.1	28	6 ABL35606	Immunosti
37	16.4	91.1	28	6 ABL35602	Immunosti
38	15.4	85.6	19	4 AAC80602	Immunogen
39	15.4	85.6	19	4 AAS09572	Immunorea
40	15.4	85.6	19	6 ABK46450	Immunosti
41	15.4	85.6	278	5 ABA12385	Human ner
42	15.4	85.6	349	4 AAL01438	Human rep
43	15.4	85.6	349	4 ABL96885	Human tes
44	15.4	85.6	827	6 AAS61882	Porcine m
45	15	83.3	1466	5 AAS80037	DNA encod

ALIGNMENTS

RESULT 1

AAC80622
ID AAC80622 standard; DNA; 20 BP.

AC AAC80622;

DT 14-FEB-2001 (first entry)

DE Immunogenic CpG oligodeoxynucleotide, SEQ ID NO:42.

KW CpG oligodeoxynucleotide; unmethylated; antigen-presenting cell;
KW immunogenic; cytokine release; natural killer cell; NK cell activation;
KW cell-mediated immune response; T-cell response; humoral response; vaccine;
KW B-cell response; antibody production; immune response induction; allergic;
KW allergy; asthma; infection; bacterial; viral; fungal; protozoal;
KW parasitic; tuberculosis; AIDS; autoimmune disease; lupus erythematosus;
KW rheumatoid arthritis; multiple sclerosis; solid tumour; cancer;
KW immune deficiency; biological warfare agent; cytostatic; antiarthritic;
KW antimicrobial; antiallergic; protozoicide; tuberculostatic;
KW antiasthmatic; dermatological; phosphorothioate; ss.

OS Synthetic.

XX WO200061151-A2.

XX 19-OCT-2000.

XX 12-APR-2000; 2000WO-US009839.

XX 12-APR-1999; 99US-0128898P.

XX (KLIN/) KLINMAN D.

XX (ISHI/) ISHII K.

XX (VERT/) VERTHELYI D.

XX Klinman D, Ishii K, Verthelyi D;

XX WPI, 2001-006880/01.

PT Novel oligonucleotides useful for the prevention and treatment of
PT allergies, cancer, and autoimmune disorders and for ameliorating symptoms
PT resulting from exposure to a bio-warfare agent.

XX Claim 4; Page 30; 46pp; English.

XX The invention relates to novel immunogenic CpG oligodeoxynucleotides

CC (AAC80581-C80723). The oligonucleotide are at least 10 bases long and
 CC comprise one of the generic sequences 5'-NNNT-CpG-WNNN-3' or 5'-RY-CpG-RY
 CC -3'. The central CpG motif is unmethylated, and the oligonucleotides
 CC optionally have phosphorothioate linkages which make them more resistant
 CC to degradation. The invention also relates to an oligonucleotide delivery
 CC complex comprising an oligonucleotide of the invention and a targeting
 CC agent, and a pharmaceutical composition comprising the oligonucleotide
 CC delivery complex. The oligonucleotides are able to induce either a cell-
 CC mediated (T-cell) response or a humoral (B-cell, antibody) response, with
 CC oligonucleotides of the sequence 5'-RY-CpG-RY-3' being able to induce a
 CC cell-mediated response, and those of the sequence 5'-NNNT-CpG-WNNN-3'
 CC being able to induce a humoral response. It is thought that after
 CC administration, the oligonucleotide acts on antigen-presenting cells
 CC (e.g., macrophages and dendritic cells), which then release cytokines,
 CC leading to activation of natural killer (NK) cells. A cell-mediated or
 CC humoral response can then occur by activation of T- or B-cells. The
 CC induction of an immune response is useful for treating, preventing or
 CC ameliorating an allergic reaction (preferably asthma), or an infection,
 CC where an immunogenic CpG oligonucleotide is administered either alone or
 CC in combination with an anti-allergenic agent or anti-infectious agent.
 CC The allergic conditions which may be treated include eczema, allergic
 CC rhinitis, hayfever, urticaria, food allergies and other atopic
 CC conditions, and the infections which may be treated include viral,
 CC bacterial, fungal and protozoal infections such as tuberculosis, AIDS,
 CC leishmania and schistosomiasis. Immune response induction may also be
 CC used in the treatment of an autoimmune disorder (e.g., lupus
 CC erythematosus, rheumatoid arthritis and multiple sclerosis), a disease
 CC associated with immune system deficiency, and symptoms resulting from
 CC exposure to an agent of biological warfare. An immunogenic CpG
 CC oligonucleotide, either alone or in combination with an anti-cancer
 CC agent, is useful for treating solid tumour cancer. The induction of an
 CC immune response is used in antisense therapy and to improve the efficacy
 CC of a vaccine. The oligonucleotide is preferably administered to
 CC lymphocytes ex vivo, producing activated lymphocytes which are then
 CC administered to the host. The present sequence represents an immunogenic
 CC CpG oligodeoxynucleotide of the invention

XX SQ Sequence 20 BP; 2 A; 4 C; 12 G; 2 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 4; Length 20;
 Best Local Similarity 100.0%; Pred. No. 64;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGCACCGGTGCAGGGGG 18
 |||||
 Db 3 TGCACCGGTGCAGGGGG 20

RESULT 2

AAS09592
 ID AAS09592 standard; DNA; 20 BP.

XX AAC09592;

XX 26-SEP-2001 (first entry)

XX Immunoreactive CpG sequence-containing oligonucleotide #42.

XX CpG sequence; immune response; non-B cell activation; interferon gamma;
 KW IFN-gamma; humoral; antibody production; interleukin-6 production;
 KW therapeutic; allergy; asthma; cancer; autoimmune disorder; infection;
 KW bio-warfare; vaccine; antisense therapy; eczema; allergic rhinitis;
 KW coryza; hay fever; urticaria; hives; food allergy; atopic condition;
 KW hepatitis; human immunodeficiency virus; HIV; malaria; Francisella;
 KW lupus erythematosus; rheumatoid arthritis; multiple sclerosis;
 KW schistosomiasis; tuberculosis; acquired immunodeficiency syndrome; AIDS;
 KW leishmania; Ebola; Anthrax; Listeria; ss.

XX Synthetic.

XX WO200151500-A1.

XX 19-JUL-2001.

XX 12-JAN-2001; 2001WO-US001122.
 XX 14-JAN-2000; 2000US-0176115P.
 XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX Klinman D, Ishii K, Verthelyi D;
 XX WPI; 2001-442129/47.

XX Oligodeoxynucleotides for inducing an immune response to treat and
 PT prevent an allergic reaction, cancer, an autoimmune disorder and symptoms
 PT resulting from exposure to bio-warfare agents, comprise multiple CpG
 PT sequences.

XX Claim 5; Page 34; 48pp; English.

XX AAS09551-AAS09662 represent oligodeoxynucleotides (ODN) of at least 10
 CC nucleotides comprising multiple CpG sequences, where one of the CpG
 CC sequences is different from another of the multiple CpG sequences. The
 CC ODN are useful for inducing an immune response, preferably a cell-
 CC mediated immune response, involving non-B cell activation, interferon
 CC gamma (IFN-gamma) production or a humoral immune response involving B
 CC cell activation, antibody and interleukin-6 production in a host, for
 CC treating, preventing or ameliorating an allergic reaction, e.g. asthma,
 CC cancer, e.g. solid tumour cancer, a disease associated with the immune
 CC system e.g. autoimmune disorder or an immune system deficiency, infection
 CC or a symptom resulting from exposure to bio-warfare agent in a human. The
 CC induction of immune response improves the efficacy of a vaccine and is
 CC used in antisense therapy. The ODN are useful for treating, preventing or
 CC ameliorating allergic reactions, including eczema, allergic rhinitis or
 CC coryza, hay fever, bronchial asthma, urticaria (hives), food allergies
 CC and other atopic conditions, for improving the efficacy of vaccines
 CC against hepatitis A, B and C, human immunodeficiency virus (HIV) and
 CC malaria, for treating immune system deficiencies, e.g. lupus
 CC erythematosus and autoimmune diseases such as rheumatoid arthritis and
 CC multiple sclerosis, infections including Francisella, schistosomiasis,
 CC tuberculosis, acquired immunodeficiency syndrome (AIDS), leishmania and
 CC symptoms resulting from exposure of bio-warfare agent, including Ebola,
 CC Anthrax and Listeria

XX Sequence 20 BP; 2 A; 4 C; 12 G; 2 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 4; Length 20;
 Best Local Similarity 100.0%; Pred. No. 64;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGCACCGGTGCAGGGGG 18
 |||||
 Db 3 TGCACCGGTGCAGGGGG 20

RESULT 3

ABL35614
 ID ABL35614 standard; DNA; 20 BP.

XX ABL35614;

XX 04-APR-2002 (first entry)

XX Immunostimulatory oligonucleotide SEQ ID NO: 540.

XX DNA/RNA hybrid; phosphorothioate backbone; immunostimulatory; vaccine;
 KW infection; allergy; cancer; hypersensitivity; bio-warfare;
 KW immunostimulant; antiallergic; cytostatic; antimicrobial; anti-HIV;
 KW immunosuppressive; protozoicide; virucide; hepatotropic; gene therapy;
 KW antiinflammatory; antibacterial; ss.

XX Synthetic.

XX Key Location/Qualifiers
 PH misc_RNA 1..20

FT /tag= a
FT /note= "optionally thymidine is replaced by uracil to
FT form RNA or DNA/RNA hybrids. Thymidine is linked to at
FT least one other base through a ribose sugar"
XX
XX
PN WO200193902-A2.
XX
XX PD 13-DEC-2001.
XX
XX PF 07-JUN-2001; 2001WO-US018276.
XX
XX PR 07-JUN-2000; 2000US-0209797P.
XX
XX PA (BIOS-) BIOSYNEXUS INC.
XX
XX PI Mond JJ, Flora M, Klinman DM;
XX
XX DR WPI; 2002-130570/17.
XX
XX PT New immunostimulatory compositions comprising RNA/DNA hybrid
XX oligonucleotides, useful for enhancing an immune response or inducing
XX PT cytokines, particularly for treating diseases, e.g. cancer, allergy or
XX PT HIV infection.
XX
XX PS Example 11; Page 62; 68pp; English.
XX
XX CC The present invention relates to an immunostimulatory composition, which
XX comprises at least one oligonucleotide comprising both an RNA region and
XX a DNA region. The composition is useful for enhancing an immune response
XX or inducing cytokines. It can be used as a vaccine adjuvant and in
XX CC treating diseases, including pathogenic infection, (non-)malignant
XX CC tumours (e.g. cancers of the brain, lung, ovary, breast, prostate or
XX CC colon, or carcinomas and sarcomas), autoimmune diseases or allergies
XX CC (e.g. allergic rhinitis, hay fever or food allergies), Lyme disease,
XX CC hepatitis, HIV or malaria. The composition is also useful for treating,
XX CC preventing or ameliorating the symptoms resulting from exposure to a bio-
XX CC warfare agent, e.g. Ebola, Anthrax or Listeria. The present sequence is
XX CC an immunostimulatory oligonucleotide described in the exemplification of
XX CC the invention
XX
XX SQ Sequence 20 BP; 2 A; 4 C; 12 G; 2 T; 0 U; 0 Other;
Query Match 100.0%; Score 18; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TGCACCGGTGCAGGGGG 18
| | | | | | | | | | | | | | | | | |
Db 3 TGCACCGGTGCAGGGGG 20
RESULT 4
ABL35578
ID ABL35578 standard; DNA; 20 BP.
XX
XX AC ABL35578;
XX
XX DT 04-APR-2002 (first entry)
XX
XX DE Immunostimulatory oligonucleotide SEQ ID NO: 504.
XX
XX KW DNA/RNA hybrid; phosphorothioate backbone; immunostimulatory; vaccine;
XX KW infection; allergy; cancer; hypersensitivity; bio-warfare;
XX KW immunostimulant; antiallergic; cytostatic; antimicrobial; anti-HIV;
XX KW immunosuppressive; protozoacide; virucide; hepatotropic; gene therapy;
XX KW antiinflammatory; antibacterial; ss.
XX
XX OS Synthetic.
XX
XX PH Key Location/Qualifiers
XX FT misc_RNA 1..20
FT /tag= a
FT /note= "optionally thymidine is replaced by uracil to
FT form RNA or DNA/RNA hybrids. Thymidine is linked to at
FT least one other base through a ribose sugar"

FT form RNA or DNA/RNA hybrids. Thymidine is linked to at
FT least one other base through a ribose sugar"
XX
XX PN WO200193902-A2.
XX
XX PD 13-DEC-2001.
XX
XX PF 07-JUN-2001; 2001WO-US018276.
XX
XX PR 07-JUN-2000; 2000US-0209797P.
XX
XX PA (BIOS-) BIOSYNEXUS INC.
XX
XX PI Mond JJ, Flora M, Klinman DM;
XX
XX DR WPI; 2002-130570/17.
XX
XX PT New immunostimulatory compositions comprising RNA/DNA hybrid
XX oligonucleotides, useful for enhancing an immune response or inducing
XX PT cytokines, particularly for treating diseases, e.g. cancer, allergy or
XX PT HIV infection.
XX
XX PS Example 11; Page 61; 68pp; English.
XX
XX CC The present invention relates to an immunostimulatory composition, which
XX comprises at least one oligonucleotide comprising both an RNA region and
XX a DNA region. The composition is useful for enhancing an immune response
XX or inducing cytokines. It can be used as a vaccine adjuvant and in
XX CC treating diseases, including pathogenic infection, (non-)malignant
XX CC tumours (e.g. cancers of the brain, lung, ovary, breast, prostate or
XX CC colon, or carcinomas and sarcomas), autoimmune diseases or allergies
XX CC (e.g. allergic rhinitis, hay fever or food allergies), Lyme disease,
XX CC hepatitis, HIV or malaria. The composition is also useful for treating,
XX CC preventing or ameliorating the symptoms resulting from exposure to a bio-
XX CC warfare agent, e.g. Ebola, Anthrax or Listeria. The present sequence is
XX CC an immunostimulatory oligonucleotide described in the exemplification of
XX CC the invention
XX
XX SQ Sequence 20 BP; 2 A; 4 C; 12 G; 2 T; 0 U; 0 Other;
Query Match 100.0%; Score 18; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TGCACCGGTGCAGGGGG 18
| | | | | | | | | | | | | | | | | |
Db 3 TGCACCGGTGCAGGGGG 20
RESULT 5
ABL35581
ID ABL35581 standard; DNA; 20 BP.
XX
XX AC ABL35581;
XX
XX DT 04-APR-2002 (first entry)
XX
XX DE Immunostimulatory oligonucleotide SEQ ID NO: 507.
XX
XX KW DNA/RNA hybrid; phosphorothioate backbone; immunostimulatory; vaccine;
XX KW infection; allergy; cancer; hypersensitivity; bio-warfare;
XX KW immunostimulant; antiallergic; cytostatic; antimicrobial; anti-HIV;
XX KW immunosuppressive; protozoacide; virucide; hepatotropic; gene therapy;
XX KW antiinflammatory; antibacterial; ss.
XX
XX OS Synthetic.
XX
XX PH Key Location/Qualifiers
XX FT misc_RNA 1..20
FT /tag= a
FT /note= "optionally thymidine is replaced by uracil to
FT form RNA or DNA/RNA hybrids. Thymidine is linked to at
FT least one other base through a ribose sugar"

```

XX PN WO200193902-A2.
XX PD
XX PF 13-DEC-2001.
XX PR
XX PP 07-JUN-2001; 2001WO-US018276.
XX PR
XX PP 07-JUN-2000; 2000US-0209797P.
XX PR
XX PA (BIOS-) BIOSYNEXUS INC.
XX PI
XX PI Mond JJ, Flora M, Klinman DM;
XX PI WPI; 2002-130570/17.
XX DR
XX DR New immunostimulatory compositions comprising RNA/DNA hybrid
XX PT oligonucleotides, useful for enhancing an immune response or inducing
XX PT cytokines, particularly for treating diseases, e.g. cancer, allergy or
XX PT HIV infection.
XX PT
XX PS Example 11; Page 61; 68pp; English.
XX PS
XX CC The present invention relates to an immunostimulatory composition, which
XX CC comprises at least one oligonucleotide comprising both an RNA region and
XX CC a DNA region. The composition is useful for enhancing an immune response
XX CC or inducing cytokines. It can be used as a vaccine adjuvant and in
XX CC treating diseases, including pathogenic infection, (non-)malignant
XX CC tumours (e.g. cancers of the brain, lung, ovary, breast, prostate or
XX CC colon, or carcinomas and sarcomas), autoimmune diseases or allergies
XX CC (e.g. allergic rhinitis, hay fever or food allergies), Lyme disease,
XX CC hepatitis, HIV or malaria. The composition is also useful for treating,
XX CC preventing or ameliorating the symptoms resulting from exposure to a bio-
XX CC warfare agent, e.g. Ebola, Anthrax or Listeria. The present sequence is
XX CC an immunostimulatory oligonucleotide described in the exemplification of
XX CC the invention
XX CC
XX SQ Sequence 20 BP; 2 A; 4 C; 12 G; 2 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGCACCGGTGCAGGGGGG 18
Db 3 TGCACCGGTGCAGGGGGG 20

RESULT 6
ABL35570
ID ABL35570 standard; DNA; 20 BP.
XX AC
XX AC ABL35570;
XX DT 04-APR-2002 (first entry)
XX DE
XX DE Immunostimulatory oligonucleotide SEQ ID NO: 496.
XX KW DNA/RNA hybrid; phosphorothioate backbone; immunostimulatory; vaccine;
XX KW infection; allergy; cancer; hypersensitivity; bio-warfare;
XX KW immunostimulant; antiallergic; cytostatic; antimicrobial; anti-HIV;
XX KW immunosuppressive; protozoacide; virucide; hepatotropic; gene therapy;
XX KW antiinflammatory; antibacterial; ss.
XX OS
XX OS Synthetic.
XX PH
XX PH Key Location/Qualifiers
XX PH misc_RNA 1..20
XX FT /+tag= a
XX FT /note= "optionally thymidine is replaced by uracil to
XX FT form RNA or DNA/RNA hybrids. Thymidine is linked to at
XX FT least one other base through a ribose sugar"
XX PN WO200193902-A2.

```

```

XX PD 13-DEC-2001.
XX PF 07-JUN-2001; 2001WO-US018276.
XX PR
XX PR 07-JUN-2000; 2000US-0209797P.
XX PA (BIOS-) BIOSYNEXUS INC.
XX PI
XX PI Mond JJ, Flora M, Klinman DM;
XX PI WPI; 2002-130570/17.
XX DR
XX DR New immunostimulatory compositions comprising RNA/DNA hybrid
XX PT oligonucleotides, useful for enhancing an immune response or inducing
XX PT cytokines, particularly for treating diseases, e.g. cancer, allergy or
XX PT HIV infection.
XX PT
XX PS Example 11; Page 61; 68pp; English.
XX PS
XX CC The present invention relates to an immunostimulatory composition, which
XX CC comprises at least one oligonucleotide comprising both an RNA region and
XX CC a DNA region. The composition is useful for enhancing an immune response
XX CC or inducing cytokines. It can be used as a vaccine adjuvant and in
XX CC treating diseases, including pathogenic infection, (non-)malignant
XX CC tumours (e.g. cancers of the brain, lung, ovary, breast, prostate or
XX CC colon, or carcinomas and sarcomas), autoimmune diseases or allergies
XX CC (e.g. allergic rhinitis, hay fever or food allergies), Lyme disease,
XX CC hepatitis, HIV or malaria. The composition is also useful for treating,
XX CC preventing or ameliorating the symptoms resulting from exposure to a bio-
XX CC warfare agent, e.g. Ebola, Anthrax or Listeria. The present sequence is
XX CC an immunostimulatory oligonucleotide described in the exemplification of
XX CC the invention
XX CC
XX SQ Sequence 20 BP; 2 A; 4 C; 12 G; 2 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGCACCGGTGCAGGGGGG 18
Db 3 TGCACCGGTGCAGGGGGG 20

RESULT 7
ABL35588
ID ABL35588 standard; DNA; 20 BP.
XX AC
XX AC ABL35588;
XX DT 04-APR-2002 (first entry)
XX DE
XX DE Immunostimulatory oligonucleotide SEQ ID NO: 514.
XX KW DNA/RNA hybrid; phosphorothioate backbone; immunostimulatory; vaccine;
XX KW infection; allergy; cancer; hypersensitivity; bio-warfare;
XX KW immunostimulant; antiallergic; cytostatic; antimicrobial; anti-HIV;
XX KW immunosuppressive; protozoacide; virucide; hepatotropic; gene therapy;
XX KW antiinflammatory; antibacterial; ss.
XX OS
XX OS Synthetic.
XX PH
XX PH Key Location/Qualifiers
XX PH misc_RNA 1..20
XX FT /+tag= a
XX FT /note= "optionally thymidine is replaced by uracil to
XX FT form RNA or DNA/RNA hybrids. Thymidine is linked to at
XX FT least one other base through a ribose sugar"
XX PN WO200193902-A2.
XX PD 13-DEC-2001.

```

```

XX PF 07-JUN-2001; 2001WO-US018276.
XX XX
XX PR 07-JUN-2000; 2000US-020979P.
XX XX
XX PA (BIOS-) BIOSYNEXUS INC.
XX XX
XX PI Mond JJ, Flora M, Klinman DM;
XX DR WPI; 2002-227118/28.
XX XX
XX PT Vaccine for immunizing patient against respiratory syncytial virus, has
XX PT epitopes of Paramyxoviridae P protein, and cytosine followed by guanine
XX PT linked by phosphate bond-oligodeoxynucleotides.
XX XX
XX PS Claim 4; Page 8; 30pp; English.
XX XX
XX CC The invention describes a vaccine comprising one or more epitopes of a
XX CC Paramyxoviridae P protein, and one or more CpG (cytosine followed by
XX CC guanine linked by phosphate bond)-oligodeoxynucleotides (ODNs). The
XX CC vaccine is useful for vaccinating a patient especially against viruses of
XX CC the Paramyxoviridae family e.g. respiratory syncytial virus (RSV), the
XX CC primary cause of viral bronchiolitis and pneumonia in infants and
XX CC children, and infectious pulmonary disease in infants. RSV has been
XX CC particularly implicated in death of infants that are premature, have
XX CC bronchopulmonary dysplasia, or congenital heart conditions. This sequence
XX CC represents an oligodeoxynucleotide that can be used in the creation of
XX CC the vaccine
XX XX
XX SQ Sequence 20 BP; 2 A; 4 C; 12 G; 2 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 18; DB 6; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 64;
XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 TGCACCGGTGCAGGGGG 18
XX |||||
XX DB 3 TGCACCGGTGCAGGGGG 20
XX
XX RESULT 9
XX ACC48296
XX ID ACC48296 standard; DNA; 20 BP.
XX XX
XX AC ACC48296;
XX XX
XX DT 11-AUG-2003 (first entry)
XX XX
XX DE CpG oligodeoxynucleotide B29 used for dendritic cell maturation.
XX XX
XX KW CpG oligodeoxynucleotide; dendritic cell; tumour; immunotherapy; vaccine;
XX KW cytostatic; immunostimulant; gene therapy; ss.
XX OS Synthetic.
XX PH Key Location/Qualifiers
XX FT modified_base 1..20
XX FT /tag= a
XX FT /mod_base= OTHER
XX FT /note= "OTHER= phosphorothioate nucleotides"
XX FT modified_base 1
XX FT /tag= a
XX FT /mod_base= OTHER
XX FT /note= "OTHER= phosphorothioate nucleotide"
XX PN WO2003020884-A2.
XX XX
XX PD 13-MAR-2003.
XX XX
XX PF 13-AUG-2002; 2002WO-US025732.
XX XX
XX PR 14-AUG-2001; 2001US-0312190P.
XX XX
XX PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX XX
XX PI Klinman DM, Gursel M, Verthelyi D;
XX XX
XX DR WPI; 2003-300874/29.
XX XX
XX PT Generating mature dendritic cells for tumor immunotherapy or as vaccines
XX PT for activating the immune system to treat diseases such as cancer,
XX PT comprises contacting a dendritic cell precursor with a D type

```

```

XX PF 07-JUN-2001; 2001WO-US018276.
XX XX
XX PR 07-JUN-2000; 2000US-020979P.
XX XX
XX PA (BIOS-) BIOSYNEXUS INC.
XX XX
XX PI Mond JJ, Flora M, Klinman DM;
XX DR WPI; 2002-130570/17.
XX XX
XX PT New immunostimulatory compositions comprising RNA/DNA hybrid
XX PT oligonucleotides, useful for enhancing an immune response or inducing
XX PT cytokines, particularly for treating diseases, e.g. cancer, allergy or
XX PT HIV infection.
XX XX
XX PS Example 11; Page 61; 68pp; English.
XX XX
XX CC The present invention relates to an immunostimulatory composition, which
XX CC comprises at least one oligonucleotide comprising both an RNA region and
XX CC a DNA region. The composition is useful for enhancing an immune response
XX CC or inducing cytokines. It can be used as a vaccine adjuvant and in
XX CC treating diseases, including pathogenic infection, (non-)malignant
XX CC tumours (e.g. cancers of the brain, lung, ovary, breast, prostate or
XX CC colon, or carcinomas and sarcomas), autoimmune diseases or allergies
XX CC (e.g. allergic rhinitis, hay fever or food allergies), Lyme disease,
XX CC hepatitis, HIV or malaria. The composition is also useful for treating,
XX CC preventing or ameliorating the symptoms resulting from exposure to a bio-
XX CC warfare agent, e.g. Ebola, Anthrax or Listeria. The present sequence is
XX CC an immunostimulatory oligonucleotide described in the exemplification of
XX CC the invention
XX XX
XX SQ Sequence 20 BP; 2 A; 4 C; 12 G; 2 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 18; DB 6; Length 20;
XX Best Local Similarity 100.0%; Pred. No. 64;
XX Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 TGCACCGGTGCAGGGGG 18
XX |||||
XX DB 3 TGCACCGGTGCAGGGGG 20
XX
XX RESULT 8
XX ABK46470
XX ID ABK46470 standard; DNA; 20 BP.
XX XX
XX AC ABK46470;
XX XX
XX DT 05-JUN-2002 (first entry)
XX XX
XX DE Immunostimulatory unmethylated CpG oligodeoxynucleotide #60.
XX XX
XX KW unmethylated CpG; oligodeoxynucleotide; ODN; virucide; vaccine;
XX KW Paramyxoviridae; P protein; respiratory syncytial virus; RSV;
XX KW viral bronchiolitis; pneumonia; infectious pulmonary disease;
XX KW bronchopulmonary dysplasia; congenital heart condition; ss.
XX OS Synthetic.
XX XX
XX PN WO200211761-A2.
XX XX
XX PD 14-FEB-2002.
XX XX
XX PR 09-AUG-2001; 2001WO-US041633.
XX XX
XX PR 10-SEP-2000; 2000US-0224011P.
XX PR 01-SEP-2000; 2000US-0229307P.
XX XX
XX PA (JACK-) JACKSON FOUND ADVANCEMENT MILITARY MED.
XX XX
XX PI Mond JJ, Prince G, Klinman DM;
XX XX

```

PT oligodeoxynucleotide.
PS Claim 11; Page 44; 69pp; English.
XX
CC The present sequence is that of D type CpG oligodeoxynucleotide D29,
CC which is used in a claimed method for generating a mature dendritic cell.
CC The method involves contacting a dendritic cell precursor, especially a
CC monocyte, with the oligonucleotide. The method is useful for generating
CC mature dendritic cells and enhancing T cell responses, thus enhancing
CC antigen presentation. Mature dendritic cells are useful for tumour
CC immunotherapy, for augmenting an immune response to an infectious agent
CC or to a vaccine, and as vaccines to prevent future infection or to
CC activate the immune system to treat diseases such as cancer. Mature
CC dendritic cells may also be used to produce activated T lymphocytes
XX
SQ Sequence 20 BP; 2 A; 4 C; 12 G; 2 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 7; Length 20;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGCACCGGTGCAGGGGG 18
Db 3 TGCACCGGTGCAGGGGG 20

RESULT 10
ACC48300
ID ACC48300 standard; DNA; 20 BP.
XX
AC ACC48300;
XX
XX
DT 11-AUG-2003 (first entry)
XX
DE CpG oligodeoxynucleotide used for dendritic cell maturation.
XX
KW CpG oligodeoxynucleotide; dendritic cell; tumour; immunotherapy; vaccine;
KW cytostatic; immunostimulant; gene therapy; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT misc_difference 1 /*tag= a
FT /*note= "N is any base (especially G) or no base"
FT misc_difference 2 /*tag= b
FT /*note= "N is any base (especially G) or no base"
FT
XX
PN WO2003020884-A2.
XX
XX
PD 13-MAR-2003.
XX
PP 13-AUG-2002; 2002WO-US025732.
XX
PR 14-AUG-2001; 2001US-0312190P.
XX
XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Klinman DM, Gursel M, Verthelyi D;
XX
DR WPI; 2003-300874/29.
XX
XX Generating mature dendritic cells for tumor immunotherapy or as vaccines
XX for activating the immune system to treat diseases such as cancer,
XX comprises contacting a dendritic cell precursor with a D type
XX oligodeoxynucleotide.
XX
PS Disclosure; Page 26; 69pp; English.
XX
CC The present sequence is that of a D type CpG oligodeoxynucleotide that is
CC an example of claimed D type oligodeoxynucleotides (see ACC48294) of the
CC invention. Mature dendritic cells are obtained by contacting a dendritic

CC cell precursor, such as a monocyte, with such an oligodeoxynucleotide.
CC The method is useful for generating mature dendritic cells and enhancing
CC T cell responses, thus enhancing antigen presentation. Mature dendritic
CC cells are useful for tumour immunotherapy, for augmenting an immune
CC response to an infectious agent or to a vaccine, and as vaccines to
CC prevent future infection or to activate the immune system to treat
CC diseases such as cancer. Mature dendritic cells may also be used to
CC produce activated T lymphocytes
XX
SQ Sequence 20 BP; 2 A; 4 C; 10 G; 2 T; 0 U; 2 Other;

Query Match 100.0%; Score 18; DB 7; Length 20;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGCACCGGTGCAGGGGG 18
Db 3 TGCACCGGTGCAGGGGG 20

RESULT 11
ACC48313
ID ACC48313 standard; DNA; 20 BP.
XX
AC ACC48313;
XX
DT 11-AUG-2003 (first entry)
XX
DE CpG oligodeoxynucleotide.
XX
KW CpG oligodeoxynucleotide; dendritic cell; tumour; immunotherapy; vaccine;
KW cytostatic; immunostimulant; gene therapy; ss.
XX
OS Synthetic.
XX
PN WO2003020884-A2.
XX
PD 13-MAR-2003.
XX
PP 13-AUG-2002; 2002WO-US025732.
XX
PR 14-AUG-2001; 2001US-0312190P.
XX
XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Klinman DM, Gursel M, Verthelyi D;
XX
DR WPI; 2003-300874/29.
XX
XX Generating mature dendritic cells for tumor immunotherapy or as vaccines
XX for activating the immune system to treat diseases such as cancer,
XX comprises contacting a dendritic cell precursor with a D type
XX oligodeoxynucleotide.
XX
PS Disclosure; Page 61; 69pp; English.
XX
CC The present sequence is that of a CpG oligodeoxynucleotide of the
CC invention. A claimed method for generating dendritic cells involves
CC contacting a dendritic cell precursor, especially a monocyte, with a D
CC type oligodeoxynucleotide (see ACC48294) containing a central
CC unmethylated CpG motif. The method is useful for generating mature
CC dendritic cells and enhancing T cell responses, thus enhancing antigen
CC presentation. Mature dendritic cells are useful for tumour immunotherapy,
CC for augmenting an immune response to an infectious agent or to a vaccine,
CC and as vaccines to prevent future infection or to activate the immune
CC system to treat diseases such as cancer. Mature dendritic cells may also
CC be used to produce activated T lymphocytes
XX
SQ Sequence 20 BP; 2 A; 4 C; 12 G; 2 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 7; Length 20;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;


```

Oy 1 TGCACCGGTGCAGGGGGG 18
Db 3 TGCACCGGTGCAGGGGGG 20

RESULT 12
ACC83118
ID ACC83118 standard; DNA; 20 BP.
XX
AC ACC83118;
XX
DT 27-AUG-2003 (first entry)
XX
DE D class CpG ODN sequence useful for encapsulating in SSCL, DV29.
XX
KW Sterically stabilised cationic liposome; SSCL; ODN; oligodeoxynucleotide;
KW tuberculosis; cytokine; leishmaniasis; AIDS-associated Kaposi's tumour;
KW thyroid; cancer; allergy; eczema; allergic rhinitis; coryza; hay fever;
KW schistosomiasis; interferon gamma; lupus erythematosus; antimicrobial;
KW asthma; urticaria; autoimmune disease; diabetes; rheumatoid arthritis;
KW CpG motif; interleukin-13; cytostatic; tularemia; malaria; psoriasis;
KW multiple sclerosis; infection; tumour; ss.
XX
OS Unidentified.
XX
FH Key Location/Qualifiers
PN modified_base 16..20
FT /tag= a
FT /mod_base= OTHER
FT /note= "Phosphorothioate backbone"
XX
PF WO2003040308-A2.
XX
PR 29-JUL-2002; 2002WO-US024235.
XX
PR 27-JUL-2001; 2001US-0308283P.
XX
PR 25-JUL-2002; 2002US-00206407.
XX
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Klinman DM, Gursel I, Ishii KJ, Kawakami K, Joshi BH, Puri RK;
XX
DR WPI; 2003-482260/45.
XX
PT Cationic liposome composition for delivering oligodeoxynucleotides
PT including a CpG motif in clinical applications, comprises a cationic
PT lipid, a co-lipid, stabilizing agent and an encapsulated oligonucleotide.
XX
PS Disclosure; Fig 10C; 110pp; English.
XX
CC The invention relates to sterically stabilised cationic liposomes (SSCL)
CC which comprises a cationic lipid, a co-lipid, stabilising agent and
CC encapsulating a K type oligodeoxynucleotide (ODN) including a CpG motif.
CC The invention is useful in pharmaceutical composition for impairing
CC growth of a solid tumour cell (e.g. human tumour cell) bearing an
CC interleukin-13 receptor in a subject; for stimulating an immune response,
CC which is expression of a cytokine (e.g. interferon gamma), particularly
CC immunotherapeutic response against tumours or stimulating an in vivo or
CC an in vitro immune cell, and for inducing an immune response against an
CC infectious agent e.g. virus, bacteria and fungus. It is also useful for
CC delivering oligodeoxynucleotides including a CpG motif in clinical
CC applications; for treating infectious diseases (e.g. tularemia, malaria,
CC francisella, schistosomiasis, tuberculosis and leishmaniasis), cancer
CC (e.g. solid tumours, AIDS-associated Kaposi's tumour, thyroid cancer
CC etc), allergy (e.g. eczema, allergic rhinitis or coryza), hay fever,
CC bronchial or allergic asthma, urticaria, food allergies), autoimmune
CC diseases (e.g. diabetes, rheumatoid arthritis, lupus erythematosus and
CC multiple sclerosis) and psoriasis. The present sequence is a D class CpG
CC ODN potentially useful for encapsulating in SSCL
XX
SQ Sequence 20 BP; 2 A; 4 C; 12 G; 2 T; 0 U; 0 Other;
Query Match 100.0%; Score 18; DB 8; Length 20;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```



```

Query Match      100.0%; Score 18; DB 8; Length 20;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGCACCGGTGCAGGGGG 18
   |||||
Db 3 TGCACCGGTGCAGGGGG 20

RESULT 14
ADD01049
ID ADD01049 standard; DNA; 20 BP.
XX
AC ADD01049;
XX
DT 01-JAN-2004 (first entry)
XX
DE CpG D oligonucleotide SEQ ID NO:13.
XX
KW vascular endothelial growth factor; VEGF; CpG oligonucleotide;
KW neovascularisation; angiogenesis; vulnery; vasotropic;
KW antiarteriosclerotic; gene therapy; skin graft; male pattern baldness;
KW atherosclerosis; ischaemia; ss.
XX
OS Synthetic.
XX
XX WO2003054161-A2.
XX
XX 03-JUL-2003.
XX
PF 19-DEC-2002; 2002WO-US040955.
XX
PR 20-DEC-2001; 2001US-0343457P.
XX
XX (UYTB-) UNIV TENNESSEE RES CORP.
XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PA Klinman DM, Zheng M, Rouse BT;
XX
XX WPI; 2003-559138/52.
XX
XX Inducing the production of vascular endothelial growth factor by a cell,
XX useful for inducing angiogenesis, comprises contacting the cell with a
XX CpG oligodeoxynucleotide.
XX
XX Example 7; SEQ ID NO 13; 37pp; English.
XX
XX The present invention describes a method for inducing the production of
XX vascular endothelial growth factor (VEGF) by a cell comprising contacting
XX the cell with a CpG oligonucleotide and therefore inducing the production
XX of VEGF by the cell. Also described: (1) inducing neovascularisation in a
XX tissue, comprising introducing a CpG oligonucleotide into an area of the
XX tissue where the formation of new blood vessels is desired, and so
XX inducing neovascularisation in the area of the tissue; (2) promoting
XX angiogenesis in an area of the subject where angiogenesis is desired,
XX comprising introducing a CpG oligonucleotide to the area, and so
XX promoting angiogenesis in the subject; and (3) screening for an agent
XX that inhibits neovascularisation, comprising administering a CpG
XX oligonucleotide to a non-human mammal and administering the agent to the
XX mammal, where inhibition of angiogenesis in the animal indicates that the
XX agent is effective in inhibiting neovascularisation. The CpG
XX oligonucleotides have vulnery, vasotropic and antiarteriosclerotic
XX activities, and can be used in gene therapy. The method and the CpG
XX oligonucleotides can be used in inducing angiogenesis or
XX neovascularisation, such as in subjects with a skin graft, subjects who
XX exhibit male pattern baldness, or subjects who have a wound or who have
XX atherosclerosis or ischaemia. The method may also be used in screening
XX for agents that inhibit neovascularisation. The present sequence
XX represents a CpG oligonucleotide which is used in the exemplification of
XX the present invention.
XX
XX Sequence 20 BP; 2 A; 4 C; 12 G; 2 T; 0 U; 0 Other;

Query Match      100.0%; Score 18; DB 6; Length 28;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGCACCGGTGCAGGGGG 18
   |||||
Db 3 TGCACCGGTGCAGGGGG 20

RESULT 15
ABL35599
ID ABL35599 standard; DNA; 28 BP.
XX
AC ABL35599;
XX
DT 04-APR-2002 (first entry)
XX
DE Immunostimulatory oligonucleotide SEQ ID NO: 525.
XX
KW DNA/RNA hybrid; phosphorothioate backbone; immunostimulatory; vaccine;
KW infection; allergy; cancer; hypersensitivity; bio-warfare;
KW immunostimulant; antiallergic; cytostatic; antimicrobial; anti-HIV;
KW immunosuppressive; protozoicide; virucide; hepatotropic; gene therapy;
KW antiinflammatory; antibacterial; ss.
XX
OS Synthetic.
XX
XX Location/Qualifiers
XX Key 1..28
XX misc_RNA /*tag= a
XX FT /note= "optionally thymidine is replaced by uracil to
XX FT form RNA or DNA/RNA hybrids. Thymidine is linked to at
XX FT least one other base through a ribose sugar"
XX
XX WO200193902-A2.
XX
XX 13-DEC-2001.
XX
XX 07-JUN-2001; 2001WO-US018276.
XX
XX 07-JUN-2000; 2000US-0209797P.
XX (BIOS-) BIOSYNEXUS INC.
XX
XX Mond JJ, Flora M, Klinman DM;
XX
XX WPI; 2002-130570/17.
XX
XX New immunostimulatory compositions comprising RNA/DNA hybrid
XX oligonucleotides, useful for enhancing an immune response or inducing
XX cytokines, particularly for treating diseases, e.g. cancer, allergy or
XX HIV infection.
XX
XX Example 11; Page 61; 68pp; English.
XX
XX The present invention relates to an immunostimulatory composition, which
XX comprises at least one oligonucleotide comprising both an RNA region and
XX a DNA region. The composition is useful for enhancing an immune response
XX or inducing cytokines. It can be used as a vaccine adjuvant and in
XX treating diseases, including pathogenic infection (non-malignant
XX tumours (e.g. cancers of the brain, lung, ovary, breast, prostate or
XX colon, or carcinomas and sarcomas), autoimmune diseases or allergies
XX (e.g. allergic rhinitis, hay fever or food allergies), Lyme disease,
XX hepatitis, HIV or malaria. The composition is also useful for treating,
XX preventing or ameliorating the symptoms resulting from exposure to a bio-
XX warfare agent, e.g. Ebola, Anthrax or Listeria. The present sequence is
XX an immunostimulatory oligonucleotide described in the exemplification of
XX the invention
XX
XX Sequence 28 BP; 10 A; 4 C; 12 G; 2 T; 0 U; 0 Other;

```

Best Local Similarity 100.0%; Pred. No. 63;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 TGCACCGGTGCACGGGG 18
Db 3 TGCACCGGTGCACGGGG 20

Search completed: July 2, 2004, 08:31:33
Job time : 135.89 secs

OM nucleic - nucleic search, using sw model

Run on: July 2, 2004, 07:36:05 ; Search time 633.732 Seconds
(without alignments)
1231.080 Million cell updates/sec

Title: US-10-068-160-13
Perfect score: 18
Sequence: 1 tgcacgggtgcaggggggg 18

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl.*

- 1: gb.ba.*
- 2: gb.htg.*
- 3: gb.in.*
- 4: gb.om.*
- 5: gb.ov.*
- 6: gb.pat.*
- 7: gb.ph.*
- 8: gb.pl.*
- 9: gb.pr.*
- 10: gb.ro.*
- 11: gb.sts.*
- 12: gb.sy.*
- 13: gb.un.*
- 14: gb.vi.*
- 15: em.ba.*
- 16: em.fun.*
- 17: em.hum.*
- 18: em.in.*
- 19: em.mu.*
- 20: em.om.*
- 21: em.or.*
- 22: em.ov.*
- 23: em.pat.*
- 24: em.ph.*
- 25: em.pl.*
- 26: em.roi.*
- 27: em.sts.*
- 28: em.un.*
- 29: em.vi.*
- 30: em.htg.hum.*
- 31: em.htg.inv.*
- 32: em.htg.other.*
- 33: em.htg.mus.*
- 34: em.htg.pin.*
- 35: em.htg.rod.*
- 36: em.htg.nam.*
- 37: em.htg.vrt.*
- 38: em.sv.*
- 39: em.htgo.hum.*
- 40: em.htgo.mus.*
- 41: em.htgo.other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	18	100.0	20	6	AX194442	AX194442 Sequence
2	18	100.0	20	6	AX352200	AX352200 Sequence
3	18	100.0	20	6	AX352208	AX352208 Sequence
4	18	100.0	20	6	AX352211	AX352211 Sequence
5	18	100.0	20	6	AX352218	AX352218 Sequence
6	18	100.0	20	6	AX352244	AX352244 Sequence
7	18	100.0	20	6	AX465392	AX465392 Sequence
8	18	100.0	28	6	AX352221	AX352221 Sequence
9	18	100.0	28	6	AX352229	AX352229 Sequence
10	18	100.0	28	6	AX352233	AX352233 Sequence
11	18	100.0	28	6	AX352241	AX352241 Sequence
12	18	100.0	40	6	AX352252	AX352252 Sequence
13	17	94.4	10782	1	AE001002	AE001002 Archaeogl
14	16.4	91.1	20	6	AX194501	AX194501 Sequence
15	16.4	91.1	20	6	AX352199	AX352199 Sequence
16	16.4	91.1	20	6	AX352203	AX352203 Sequence
17	16.4	91.1	20	6	AX352210	AX352210 Sequence
18	16.4	91.1	20	6	AX352214	AX352214 Sequence
19	16.4	91.1	20	6	AX352247	AX352247 Sequence
20	16.4	91.1	28	6	AX352220	AX352220 Sequence
21	16.4	91.1	28	6	AX352224	AX352224 Sequence
22	16.4	91.1	28	6	AX352232	AX352232 Sequence
23	16.4	91.1	28	6	AX352236	AX352236 Sequence
24	16.4	91.1	124270	10	AC091518	AC091518 Mus muscu
25	16.4	91.1	155724	4	AC091316	AC091316 Sus scrof
26	16.4	91.1	201320	2	AC073816	AC073816 Mus muscu
27	16.4	91.1	260424	2	AC131745	AC131745 Mus muscu
28	16.4	91.1	307820	2	AC130831	AC130831 Mus muscu
29	16.4	91.1	347365	1	BX569691	BX569691 Synchoco
30	16	88.9	13787	1	AE013603	AE013603 Yersinia
31	16	88.9	47225	2	AC099869	AC099869 Mus muscu
32	16	88.9	110000	2	AC105643	Continuation (5 of
33	16	88.9	210644	2	AC116555	AC116555 Mus muscu
34	16	88.9	235050	1	AY414158	AY414158 Yersinia
35	16	88.9	240918	2	AC137254	AC137254 Rattus no
36	16	88.9	264464	2	AC107410	AC107410 Rattus no
37	16	88.9	323991	2	AC098512	AC098512 Rattus no
38	15.4	85.6	19	6	AX194422	AX194422 Sequence
39	15.4	85.6	19	6	AX465372	AX465372 Sequence
40	15.4	85.6	342	11	AU027239	AU027239 Rattus no
41	15.4	85.6	540	4	AY316132	AY316132 Felis cat
42	15.4	85.6	827	6	AX283735	AX283735 Sequence
43	15.4	85.6	1236	14	AF082811	AF082811 Cercopith
44	15.4	85.6	1245	14	AF082813	AF082813 Cercopith
45	15.4	85.6	1246	14	AF082814	AF082814 Cercopith

ALIGNMENTS

RESULT 1	AX194442	Sequence 42 from Patent WO0151500.	20 bp	DNA	linear	PAT 28-AUG-2001
LOCUS	AX194442	Sequence 42 from Patent WO0151500.				
DEFINITION	AX194442					
ACCESSION	AX194442					
VERSION	AX194442.1	GI:15385098				
KEYWORDS		synthetic construct				
SOURCE		synthetic construct				
ORGANISM		artificial sequences.				
REFERENCE	1					
AUTHORS		Klinman, D., Ishii, K. and Verthelyi, D.				
TITLE		Oligodeoxynucleotide and its use to induce an immune response				
JOURNAL		Patent: WO 0151500-A 42 19-JUL-2001;				
		Secretary of the Department of Health and Human Services (US)				

FEATURES	source	Location/Qualifiers	Best Local Similarity	Score	DB	Length	Matches	Conservative	Mismatches	Indels	Gaps
ORIGIN											
Query Match		100.0%; Score 18; DB 6; Length 20;									
Best Local Similarity		100.0%; Pred. No. 4.2e+02;									
Matches	18;	Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
QY	1	TGCACCGGTGCAGGGGG 18									
DB	3	TGCACCGGTGCAGGGGG 20									
ORIGIN											
LOCUS	AX352200	20 bp DNA									
DEFINITION	Sequence 496 from Patent WO0193902.										
ACCESSION	AX352200										
VERSION	AX352200.1	GI:18617483									
KEYWORDS											
SOURCE		synthetic construct									
ORGANISM		artificial sequences.									
REFERENCE	1	Mond, J.J., Flora, M. and Klimman, D.M.									
AUTHORS		Immunostimulatory rna/dna hybrid molecules									
TITLE		Patent: WO 0193902-A 496 13-DEC-2001;									
JOURNAL		Biosynexus Incorporated (US)									
FEATURES		Location/Qualifiers									
source		1. .20									
		/organism="synthetic construct"									
		/mol_type="unassigned DNA"									
		/db_xref="taxon:32630"									
		/note="Synthetic HDR"									
ORIGIN											
Query Match		100.0%; Score 18; DB 6; Length 20;									
Best Local Similarity		100.0%; Pred. No. 4.2e+02;									
Matches	18;	Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
QY	1	TGCACCGGTGCAGGGGG 18									
DB	3	TGCACCGGTGCAGGGGG 20									
ORIGIN											
LOCUS	AX352208	20 bp DNA									
DEFINITION	Sequence 504 from Patent WO0193902.										
ACCESSION	AX352208										
VERSION	AX352208.1	GI:18617491									
KEYWORDS											
SOURCE		synthetic construct									
ORGANISM		artificial sequences.									
REFERENCE	1	Mond, J.J., Flora, M. and Klimman, D.M.									
AUTHORS		Immunostimulatory rna/dna hybrid molecules									
TITLE		Patent: WO 0193902-A 504 13-DEC-2001;									
JOURNAL		Biosynexus Incorporated (US)									
FEATURES		Location/Qualifiers									
source		1. .20									
		/organism="synthetic construct"									
		/mol_type="unassigned DNA"									
		/db_xref="taxon:32630"									
		/note="Synthetic HDR"									
ORIGIN											
Query Match		100.0%; Score 18; DB 6; Length 20;									
Best Local Similarity		100.0%; Pred. No. 4.2e+02;									
Matches	18;	Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
QY	1	TGCACCGGTGCAGGGGG 18									
DB	3	TGCACCGGTGCAGGGGG 20									
ORIGIN											
LOCUS	AX352218	20 bp DNA									
DEFINITION	Sequence 514 from Patent WO0193902.										
ACCESSION	AX352218										
VERSION	AX352218.1	GI:18617501									

AX352244
LOCUS AX352244 20 bp DNA linear PAT 06-FEB-2002
DEFINITION Sequence 540 from Patent WO0193902.
ACCESSION AX352244
VERSION AX352244.1 GI:18617527
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE
AUTHORS Mond, J.J., Flora, M. and Klinman, D.M.
TITLE Immunostimulatory rna/dna hybrid molecules
JOURNAL Patent: WO 0193902-A 540 13-DEC-2001;
Biosynexus Incorporated (US)
FEATURES
source Location/Qualifiers
1..20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic HDR"
ORIGIN
Query Match 100.0%; Score 18; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.2e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 18; Conservative 0;
Qy 1 TGCACCGGTGCAGGGGG 18
Db 3 TGCACCGGTGCAGGGGG 20
RESULT 7
AX465392
LOCUS AX465392 20 bp DNA linear PAT 16-JUL-2002
DEFINITION Sequence 60 from Patent WO0211761.
ACCESSION AX465392
VERSION AX465392.1 GI:21899755
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE
AUTHORS Mond, J.J., Prince, G. and Klinman, D.M.
TITLE Vaccine against RSV
JOURNAL Patent: WO 0211761-A 60 14-FEB-2002;
HENRY M. JACKSON FOUNDATION FOR THE ADVANCEMENT OF MILITARY
MEDICINE (US)
FEATURES
source Location/Qualifiers
1..20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic oligonucleotide"
ORIGIN
Query Match 100.0%; Score 18; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 4.2e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 18; Conservative 0;
Qy 1 TGCACCGGTGCAGGGGG 18
Db 3 TGCACCGGTGCAGGGGG 20
RESULT 8
AX352221
LOCUS AX352221 28 bp DNA linear PAT 06-FEB-2002
DEFINITION Sequence 517 from Patent WO0193902.
ACCESSION AX352221
VERSION AX352221.1 GI:18617504
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE
AUTHORS Mond, J.J., Flora, M. and Klinman, D.M.
TITLE Immunostimulatory rna/dna hybrid molecules
JOURNAL Patent: WO 0193902-A 525 13-DEC-2001;
Biosynexus Incorporated (US)
FEATURES
source Location/Qualifiers
1..28
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic HDR"

artificial sequences.
REFERENCE
AUTHORS Mond, J.J., Flora, M. and Klinman, D.M.
TITLE Immunostimulatory rna/dna hybrid molecules
JOURNAL Patent: WO 0193902-A 517 13-DEC-2001;
Biosynexus Incorporated (US)
FEATURES
source Location/Qualifiers
1..28
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic HDR"
ORIGIN
Query Match 100.0%; Score 18; DB 6; Length 28;
Best Local Similarity 100.0%; Pred. No. 4.1e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 18; Conservative 0;
Qy 1 TGCACCGGTGCAGGGGG 18
Db 3 TGCACCGGTGCAGGGGG 20
RESULT 9
AX352229
LOCUS AX352229 28 bp DNA linear PAT 06-FEB-2002
DEFINITION Sequence 525 from Patent WO0193902.
ACCESSION AX352229
VERSION AX352229.1 GI:18617512
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE
AUTHORS Mond, J.J., Flora, M. and Klinman, D.M.
TITLE Immunostimulatory rna/dna hybrid molecules
JOURNAL Patent: WO 0193902-A 525 13-DEC-2001;
Biosynexus Incorporated (US)
FEATURES
source Location/Qualifiers
1..28
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic HDR"
ORIGIN
Query Match 100.0%; Score 18; DB 6; Length 28;
Best Local Similarity 100.0%; Pred. No. 4.1e+02; Mismatches 0; Indels 0; Gaps 0;
Matches 18; Conservative 0;
Qy 1 TGCACCGGTGCAGGGGG 18
Db 3 TGCACCGGTGCAGGGGG 20
RESULT 10
AX352233
LOCUS AX352233 28 bp DNA linear PAT 06-FEB-2002
DEFINITION Sequence 529 from Patent WO0193902.
ACCESSION AX352233
VERSION AX352233.1 GI:18617516
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE
AUTHORS Mond, J.J., Flora, M. and Klinman, D.M.
TITLE Immunostimulatory rna/dna hybrid molecules
JOURNAL Patent: WO 0193902-A 529 13-DEC-2001;
Biosynexus Incorporated (US)
FEATURES
source Location/Qualifiers
1..28
/organism="synthetic construct"

1 TGCACCGGTGCAGGGGG 18
 |||||
16 TGCACCGGTGCAGGGGG 33

Accession	Length	Type	Source
AE001002	10782 bp	DNA	linear BCT 17-MAR-2003

genome.
AE001002 AE000782
AE001002.1 GI:2689325

Archaeoglobus fulgidus DSM 4304
Archaeoglobus fulgidus DSM 4304
Archaea: Euryarchaeota: Archaeoglobales;
Archaeoglobaceae; Archaeoglobus.
1 (bases 1 to 10782)
Klenk, H.P., Clayton, R.A., Tomb, J., White, O., Nelson, K.E.,
Ketchum, K.A., Dodson, R.J., Gwinn, M., Hickey, E.K., Peterson, J.D.,
Richardson, D.L., Kierlavage, A.R., Graham, D.E., Kyrtides, N.C.,
Fleischmann, R.D., Quackenbush, J., Lee, N.H., Sutton, C.G., Gill, S.,
Kirkness, E.F., Dougherty, B.A., McKenney, K., Adams, M.D., Loftus, B.,
Peterson, S., Reich, C.I., McNeil, L.K., Badger, J.H., Glodek, A.,
Zhou, L., Overbeek, R., Gocayne, J.D., Weidman, J.F., McDonald, L.,
Tuttleback, T., Cotton, M.D., Spriggs, T., Atlach, P., Kaine, B.P.,
Sykes, S.M., Sadow, P.W., D'Andrea, K.P., Bowman, C., Fujii, C.,
Garland, S.A., Mason, T.M., Olsen, G.J., Fraser, C.M., Smith, H.O.,
Woese, C.R. and Venter, J.C.

The complete genome sequence of the hyperthermophilic, sulphate-reducing archaeon *Archaeoglobus fulgidus* Nature 390 (6558), 364-370 (1997)

:

Richardson, D. L., Kerlavage, A. R., Graham, D. E., Kyrpides, N. C., Fleischmann, R. D., Quackenbush, J., Lee, N. H., Sutton, G. G., Gill, S., Kirkness, E. F., Dougherty, B. A., McKenney, K., Adams, M. D., Loftus, B.,

Zhou, L., Overbeek, R., Goeyne, J. D., Weidman, J. F., McDonald, L., Utterback, T., Cotton, M. D., Spriggs, T., Artiach, P., Kaine, B. P., Sykes, S. M., Sadow, P. W., D'Andrea, K. P., Bowman, C., Fujii, C.,

Direct Submission
Submitted (15-DEC-1997) The Institute for Genomic Research, 9712
Medical Center Dr, Rockville, MD 20850, USA
In order to show the genes in ascending order on the genome, the
origin of this version has been moved by TIGR to position 2093570
of the original version and the opposite strand is shown from the
original version.
On Dec 16, 1997 this sequence version replaced gi:2649104.
Location/Qualifiers
1. .10782

```

/organism="Archaeoglobus fulgidus DSM 4304"
/mol_type="genomic DNA"
/db_xref="taxon:224325"
/complement(159..1019)
/gene="AFL454"
/complement(159..1019)
/gene="AFL454"
/note="hypothetical protein; identified by GeneMark;
putative"
/codon_start=1
/transl_table=11

```

454¹¹

```

/db xref="GI:2649115"
/translation="MKFRTLFNLLTACILLFADVRADTFQVDYKIYESNQCGGKSKY
VEFHVLPTKRVGLLLLSYIWAGNEAITPCEPSSWRDLVEVSPNQAGTSKFYYEKL

```

/CD_Xref="GI:26493113"
translation="MKFRTLFNLLTACILLFADVRADTFQVDYKIYESNQCGGKSYK
VVEFVLVPTKRVGLLLSYIWAGNEAITCEPSSWRDLVEVSPNAGTSKFYYEKL
PESGNIYLKISSGKEEQKLYFPFALQATTITATASQAPATSHQVDLATQINSAVSL

```

F#
5471..5543
/gene="tRNA-Thr-1"
5471..5543
/gene="tRNA-Thr-1"
/product="tRNA-Thr"
/note="codon recognized: ACC"
complement(5605..5877)
/gene="AF1459"
complement(5605..5877)
/gene="AF1459"
/note="similar to GB:L77117 SP:Q57735 PID:I499069 percent identity: 35.38; identified by sequence similarity; putative"
/codon_start=1
/transl_table=11
/product="conserved hypothetical protein"
/protein_id="AAB89785.1"
/db_xref="GI:2649106"
DELKKGGLVRIQDSGRYYSLTDKGRPFLEKYQKIREFEEFGI"
translatability=1
complement(5887..6570)
/gene="AF1460"
complement(5887..6570)
/gene="AF1460"
/note="hypothetical protein; identified by GeneMark; putative"
/codon_start=1
/transl_table=11
/product="A. fulgidus predicted coding region AF1460"
/protein_id="AAB89791.1"
/db_xref="GI:2649112"
translatability=1
nucleotide="MPPPMIPPKLPPLPEFAAEALYLSIIFLICLIYHRLREVYKLS
DYRGPHFSNTPFLGAYLFRFVLVLLSGVMFEETLEGIRGIMAPSMAPLAYSG
SAAUITYTLLMWLERPFCGEWINGVALVTSLSRMPLVFLISOLALVFLLVA
RIFVNSHFRESRSKRYPHYILLFVFWLNINISLTFELPLEFPFPAITLVSAVILI
IAVRVKKL"
6558..6891
/gene="AF1461"
6558..6891
/gene="AF1461"
/note="similar to GP:I747410 percent identity: 50.98; identified by sequence similarity; putative"
/codon_start=1
/transl_table=11
/product="iron-sulfur cluster binding protein, putative"
/protein_id="AAB89787.1"
/db_xref="GI:2649108"
translatability=1
nucleotide="WRIGSDSVVVVEQLSGCIGCGTCVCPTDVRLEGGRAVIKYK
EDQCCHLCRLGYCPVDATILSPKSLPIVANG"
7028..7579
/gene="AF1462"
7028..7579
/gene="AF1462"
/note="hypothetical protein; identified by GeneMark; putative"
/codon_start=1
/transl_table=11
/product="A. fulgidus predicted coding region AF1462"
/protein_id="AAB89790.1"
/db_xref="GI:2649111"

Query Match      94.4%; Score 17; DB 1; Length 10782;
Best Local Similarity 100.0%; Pred. No. 6.5e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TGCACCGGTGCAGGGGG 17
          |||||
DB     8164 TGCACCGGTGCAGGGGG 8180

RESULT 14
X194501

```

Fri Jul 2 14:53:27 2004

LOCUS AX194501 20 bp DNA linear PAT 28-AUG-2001

DEFINITION Sequence 101 from Patent WO0151500.

ACCESSION AX194501

VERSION AX194501.1 GI:15385157

KEYWORDS synthetic construct

SOURCE synthetic construct

ORGANISM artificial sequences.

REFERENCE 1

AUTHORS Klinman,D., Ishii,K. and Verthelyi,D.

TITLE Oligodeoxynucleotide and its use to induce an immune response

JOURNAL Patent: WO 0151500-A 101 19-JUL-2001;

SECRETARY of the Department of Health and Human Services (US)

FEATURES

source

1..20

/organism="synthetic construct"

/mol_type="unassigned DNA"

/db_xref="taxon:32630"

/note="Synthetic DNA"

ORIGIN

Query Match 91.1%; Score 16.4; DB 6; Length 20;

Best Local Similarity 94.4%; Pred. No. 2.7e+03;

Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TGCACCGGTGCAGGGGG 18

Db 3 TGCACCGGTGCAGGGGG 20

RESULT 15

AX352199

LOCUS AX352199 20 bp DNA linear PAT 06-FEB-2002

DEFINITION Sequence 495 from Patent WO0193902.

ACCESSION AX352199

VERSION AX352199.1 GI:18617482

KEYWORDS synthetic construct

SOURCE synthetic construct

ORGANISM artificial sequences.

REFERENCE 1

AUTHORS Mond,J.J., Flora,M. and Klinman,D.M.

TITLE Immunostimulatory rna/dna hybrid molecules

JOURNAL Patent: WO 0193902-A 495 13-DEC-2001;

BIOSYNEXUS Incorporated (US)

FEATURES

source

1..20

/organism="synthetic construct"

/mol_type="unassigned DNA"

/db_xref="taxon:32630"

/note="Synthetic HDR"

ORIGIN

Query Match 91.1%; Score 16.4; DB 6; Length 20;

Best Local Similarity 94.4%; Pred. No. 2.7e+03;

Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TGCACCGGTGCAGGGGG 18

Db 3 TGCACCGGTGCAGGGGG 20

Search completed: July 2, 2004, 10:07:58

Job time : 636.732 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 2, 2004, 08:09:30 ; Search time 28.2073 Seconds
{without alignments}
354.132 Million cell updates/sec

Title: US-10-068-160-13

Perfect score: 18

Sequence: 1 tgcaccggtgcaggggg 18

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents_NA.*
1: /cgn2_6/ptodata/2/ina/5A_COMB.seq.*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq.*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq.*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq.*
5: /cgn2_6/ptodata/2/ina/ECTUS_COMB.seq.*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	14.8	82.2	1443	3	US-08-959-381A-3
C 2	14.8	82.2	1446	4	US-09-170-496D-81
C 3	14.8	82.2	1446	3	US-09-170-496D-207
C 4	14.8	82.2	1626	3	US-08-959-381A-4
5	14.8	82.2	3358	3	US-09-248-571-2
6	14.8	82.2	3358	4	US-09-553-736-2
7	14.8	82.2	24707	4	US-09-740-027-3
8	14.8	82.2	38653	4	US-09-922-445-1
9	14.4	80.0	265	4	US-09-313-294A-385
10	14.4	80.0	2194	4	US-09-023-655-668
11	14.4	80.0	732	4	US-09-252-991A-736
C 12	14	77.8	1350	4	US-09-252-991A-677
C 13	14	77.8	7168	3	US-08-840-316-4
C 14	14	77.8	7168	3	US-08-809-523-4
C 15	14	77.8	7168	3	US-08-471-971-4
C 16	14	77.8	7168	4	US-09-402-776-4
C 17	14	77.8	7168	5	PCT-US93-08849A-4
C 18	14	77.8	7168	5	PCT-US93-08849-4
C 19	14	77.8	7195	3	US-08-478-507-6
C 20	14	77.8	7195	3	US-09-128-275A-6
C 21	14	77.8	7195	4	US-09-553-427-6
C 22	13.8	76.7	96	4	US-08-342-681C-107
23	13.8	76.7	106	1	US-08-441-591-18
24	13.8	76.7	106	1	US-08-441-591-19
25	13.8	76.7	106	1	US-08-303-362A-18
26	13.8	76.7	106	1	US-08-303-362A-19
27	13.8	76.7	106	5	PCT-US95-05600-35

28	13.8	76.7	106	5	PCT-US95-05600-36
29	13.8	76.7	107	1	US-08-441-591-20
30	13.8	76.7	107	1	US-08-303-362A-20
31	13.8	76.7	107	5	PCT-US95-05600-37
C 32	13.8	76.7	204	4	US-09-313-294A-7594
33	13.8	76.7	382	4	US-09-833-381-178
34	13.8	76.7	633	4	US-09-489-039A-2752
C 35	13.8	76.7	672	4	US-09-511-881A-1
C 36	13.8	76.7	672	4	US-09-511-881A-2
37	13.8	76.7	750	4	US-09-833-381-1453
C 38	13.8	76.7	885	4	US-09-252-991A-7532
39	13.8	76.7	899	4	US-09-171-209-50
40	13.8	76.7	912	4	US-09-252-991A-7811
C 41	13.8	76.7	1038	1	US-08-031-148-3
C 42	13.8	76.7	1038	3	US-08-415-838-3
C 43	13.8	76.7	1038	4	US-09-205-169-3
44	13.8	76.7	1242	4	US-09-252-991A-7949
C 45	13.8	76.7	1359	4	US-09-489-039A-2500

ALIGNMENTS

RESULT 1
US-08-959-381A-3/c
; Sequence 3, Application US/08959381A
; Patent No. 6048711
; GENERAL INFORMATION:
; APPLICANT: HINUMA, SHUJI
; APPLICANT: FUKUSUMI, SHUJI
; TITLE OF INVENTION: NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR
; TITLE OF INVENTION: POLYNUCLEOTIDES
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ratner & Prestia
; STREET: P.O. Box 980
; CITY: Valley Forge
; STATE: PA
; COUNTRY: USA
; ZIP: 19482
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/959,381A
; FILING DATE: 28-OCT-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 286823/1996
; FILING DATE: 29-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Prestia, Paul F
; REGISTRATION NUMBER: 23,031
; REFERENCE/DOCKET NUMBER: TAK-50003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-407-0700
; TELEFAX: 610-407-0700
; TELEX: 846169
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1443 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
US-08-959-381A-3

Query Match 82.2% ; Score 14.8; DB 3; Length 1443;
Best Local Similarity 88.9%; Pred. No. 2.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
QY      1  TGCACCGGTGCAGGGGG 18
Db      94  TCCCCAGGTGCAGGGGG 77

RESULT 2
US-09-170-496D-81/c
; Sequence 81, Application US/09170496D
; Patent No. 6555339
; GENERAL INFORMATION:
; APPLICANT: Behan, Dominic P.
; APPLICANT: Chalmers, Derek T.
; APPLICANT: Liaw, Chen W.
; TITLE OF INVENTION: No. 6555339-Endogenous, Constitutively Activated Human G Protein-
; FILE REFERENCE: AREN-0040
; CURRENT APPLICATION NUMBER: US/09/170,496D
; CURRENT FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 294
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 81
; LENGTH: 1446
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-170-496D-81

Query Match      82.2%; Score 14.8; DB 4; Length 1446;
Best Local Similarity 88.9%; Pred. No. 2.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1  TGCACCGGTGCAGGGGG 18
Db      94  TCCCCAGGTGCAGGGGG 77

RESULT 3
US-09-170-496D-207/c
; Sequence 207, Application US/09170496D
; Patent No. 6555339
; GENERAL INFORMATION:
; APPLICANT: Behan, Dominic P.
; APPLICANT: Chalmers, Derek T.
; APPLICANT: Liaw, Chen W.
; TITLE OF INVENTION: No. 6555339-Endogenous, Constitutively Activated Human G Protein-
; FILE REFERENCE: AREN-0040
; CURRENT APPLICATION NUMBER: US/09/170,496D
; CURRENT FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 294
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 207
; LENGTH: 1446
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-170-496D-207

Query Match      82.2%; Score 14.8; DB 4; Length 1446;
Best Local Similarity 88.9%; Pred. No. 2.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1  TGCACCGGTGCAGGGGG 18
Db      94  TCCCCAGGTGCAGGGGG 77

RESULT 4
US-08-959-381A-4/c
; Sequence 4, Application US/08959381A
; Patent No. 6048711
; GENERAL INFORMATION:
; APPLICANT: HINUMA, SHUJI
; APPLICANT: FUKUSUMI, SHOJI
```

```
; APPLICANT: KAWAMATA, YUJI
; TITLE OF INVENTION: NOVEL HUMAN G-PROTEIN COUPLED RECEPTOR
; TITLE OF INVENTION: POLYNUCLEOTIDES
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ratner & Prestia
; STREET: P.O. Box 980
; CITY: Valley Forge
; STATE: PA
; COUNTRY: USA
; ZIP: 19482
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/959,381A
; FILING DATE: 28-OCT-1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 286823/1996
; FILING DATE: 29-OCT-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Prestia, Paul F
; REGISTRATION NUMBER: 23,031
; REFERENCE/DOCKET NUMBER: TAK-50003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-407-0700
; TELEFAX: 610-407-0700
; TELEX: 846169
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1626 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-959-381A-4

Query Match      82.2%; Score 14.8; DB 3; Length 1626;
Best Local Similarity 88.9%; Pred. No. 2.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1  TGCACCGGTGCAGGGGG 18
Db      277  TCCCCAGGTGCAGGGGG 260

RESULT 5
US-09-248-571-2
; Sequence 2, Application US/09248571
; Patent No. 6136539
; GENERAL INFORMATION:
; APPLICANT: BASBAUM, CAROL
; APPLICANT: GALLOP, MARIANNE
; APPLICANT: DAIZONG, LI
; APPLICANT: GEBREMICHAEL, ASSEFA
; APPLICANT: GENSCH, ERIN
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR INHIBITION OF MUC-5 MUCIN
; FILE REFERENCE: UCSF12/02
; CURRENT APPLICATION NUMBER: US/09/248,571
; CURRENT FILING DATE: 1999-02-11
; EARLIER APPLICATION NUMBER: 60/074,398
; EARLIER FILING DATE: 1998-02-11
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 3358
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-248-571-2
```

Query Match 82.2%; Score 14.8; DB 3; Length 3358;
Best Local Similarity 88.9%; Pred. No. 2.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TGCACCGGTGCAGGGGG 18
|||||
Db 999 TGCACCCATGCAGGGGG 1016

RESULT 6
US-09-553-736-2
; Sequence 2, Application US/09553736
; Patent No. 6440672
; GENERAL INFORMATION:
; APPLICANT: BASBAUM, Carol
; APPLICANT: GALLUP, Marianne
; APPLICANT: DAIZONG, Li
; APPLICANT: GEREMICHAEL, Assefa
; APPLICANT: GENSCH, Erin
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE INHIBITION OF MUC-5
; FILE REFERENCE: UCSF-013/0305
; CURRENT APPLICATION NUMBER: US/09/553,736
; CURRENT FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 09/248,571
; PRIOR FILING DATE: 1999-02-11
; PRIOR APPLICATION NUMBER: US 60/074,398
; PRIOR FILING DATE: 1998-02-11
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 3358
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-553-736-2

Query Match 82.2%; Score 14.8; DB 4; Length 3358;
Best Local Similarity 88.9%; Pred. No. 2.4e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TGCACCGGTGCAGGGGG 18
|||||
Db 999 TGCACCCATGCAGGGGG 1016

RESULT 7
US-09-740-027-3
; Sequence 3, Application US/09740027
; Patent No. 6485939
; GENERAL INFORMATION:
; APPLICANT: YE, Jane et al
; TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER COFACTOR
; FILE REFERENCE: CLO01052
; CURRENT APPLICATION NUMBER: US/09/740,027
; CURRENT FILING DATE: 2000-12-20
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 24707
; TYPE: DNA
; ORGANISM: Human
US-09-740-027-3

Query Match 82.2%; Score 14.8; DB 4; Length 24707;
Best Local Similarity 88.9%; Pred. No. 2.3e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TGCACCGGTGCAGGGGG 18
|||||
Db 17471 TGCACGGGGCGAGGGAGG 17488

RESULT 8
US-09-922-445-1/c
; Sequence 1, Application US/09922445
; Patent No. 6528268
; GENERAL INFORMATION:
; APPLICANT: Andersson, Maria K.
; APPLICANT: Berglund, Lars G. T.
; APPLICANT: Reneland, Rikard H.
; APPLICANT: Adam, Gail I. R.
; TITLE OF INVENTION: REAGENTS AND METHODS FOR DETECTION OF HEART FAILURE
; FILE REFERENCE: G312605
; CURRENT APPLICATION NUMBER: US/09/922,445
; CURRENT FILING DATE: 2001-08-03
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 38653
; TYPE: DNA
; ORGANISM: homo sapiens
; FEATURE:
; NAME/KEY: 5'UTR
; LOCATION: (1)..(26156)
; OTHER INFORMATION:
; NAME/KEY: misc feature
; LOCATION: (24801)..(24801)
; OTHER INFORMATION: nucleotide 24801 is a single nucleotide polymorphism which can be
; OTHER INFORMATION: A or G
; NAME/KEY: misc feature
; LOCATION: (24941)..(24941)
; OTHER INFORMATION: nucleotide 24941 is a single nucleotide polymorphism which can be
; OTHER INFORMATION: T or C
; NAME/KEY: exon
; LOCATION: (26157)..(26252)
; OTHER INFORMATION:
; NAME/KEY: Intron
; LOCATION: (26253)..(26401)
; OTHER INFORMATION:
; NAME/KEY: exon
; LOCATION: (26402)..(26543)
; OTHER INFORMATION:
; NAME/KEY: Intron
; LOCATION: (26544)..(27024)
; OTHER INFORMATION:
; NAME/KEY: exon
; LOCATION: (27025)..(27178)
; OTHER INFORMATION:
; NAME/KEY: Intron
; LOCATION: (27179)..(30519)
; OTHER INFORMATION:
; NAME/KEY: misc feature
; LOCATION: (27645)..(27645)
; OTHER INFORMATION: nucleotide 27645 is a single nucleotide polymorphism which can be
; OTHER INFORMATION: C or G
; NAME/KEY: exon
; LOCATION: (30520)..(30681)
; OTHER INFORMATION:
; NAME/KEY: Intron
; LOCATION: (30682)..(30894)
; OTHER INFORMATION:
; NAME/KEY: exon
; LOCATION: (30895)..(31027)
; OTHER INFORMATION:
; NAME/KEY: Intron
; LOCATION: (31028)..(31747)
; OTHER INFORMATION:
; NAME/KEY: exon
; LOCATION: (31748)..(31841)
; OTHER INFORMATION:
; NAME/KEY: Intron
; LOCATION: (31842)..(32400)
; OTHER INFORMATION:

NAME/KEY: misc feature
LOCATION: (32163)..
OTHER INFORMATION: nucleotide 32163 is a single nucleotide polymorphism which can be
NAME/KEY: exon
LOCATION: (32401)..
OTHER INFORMATION:
NAME/KEY: Intron
LOCATION: (32529)..
OTHER INFORMATION:
NAME/KEY: misc feature
LOCATION: (32614)..
OTHER INFORMATION: nucleotide 32614 is a single nucleotide polymorphism which can be
NAME/KEY: exon
LOCATION: (33415)..
OTHER INFORMATION:
NAME/KEY: Intron
LOCATION: (33598)..
OTHER INFORMATION:
NAME/KEY: exon
LOCATION: (34315)..
OTHER INFORMATION:
NAME/KEY: Intron
LOCATION: (34589)..
OTHER INFORMATION:
NAME/KEY: exon
LOCATION: (36405)..
OTHER INFORMATION:
NAME/KEY: Intron
LOCATION: (36524)..
OTHER INFORMATION:
NAME/KEY: exon
LOCATION: (38342)..
OTHER INFORMATION:
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: Genbank/AC004923
DATABASE ENTRY DATE: 1999-12-21
RELEVANT RESIDUES: (1)..
US-09-922-445-1

Query Match 82.2%; Score 14.8; DB 4; Length 38653;
Best Local Similarity 88.9%; Pred. No. 2.3e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TGCACCGGTGCAGGGGG 18
DB 14712 TGCACGTGGGCAGGGGG 14695

RESULT 9
US-09-313-294A-385
Sequence 385, Application US/09313294A
Patent No. 6476212
GENERAL INFORMATION:
APPLICANT: Lalgudi, Raghunath V.
APPLICANT: Ito, Laura I.
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR
FILE REFERENCE: PL-0017 US
CURRENT APPLICATION NUMBER: US/09/313,294A
CURRENT FILING DATE: 1999-05-14
NUMBER OF SEQ ID NOS: 7600
SOFTWARE: PERL Program
SEQ ID NO 385
LENGTH: 265
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No. 6476212 700549120HI
NAME/KEY: unsure
LOCATION: 3, 7, 39, 240

OTHER INFORMATION: a, t, c, g, or other
US-09-313-294A-385
Query Match 80.0%; Score 14.4; DB 4; Length 265;
Best Local Similarity 93.8%; Pred. No. 3.7e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GCACCGGTGCAGGGGG 17
DB 89 GCACCGGAGCAGGGGG 104

RESULT 10
US-09-023-655-668
Sequence 668, Application US/09023655
Patent No. 6607879
GENERAL INFORMATION:
APPLICANT: Cocks, Benjamin G.
APPLICANT: Susan G. Stuart
APPLICANT: Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
NUMBER OF SEQUENCES: 1508
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,655
FILING DATE: HEREWITH
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0001 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166

INFORMATION FOR SEQ ID NO: 668:
SEQUENCE CHARACTERISTICS:
LENGTH: 2194 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: BSIHET02
CLONE: 409041
US-09-023-655-668

Query Match 80.0%; Score 14.4; DB 4; Length 2194;
Best Local Similarity 93.8%; Pred. No. 3.6e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GCACCGGTGCAGGGGG 17
DB 2116 GCACCGGTTCAGGGGG 2131

RESULT 11
US-09-252-991A-736
Sequence 736, Application US/09252991A

Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 735
; LENGTH: 732
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-736

Query Match 77.8%; Score 14; DB 4; Length 732;
Best Local Similarity 100.0%; Pred. No. 5.6e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GCACCGGTGCAGGG 15
Db 523 GCACCGGTGCAGGG 536
|||||

RESULT 12
US-09-252-991A-677/c
; Sequence 677, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 677
; LENGTH: 1350
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-677

Query Match 77.8%; Score 14; DB 4; Length 1350;
Best Local Similarity 100.0%; Pred. No. 5.6e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GCACCGGTGCAGGG 15
Db 678 GCACCGGTGCAGGG 665
|||||

RESULT 13
US-08-840-316-4/c
; Sequence 4, Application US/08840316
; Patent No. 6054567
; GENERAL INFORMATION:
; APPLICANT: Emerson, Suzanne U., Purcell, Robert H.,
; APPLICANT: Tsarev, Sergei. A., and Robinson, Robin A.
; TITLE OF INVENTION: Recombinant Proteins Of
; TITLE OF INVENTION: A Pakistani Strain Of Hepatitis E And Their
; TITLE OF INVENTION: Use In Diagnostic Methods And Vaccines
; NUMBER OF SEQUENCES: 111
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN
; STREET: 345 PARK AVENUE

Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 677
; LENGTH: 1350
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-677

Query Match 77.8%; Score 14; DB 3; Length 7168;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 CCGGTGCAGGGGG 18
Db 2263 CCGGTGCAGGGGG 2250
|||||

RESULT 14
US-08-809-523-4/c
; Sequence 4, Application US/08809523
; Patent No. 6207416
; GENERAL INFORMATION:
; APPLICANT: Tsarev, Sergei. A., Emerson,
; APPLICANT: Suzanne U., Purcell, Robert H.
; TITLE OF INVENTION: Recombinant Proteins Of
; TITLE OF INVENTION: A Pakistani Strain Of Hepatitis E And Their
; TITLE OF INVENTION: Use In Diagnostic Methods And Vaccines
; NUMBER OF SEQUENCES: 107
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
; STREET: 345 PARK AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10154

COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/809,523
FILING DATE: 28-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/13102
FILING DATE: 03-OCT-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US08/316,765
FILING DATE: 03-OCT-1994

Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 735
; LENGTH: 732
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-736

Query Match 77.8%; Score 14; DB 4; Length 732;
Best Local Similarity 100.0%; Pred. No. 5.6e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GCACCGGTGCAGGG 15
Db 523 GCACCGGTGCAGGG 536
|||||

RESULT 12
US-09-252-991A-677/c
; Sequence 677, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 677
; LENGTH: 1350
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-677

Query Match 77.8%; Score 14; DB 4; Length 1350;
Best Local Similarity 100.0%; Pred. No. 5.6e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GCACCGGTGCAGGG 15
Db 678 GCACCGGTGCAGGG 665
|||||

RESULT 13
US-08-840-316-4/c
; Sequence 4, Application US/08840316
; Patent No. 6054567
; GENERAL INFORMATION:
; APPLICANT: Emerson, Suzanne U., Purcell, Robert H.,
; APPLICANT: Tsarev, Sergei. A., and Robinson, Robin A.
; TITLE OF INVENTION: Recombinant Proteins Of
; TITLE OF INVENTION: A Pakistani Strain Of Hepatitis E And Their
; TITLE OF INVENTION: Use In Diagnostic Methods And Vaccines
; NUMBER OF SEQUENCES: 111
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN
; STREET: 345 PARK AVENUE

Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 735
; LENGTH: 732
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-736

Query Match 77.8%; Score 14; DB 3; Length 7168;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 CCGGTGCAGGGGG 18
Db 2263 CCGGTGCAGGGGG 2250
|||||

RESULT 14
US-08-809-523-4/c
; Sequence 4, Application US/08809523
; Patent No. 6207416
; GENERAL INFORMATION:
; APPLICANT: Tsarev, Sergei. A., Emerson,
; APPLICANT: Suzanne U., Purcell, Robert H.
; TITLE OF INVENTION: Recombinant Proteins Of
; TITLE OF INVENTION: A Pakistani Strain Of Hepatitis E And Their
; TITLE OF INVENTION: Use In Diagnostic Methods And Vaccines
; NUMBER OF SEQUENCES: 107
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
; STREET: 345 PARK AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10154

COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/809,523
FILING DATE: 28-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/13102
FILING DATE: 03-OCT-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US08/316,765
FILING DATE: 03-OCT-1994

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/947,263
; FILING DATE: 18-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Richard W. Bork
; REGISTRATION NUMBER: 36,459
; REFERENCE/DOCKET NUMBER: 2026-4032US4
; TELEPHONE: (212) 758-4800
; TELEFAX: (212) 751-6849
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7168 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-809-523-4

Query Match 77.8%; Score 14; DB 3; Length 7168;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CCGGTGCAGGGGGG 18
|||||
DB 2263 CCGGTGCAGGGGGG 2250

RESULT 15

US-08-471-971-4/c
; Sequence 4, Application US/08471971
; Patent No 6287759
; GENERAL INFORMATION:
; APPLICANT: Tsarev, Sergei. A.; Emerson,
; APPLICANT: Suzanne U.; Purcell, Robert H.
; TITLE OF INVENTION: Recombinant Proteins Of
; TITLE OF INVENTION: A Pakistani Strain Of Hepatitis E And Their
; TITLE OF INVENTION: Use In Diagnostic Methods And Vaccines
; NUMBER OF SEQUENCES: 107
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN
; STREET: 345 PARK AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/471,971
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US08/316,765
; FILING DATE: 03-OCT-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US07/947,263
; FILING DATE: 18-SEP-1992
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Richard W. Bork
; REGISTRATION NUMBER: 36,459
; REFERENCE/DOCKET NUMBER: 2026-4032US2
; TELEPHONE: (212) 758-4800
; TELEFAX: (212) 751-6849
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7168 base pairs
; TYPE: nucleic acid

; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-471-971-4

Query Match 77.8%; Score 14; DB 3; Length 7168;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CCGGTGCAGGGGGG 18
|||||
DB 2263 CCGGTGCAGGGGGG 2250

Search completed: July 2, 2004, 13:37:23
Job time : 29.2073 secs


```
; SEQ ID NO 540
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic HDR
US-09-874-991C-540

Query Match      100.0%; Score 18; DB 13; Length 20;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGCACCGGTGCAGGGGG 18
   |||||
Db 3 TGCACCGGTGCAGGGGG 20

RESULT 7
US-10-068-160-2
; Sequence 2, Application US/10068160
; Publication No. US20030060440A1
; GENERAL INFORMATION:
; APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA, REPRESENTED BY THE
; APPLICANT: SECRETARY, DEPARTMENT OF HEALTH AND HUMAN SERVICES
; APPLICANT: KLINMAN, Dennis
; APPLICANT: VERTHELYI, Ken
; TITLE OF INVENTION: OLIGODEOXYNUCLEOTIDE AND ITS USE TO INDUCE AN IMMUNE RESPONSE
; FILE REFERENCE: 4239-61999
; CURRENT APPLICATION NUMBER: US/10/068,160
; CURRENT FILING DATE: 2002-02-06
; PRIOR APPLICATION NUMBER: 60/128,898
; PRIOR FILING DATE: 1999-04-12
; NUMBER OF SEQ ID NOS: 120
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide
US-10-068-160-2

Query Match      100.0%; Score 18; DB 15; Length 20;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGCACCGGTGCAGGGGG 18
   |||||
Db 3 TGCACCGGTGCAGGGGG 20

RESULT 8
US-10-194-035-42
; Sequence 42, Application US/10194035
; Publication No. US20030144229A1
; GENERAL INFORMATION:
; APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS REPRESENTED BY THE
; APPLICANT: SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES
; APPLICANT: KLINMAN, Dennis
; APPLICANT: ISHII, Ken
; APPLICANT: VERTHELYI, Daniela
; TITLE OF INVENTION: OLIGODEOXYNUCLEOTIDE AND ITS USE TO INDUCE AN IMMUNE RESPONSE
; FILE REFERENCE: 4239-63317
; CURRENT APPLICATION NUMBER: US/10/194,035
; CURRENT FILING DATE: 2002-07-12
; PRIOR APPLICATION NUMBER: PCT/US01/01122
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: US 60/176,115
; PRIOR FILING DATE: 2000-01-14
; NUMBER OF SEQ ID NOS: 119
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 42
```

```
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
US-10-194-035-42

Query Match      100.0%; Score 18; DB 15; Length 20;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGCACCGGTGCAGGGGG 18
   |||||
Db 3 TGCACCGGTGCAGGGGG 20

RESULT 9
US-10-666-022-2
; Sequence 2, Application US/10666022
; Publication No. US20040105872A1
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America, as represented by the
; APPLICANT: Secretary of the Department of Health and Human Services
; APPLICANT: Klinman, Dennis M.
; APPLICANT: Verthelyi, Daniela
; TITLE OF INVENTION: METHOD OF TREATING AND PREVENTING INFECTIONS IN IMMUNOCOMPROMISED
; FILE REFERENCE: 4239-66899
; CURRENT APPLICATION NUMBER: US/10/666,022
; CURRENT FILING DATE: 2003-09-17
; PRIOR APPLICATION NUMBER: US 60/411,944
; PRIOR FILING DATE: 2002-09-18
; NUMBER OF SEQ ID NOS: 181
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic
; NAME/KEY: misc feature
; LOCATION: (1)..(20)
; OTHER INFORMATION: n is a, c, g, or t, or no nucleotide
US-10-666-022-2

Query Match      100.0%; Score 18; DB 17; Length 20;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGCACCGGTGCAGGGGG 18
   |||||
Db 3 TGCACCGGTGCAGGGGG 20

RESULT 10
US-10-666-022-178
; Sequence 178, Application US/10666022
; Publication No. US20040105872A1
; GENERAL INFORMATION:
; APPLICANT: The Government of the United States of America, as represented by the
; APPLICANT: Secretary of the Department of Health and Human Services
; APPLICANT: Klinman, Dennis M.
; APPLICANT: Verthelyi, Daniela
; TITLE OF INVENTION: METHOD OF TREATING AND PREVENTING INFECTIONS IN IMMUNOCOMPROMISED
; FILE REFERENCE: 4239-66899
; CURRENT APPLICATION NUMBER: US/10/666,022
; CURRENT FILING DATE: 2003-09-17
; PRIOR APPLICATION NUMBER: US 60/411,944
; PRIOR FILING DATE: 2002-09-18
; NUMBER OF SEQ ID NOS: 181
; SOFTWARE: PatentIn version 3.1
```

```

; SEQ ID NO 178
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic
US-10-666-022-178

Query Match      100.0%; Score 18; DB 13; Length 28;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGCACCGGTGCAGGGGG 18
    |||||
Db 3 TGCACCGGTGCAGGGGG 20

RESULT 13
US-09-874-991C-529
; Sequence 529, Application US/09874991C
; Publication No. US20040052763A1
; GENERAL INFORMATION:
; APPLICANT: MOND, JAMES J.
; APPLICANT: FLORA, MICHAEL
; APPLICANT: KLINMAN, DENNIS M.
; TITLE OF INVENTION: IMMUNOSTIMULATORY RNA/DNA HYBRID MOLECULES
; FILE REFERENCE: 07787.0042-0
; CURRENT APPLICATION NUMBER: US/09/874,991C
; CURRENT FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: 60/209,797
; PRIOR FILING DATE: 2000-06-07
; NUMBER OF SEQ ID NOS: 620
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 529
; LENGTH: 28
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic HDR
US-09-874-991C-529

Query Match      100.0%; Score 18; DB 13; Length 28;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGCACCGGTGCAGGGGG 18
    |||||
Db 11 TGCACCGGTGCAGGGGG 28

RESULT 14
US-09-874-991C-537
; Sequence 537, Application US/09874991C
; Publication No. US20040052763A1
; GENERAL INFORMATION:
; APPLICANT: MOND, JAMES J.
; APPLICANT: FLORA, MICHAEL
; APPLICANT: KLINMAN, DENNIS M.
; TITLE OF INVENTION: IMMUNOSTIMULATORY RNA/DNA HYBRID MOLECULES
; FILE REFERENCE: 07787.0042-0
; CURRENT APPLICATION NUMBER: US/09/874,991C
; CURRENT FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: 60/209,797
; PRIOR FILING DATE: 2000-06-07
; NUMBER OF SEQ ID NOS: 620
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 537
; LENGTH: 28
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic HDR
US-09-874-991C-537

Query Match      100.0%; Score 18; DB 13; Length 28;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGCACCGGTGCAGGGGG 18
    |||||
Db 11 TGCACCGGTGCAGGGGG 28

```

```

; SEQ ID NO 178
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic
US-10-666-022-178

Query Match      100.0%; Score 18; DB 17; Length 20;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGCACCGGTGCAGGGGG 18
    |||||
Db 3 TGCACCGGTGCAGGGGG 20

RESULT 11
US-09-874-991C-517
; Sequence 517, Application US/09874991C
; Publication No. US20040052763A1
; GENERAL INFORMATION:
; APPLICANT: MOND, JAMES J.
; APPLICANT: FLORA, MICHAEL
; APPLICANT: KLINMAN, DENNIS M.
; TITLE OF INVENTION: IMMUNOSTIMULATORY RNA/DNA HYBRID MOLECULES
; FILE REFERENCE: 07787.0042-0
; CURRENT APPLICATION NUMBER: US/09/874,991C
; CURRENT FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: 60/209,797
; PRIOR FILING DATE: 2000-06-07
; NUMBER OF SEQ ID NOS: 620
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 517
; LENGTH: 28
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic HDR
US-09-874-991C-517

Query Match      100.0%; Score 18; DB 13; Length 28;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGCACCGGTGCAGGGGG 18
    |||||
Db 3 TGCACCGGTGCAGGGGG 20

RESULT 12
US-09-874-991C-525
; Sequence 525, Application US/09874991C
; Publication No. US20040052763A1
; GENERAL INFORMATION:
; APPLICANT: MOND, JAMES J.
; APPLICANT: FLORA, MICHAEL
; APPLICANT: KLINMAN, DENNIS M.
; TITLE OF INVENTION: IMMUNOSTIMULATORY RNA/DNA HYBRID MOLECULES
; FILE REFERENCE: 07787.0042-0
; CURRENT APPLICATION NUMBER: US/09/874,991C
; CURRENT FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: 60/209,797
; PRIOR FILING DATE: 2000-06-07
; NUMBER OF SEQ ID NOS: 620
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 525
; LENGTH: 28
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic HDR
US-09-874-991C-525

```

Db 11 TGCACCGGTGCAGGGGG 28

RESULT 15

US-09-874-991C-548
; Sequence 548, Application US/09874991C
; Publication No. US20040052763A1
; GENERAL INFORMATION:
; APPLICANT: MOND, JAMES J.
; APPLICANT: FLORA, MICHAEL
; APPLICANT: KLINMAN, DENNIS M.
; TITLE OF INVENTION: IMMUNOSTIMULATORY RNA/DNA HYBRID MOLECULES
; FILE REFERENCE: 07787.0042-0
; CURRENT APPLICATION NUMBER: US/09/874,991C
; CURRENT FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: 60/209,797
; PRIOR FILING DATE: 2000-06-07
; NUMBER OF SEQ ID NOS: 820
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 548
; LENGTH: 40
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic HDR
US-09-874-991C-548

Query Match 100.0%; Score 18; DB 13; Length 40;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGCACCGGTGCAGGGGG 18
Db 16 TGCACCGGTGCAGGGGG 33

Search completed: July 2, 2004, 13:58:24
Job time : 139.732 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 2, 2004, 07:38:45 ; Search time 1348.02 Seconds
(without alignments)
398.746 Million cell updates/sec

Title: US-10-068-160-13
Perfect score: 18
Sequence: 1 tgcaccggtgcagg999 18

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hci:*
9: gb_estl:*
10: gb_est2:*
11: gb_hci:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_phg:*
27: em_gss_vrl:*
28: gb_gsal:*
29: gb_gses2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	17	94.4	840	29	CG271799 OG0D226TV
C 2	16.4	91.1	245	10	AW325275 TENU4637
C 3	16.4	91.1	277	28	AQ444154 GSSTC0207
C 4	16.4	91.1	339	14	CB076094 hf37c06.9

RESULT 1
CG271799
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

CG271799
OG0D226TV ZM 0.7 1.5 KB Zea mays genomic clone ZMMBMA0596F04,
genomic survey sequence.
CG271799
CG271799.1 GI:34183940
GSS.
Zea mays
Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (base i to 840)
Whitelaw,C.A., Quackenbush,J., Van Aken,S., Utterback,T.,
Resnick,A., Fraser,C.N., Budiman,M.A., Bedell,J.A., Rohlfing,T.,
Citek,R.W., Numborg,A., Robbins,D. and Lakey,N.
Consortium for Maize Genomics
Unpublished (2002)
Other GSSs: OG0D226TH
Contact: Cathy Whitelaw
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer: TP

ALIGNMENTS

C	5	16.4	91.1	440	14	CB087291
C	6	16.4	91.1	509	14	CB087214
C	7	16.4	91.1	562	9	AI370313
C	8	16.4	91.1	598	14	CB087325
C	9	16.4	91.1	610	29	CG592380
C	10	16.4	91.1	684	12	BMG24520
C	11	16.4	91.1	692	12	BMG20160
C	12	16.4	91.1	708	12	BMG21890
C	13	16.4	91.1	779	28	CG109078
C	14	16.4	91.1	799	28	CK133230
C	15	16.4	91.1	866	14	CK151795
C	16	16.4	91.1	1005	29	CNS04021
C	17	16.4	91.1	1120	28	CD214014
C	18	16.4	91.1	1200	14	CD256849
C	19	16	88.9	553	14	CB334319
C	20	16	88.9	700	12	BI897515
C	21	16	88.9	969	29	CNS03H3D
C	22	16	88.9	982	29	CNS042UH
C	23	16	88.9	1200	13	EX426076
C	24	16	88.9	1309	12	BM559504
C	25	15.4	85.6	105	14	CB486533
C	26	15.4	85.6	160	14	CB016628
C	27	15.4	85.6	220	29	CG222603
C	28	15.4	85.6	253	10	BE148995
C	29	15.4	85.6	274	9	AV108043
C	30	15.4	85.6	331	9	AI216300
C	31	15.4	85.6	332	13	BM268033
C	32	15.4	85.6	332	14	CB406325
C	33	15.4	85.6	344	28	AQ067086
C	34	15.4	85.6	375	13	BY315784
C	35	15.4	85.6	391	14	CD598131
C	36	15.4	85.6	397	29	CB437108
C	37	15.4	85.6	402	29	CE182406
C	38	15.4	85.6	405	12	BM487257
C	39	15.4	85.6	408	9	AI146003
C	40	15.4	85.6	411	10	BF386534
C	41	15.4	85.6	411	10	AW264336
C	42	15.4	85.6	418	12	BG381382
C	43	15.4	85.6	429	10	BP412974
C	44	15.4	85.6	450	9	AW024189
C	45	15.4	85.6	458	13	CA111141

CB087291 hf98g11.9
CB087214 hf97e04.9
AI370313 qv76e01.x
CB087525 bk03f05.9
CG592380 ZMMBMA029
BMG24520 170006874
BMG20160 170006874
BMG21890 170006874
CG109078 NDL.50B23
CK133230 NDL.50B22
CK151795 FGAS03452
AL29542 Tetradon
CC214014 CH261-3F1
CD256849 AGENCOURT
CB334319 3529.1_24
BI897515 fm62g02.Y
AL243778 Tetradon
AL21970 Tetradon
EX426076 EX426076
BM559504 AGENCOURT
CB486533 onykptc10
CB016628 pgn1c.pk0
CG222603 OGUKS09TV
BE148995 CM0-HT024
AV108043 AV108043
AI216300 qg76c11.x
BM268033 BX268033
CB406325 OSTR070G1
AQ067086 HS 2233.A
BY315784 BY315784
CD598131 RK112A1D0
CE437108 tigr-gss-
CE182406 tigr-gss-
BM487257 psm2n.pk0
AI146003 UI-R-BT0-
BF386534 UI-R-CA1-
AW264336 xq98e07.x
BG381382 UI-R-CS0-
BP412974 UI-R-BT1-
AW024189 wv01f06.x
CA111141 SCACLB104

```

FEATURES
  source
    Class: sheared ends.
    Location/Qualifiers
      1..840
        /organism="Zea mays"
        /mol_type="genomic DNA"
        /strain="B73"
        /db_xref="taxon:4577"
        /clone="ZMBM0696F04"
        /clone_lib="ZM 0.7 1.5 KB"
        /notes="Vector: pBCSK-; Site 1: HincII; 0.7-1.5 kb
        methylation filtered genomic DNA library"
ORIGIN
  Query Match          94.4%; Score 17; DB 29; Length 840;
  Best Local Similarity 100.0%; Pred. No. 6.3e+03;
  Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
  QY 2 GCACCGGTGCAGGGGG 18
  |||||
  DB 502 GCACCGGTGCAGGGGG 518

RESULT 2
AW325275/c
LOCUS
DEFINITION
  TENU6637 T. cruzi epimastigote normalized cDNA library Trypanosoma
  cruzi cDNA clone 25h9 5', mRNA sequence.
ACCESSION
  AW325275
VERSION
  AW325275.1 GI:6761196
SOURCE
  Trypanosoma cruzi
  Trypanosoma cruzi
  Trypanosoma; Kinetoplastida; Trypanosomatidae;
  Eukaryota; Euglenozoa; Schizotrypanum.
REFERENCE
  1 (bases 1 to 245)
  Porcel, B.M., Iran, A.-N., Tammi, M., Nyarady, Z., Rydaker, M.,
  Urmenyi, T.P., Rondinelli, E., Pettersson, U., Andersson, B. and
  Aslund, L.
  Gene survey of the pathogenic protozoan Trypanosoma cruzi
  20414748
  Genome Res. 10 (8), 1103-1107 (2000)
  10958628
  Contact: Aslund L
  Department of Medical Genetics
  Uppsala University
  Biomedical Center, Box 589, S-751 23 Uppsala, Sweden
  Tel: 46 18 471 45 85
  Fax: 46 18 52 68 49
  Email: lena.aslund@medgen.uu.se
  Seq primer: T7 primer
  High quality sequence stop: 245.
FEATURES
  source
    Location/Qualifiers
      1..245
        /organism="Trypanosoma cruzi"
        /mol_type="mRNA"
        /strain="Cl-Brenner"
        /db_xref="taxon:5693"
        /clone="25h9"
        /cell_type="epimastigote"
        /clone_lib="T. cruzi epimastigote normalized cDNA Library"
        /notes="cDNA library constructed with oligo dt primed
        epimastigote mRNA and cloned in pT7c318D phagemid with
        modified polylinker (Pharmacia)"
ORIGIN
  Query Match          91.1%; Score 16.4; DB 10; Length 245;
  Best Local Similarity 94.4%; Pred. No. 1e+04;
  Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
  QY 1 TGCACCGGTGCAGGGGG 18
  |||||
  DB 65 TGCATCGGTGCAGGGGG 48

FEATURES
  source
    Location/Qualifiers
      1..277
        /organism="Trypanosoma cruzi"
        /mol_type="genomic DNA"
        /strain="Cl-Brenner"
        /db_xref="taxon:5693"
        /clone="G1017"
        /cell_type="epimastigote"
        /clone_lib="Trypanosoma cruzi random genomic library"
        /notes="Vector: pBS(-) (Stratagene); T. cruzi DNA was
        randomly sheared using a nebulizer and the 1 to 2 Kb range
        was gel purified and cloned into the dephosphorylated
        HincII site of the vector"
ORIGIN
  Query Match          91.1%; Score 16.4; DB 28; Length 277;
  Best Local Similarity 94.4%; Pred. No. 1e+04;
  Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
  QY 1 TGCACCGGTGCAGGGGG 18
  |||||
  DB 238 TGCATCGGTGCAGGGGG 221

RESULT 3
AQ444154/c
LOCUS
DEFINITION
  CSSTc0207 Trypanosoma cruzi random genomic library Trypanosoma
  cruzi genomic clone G1017, genomic survey sequence.
ACCESSION
  AQ444154
VERSION
  AQ444154.3 GI:10130745
KEYWORDS
  GSS.
SOURCE
  Trypanosoma cruzi
  Trypanosoma cruzi
  Trypanosoma; Kinetoplastida; Trypanosomatidae;
  Eukaryota; Euglenozoa; Schizotrypanum.
REFERENCE
  1 (bases 1 to 277)
  Aguerro, F., Verdun, R., Frasch, A.C.C. and Sanchez, D.O.
  A random sequencing approach for the analysis of the trypanosoma
  cruzi genome: general structure, large gene and repetitive DNA
  families, and Gene discovery
  Genome Res. 10 (12), 1996-2005 (2000)
  20568489
  11116094
  On Sep 14, 2000 this sequence version replaced gi:9372108.
  Contact: Sanchez D.O.
  Instituto de Investigaciones Biotecnologicas (Univ. Nac. de Gral
  San Martin)
  Av. Gral. Paz S/N, INTI, Edificio 24, B 1650 KNA, San Martin, Buenos
  Aires, Argentina
  Tel: (54-11) 4752-9639
  Fax: (54-11) 4752-9639
  Email: dsanchez@iib.unsam.edu.ar
  Sequences were basecalled with phred and vector was masked with
  crossmatch (see http://genome.washington.edu). Sequences were then
  trimmed from both ends to remove low quality bases and masked
  vector.
  Seq primer: T7
  Class: shotgun.
FEATURES
  source
    Location/Qualifiers
      1..277
        /organism="Trypanosoma cruzi"
        /mol_type="genomic DNA"
        /strain="Cl-Brenner"
        /db_xref="taxon:5693"
        /clone="G1017"
        /cell_type="epimastigote"
        /clone_lib="Trypanosoma cruzi random genomic library"
        /notes="Vector: pBS(-) (Stratagene); T. cruzi DNA was
        randomly sheared using a nebulizer and the 1 to 2 Kb range
        was gel purified and cloned into the dephosphorylated
        HincII site of the vector"
ORIGIN
  Query Match          91.1%; Score 16.4; DB 28; Length 277;
  Best Local Similarity 94.4%; Pred. No. 1e+04;
  Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
  QY 1 TGCACCGGTGCAGGGGG 18
  |||||
  DB 238 TGCATCGGTGCAGGGGG 221

RESULT 4
CB076094/c
LOCUS
DEFINITION
  hf37c06.g1 Hedyotis terminalis flower - Stage 2 (NYBG) Hedyotis
  terminalis cDNA clone hf37c06, mRNA sequence.
ACCESSION
  CB076094
VERSION
  CB076094.1 GI:27889531
KEYWORDS
  EST.
SOURCE
  Hedyotis terminalis
  Hedyotis terminalis
  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
  asterids; lamids; Gentianales; Rubiaceae; Rubioideae;

```

Spermacoceae; Hedyotis.
1 (bases 1 to 339)
Levesque,M.P., Twigg,R.W., Motley,T., Katari,M.S., Dedhia,N.N.,
O'Shaughnessy,A.L., Ballija,V., Martienssen,R.A., McCombie,R.W.,
Benfey,P. and Stevenson,D.
Expressed tag sequences from Hedyotis terminalis flower - Stage 2
(NYBG)
Unpublished (2003)
Contact: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8894
Fax: 516 367 8874
Email: mcombie@cshl.org
Plate: h37 row: c column: 06
Seq primer: -2LM13UnivRev
High quality sequence stop: 339.
Location/Qualifiers
1. .339
/organism="Hedyotis terminalis"
/mol_type="mRNA"
/db_xref="taxon:219667"
/dev_stage="pre-anthesis; Stage 2"
/clone_lib="Hedyotis terminalis flower - Stage 2 (NYBG)"
/note="Organ: flower; Vector: pBK-CMV; Site 1: XhoI;
Site 2: Eco RI; Date: Completed 12/18/01. Submitted to
CSHL 12/21/01 Library: Stratagene ZAP Express cDNA
Synthesis Kit. The library was size-fractionated to enrich
for large inserts. Sample: collected on the island of
Hawaii, Hawaii; NYBG herbarium voucher TM2562"

ORIGIN
Query Match 91.1%; Score 16.4; DB 14; Length 339;
Best Local Similarity 94.4%; Pred. No. 1e+04;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Cy 1 TGCACCGGTGCAGGGGG 18
|||||
Db 97 TGCACCTGTCAGGGGG 80
|||||

RESULT 5
CB087291/c
LOCUS
DEFINITION
440 bp mRNA linear EST 27-JAN-2003
centranthoides cDNA clone hj98g11, mRNA sequence.
ACCESSION
CB087291 GI:27911483
VERSION
EST.
KEYWORDS
Hedyotis centranthoides
Hedyotis centranthoides
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Gentianales; Rubiaceae; Rubioidae;
Spermacoceae; Hedyotis.
1 (bases 1 to 440)
Levesque,M.P., Twigg,R.W., Motley,T., Katari,M.S., Dedhia,N.N.,
O'Shaughnessy,A.L., Ballija,V., Martienssen,R.A., McCombie,R.W.,
Benfey,P. and Stevenson,D.
Expressed tag sequences from Hedyotis centranthoides flower - Stage
2 (NYBG)
Unpublished (2003)
Contact: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8894
Fax: 516 367 8874
Email: mcombie@cshl.org
Plate: h37 row: g column: 11
Seq primer: -2LM13UnivRev

High quality sequence stop: 440.
Location/Qualifiers
1. .440
/organism="Hedyotis centranthoides"
/mol_type="mRNA"
/db_xref="taxon:219666"
/clone_lib="Hj98g11"
/dev_stage="pre-anthesis; Stage 2"
/clone_lib="Hedyotis centranthoides flower - Stage 2
(NYBG)"
/note="Organ: flower; Vector: pBK-CMV; Site 1: XhoI;
Site 2: Eco RI; Date: Completed 12/18/01. Submitted to
CSHL 12/21/01 Library: Stratagene ZAP Express cDNA
Synthesis Kit. The library was size-fractionated to enrich
for large inserts. Sample: collected on the island of
Hawaii, Hawaii; NYBG herbarium voucher TM2563"

ORIGIN
Query Match 91.1%; Score 16.4; DB 14; Length 440;
Best Local Similarity 94.4%; Pred. No. 1.1e+04;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Cy 1 TGCACCGGTGCAGGGGG 18
|||||
Db 129 TGCACCTGTCAGGGGG 112
|||||

RESULT 6
CB087214/c
LOCUS
DEFINITION
509 bp mRNA linear EST 27-JAN-2003
hij97e04.g1 Hedyotis centranthoides flower - Stage 2 (NYBG) Hedyotis
centranthoides cDNA clone hj97e04, mRNA sequence.
ACCESSION
CB087214.1 GI:27911406
VERSION
EST.
KEYWORDS
Hedyotis centranthoides
Hedyotis centranthoides
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Gentianales; Rubiaceae; Rubioidae;
Spermacoceae; Hedyotis.
1 (bases 1 to 509)
Levesque,M.P., Twigg,R.W., Motley,T., Katari,M.S., Dedhia,N.N.,
O'Shaughnessy,A.L., Ballija,V., Martienssen,R.A., McCombie,R.W.,
Benfey,P. and Stevenson,D.
Expressed tag sequences from Hedyotis centranthoides flower - Stage
2 (NYBG)
Unpublished (2003)
Contact: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
Fax: 516 367 8874
Email: mcombie@cshl.org
Plate: hj97 row: e column: 04
Seq primer: -2LM13UnivRev
High quality sequence stop: 509.
Location/Qualifiers
1. .509
/organism="Hedyotis centranthoides"
/mol_type="mRNA"
/db_xref="taxon:219666"
/clone_lib="Hj97e04"
/dev_stage="pre-anthesis; Stage 2"
/clone_lib="Hedyotis centranthoides flower - Stage 2
(NYBG)"
/note="Organ: flower; Vector: pBK-CMV; Site 1: XhoI;
Site 2: Eco RI; Date: Completed 12/18/01. Submitted to
CSHL 12/21/01 Library: Stratagene ZAP Express cDNA
Synthesis Kit. The library was size-fractionated to enrich
for large inserts. Sample: collected on the island of
Hawaii, Hawaii; NYBG herbarium voucher TM2563"

FEATURES
source

Tel: 520 626 3967
Fax: 520 621 9288
Email: <http://genome.arizona.edu>
PCR Primers
FORWARD: T7
BACKWARD: M13r
Plate: 0292 row: G column: 11
Seq primer: T7
Class: BAC ends.

FEATURES

Location/Qualifiers
1..610
/organism="Zea mays subsp. mays"
/mol_type="genomic DNA"
/cultiivar="B73"
/sub_species="mays"
/db_xref="taxon:4578"
/clone="ZMWBB0292G11"
/lab_host="DH10B"
/clone_lib="ZMWBBb"
/note="Vector: pBelobAC11; Site 1: HindIII; Site 2: HindIII; Zea mays L. ssp. mays"

ORIGIN

Query Match 91.1%; Score 16.4; DB 29; Length 610;
Best Local Similarity 94.4%; Pred. No. 1.1e+04;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TGCACCGGTTCAGGGGG 18
Db 525 TGCACCGGTTCAGGGGG 542

RESULT 10

BM624520/c
LOCUS BM624520 684 bp mRNA linear EST 26-FEB-2002
DEFINITION 17000687491457 A.Gam.ad.cdNA1 Anopheles gambiae cDNA clone
19600449632784 5', mRNA sequence.

ACCESSION BM624520

VERSION EST

KEYWORDS BM624520.1 GI:18924031

SOURCE Anopheles gambiae (African malaria mosquito)

ORGANISM Anopheles gambiae

Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;

Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;

Anopheles.

1 (bases 1 to 684)

Holt, R.A., Lin, J.-J., Murphy, S.D., Evans, C.A., Kraft, C.L.,

Charlab, R., Collins, F.H., Venter, J.C. and Hoffman, S.L.

Celera Genomics

Unpublished (2002)

Contact: Holt R.A.

45 W. Gude Dr., Rockville, MD 20850, USA

Tel: 2404533151

Fax: 2404534580

Email: HoltRA@celera.com

Plate: NU01004ABX row: 1 column: 06

Seq primer: M13 Reverse.

Location/Qualifiers

1..684

/organism="Anopheles gambiae"

/mol_type="mRNA"

/strain="RSP-ST (Reduced susc. to Permethrin - std.

chromosome)"

/db_xref="taxon:7165"

/clone="19600449632784"

/dev_stage="Adult"

/lab_host="DH10B"

/clone_lib="A.Gam.ad.cdNA1"

/note="Vector: pSport1; Site 1: SalI; Site 2: NotI; Whole

adult mosquitoes (mixed sex) frozen on liquid nitrogen.

cDNA inserts >500 bp cloned directionally into pSport 1.

Not 1 site is 3'. Clones available through the Malaria

Research and Reference Reagent Resource Center
(www.malaria.mr4.org).

ORIGIN

Query Match 91.1%; Score 16.4; DB 12; Length 684;
Best Local Similarity 94.4%; Pred. No. 1.1e+04;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TGCACCGGTTCAGGGGG 18
Db 168 TGCACCGGTTCAGGGGG 151

RESULT 11

BM620160/c

LOCUS BM620160 692 bp mRNA linear EST 25-FEB-2002

DEFINITION 17000687442189 A.Gam.ad.cdNA1 Anopheles gambiae cDNA clone

19600449668094 5', mRNA sequence.

ACCESSION BM620160

VERSION EST

KEYWORDS BM620160.1 GI:18918578

SOURCE Anopheles gambiae (African malaria mosquito)

ORGANISM Anopheles gambiae

Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;

Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;

Anopheles.

1 (bases 1 to 692)

Holt, R.A., Lin, J.-J., Murphy, S.D., Evans, C.A., Kraft, C.L.,

Charlab, R., Collins, F.H., Venter, J.C. and Hoffman, S.L.

Celera Genomics

Unpublished (2002)

Contact: Holt R.A.

45 W. Gude Dr., Rockville, MD 20850, USA

Tel: 2404533151

Fax: 2404534580

Email: HoltRA@celera.com

Plate: NU01004ABX row: H column: 12

Seq primer: M13 Reverse.

Location/Qualifiers

1..692

/organism="Anopheles gambiae"

/mol_type="mRNA"

/strain="RSP-ST (Reduced susc. to Permethrin - std.

chromosome)"

/db_xref="taxon:7165"

/clone="19600449668094"

/dev_stage="Adult"

/lab_host="DH10B"

/clone_lib="A.Gam.ad.cdNA1"

/note="Vector: pSport1; Site 1: SalI; Site 2: NotI; Whole

adult mosquitoes (mixed sex) frozen on liquid nitrogen.

cDNA inserts >500 bp cloned directionally into pSport 1.

Not 1 site is 3'. Clones available through the Malaria

Research and Reference Reagent Resource Center

(www.malaria.mr4.org).

ORIGIN

Query Match 91.1%; Score 16.4; DB 12; Length 692;
Best Local Similarity 94.4%; Pred. No. 1.1e+04;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TGCACCGGTTCAGGGGG 18
Db 183 TGCACCGGTTCAGGGGG 166

RESULT 12

BM621890/c

LOCUS BM621890 708 bp mRNA linear EST 25-FEB-2002

DEFINITION 17000687447901 A.Gam.ad.cdNA1 Anopheles gambiae cDNA clone

19600449620865 5', mRNA sequence.

ACCESSION BM621890

BM621890.1 GI:18920308
EST.
Anopheles gambiae (African malaria mosquito)
Anopheles gambiae
ORGANISM
Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
1 (bases 1 to 708)
Holt, R.A., Lin, J.-J., Murphy, S.D., Evans, C.A., Kraft, C.L., Charlab, R., Collins, F.H., Venter, J.C. and Hoffman, S.L.
Celera Anopheles gambiae EST project
Unpublished (2002)
Contact: Holt, R.A.
Celera Genomics
45 W. Gude Dr., Rockville, MD 20850, USA
Tel: 240-453-3151
Fax: 240-453-4580
Email: HoltRA@celera.com
Plate: NU01004NBU row: H column: 15
Seq primer: M13 Reverse.
Location/Qualifiers
1..708
/organism="Anopheles gambiae"
/mol_type="mRNA"
/strain="RSP-ST (Reduced susc. to Permethrin - std. chromosome)"
/db_xref="taxon:7165"
/clone="19600449620865"
/dev_stage="Adult"
/lab_host="DHI08"
/clone_lib="A.Gam.ad.cDNA1"
/notes="Vector: pSport1; Site 1: SalI; Site 2: NotI; Whole adult mosquitoes (mixed sex) frozen on liquid nitrogen. cDNA inserts >500 bp cloned directionally into pSport 1. Not 1 site is 3'. Clones available through the Malaria Research and Reference Reagent Resource Center (www.malaria.mr4.org)."
799 bp DNA linear GSS 16-APR-2003

Query Match 91.1%; Score 16.4; DB 12; Length 708;
Best Local Similarity 94.4%; Pred. No. 1.1e+04;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TGCACCGGTGCACGGGGG 18
|||||
DB 153 TGCACCGGTGCACGGGGG 136
|||||

RESULT 13
CC109078/c
LOCUS
DEFINITION
NDL.50B23.T7 Notre Dame Liverpool Aedes aegypti genomic clone
ACCESSION
CC109078
VERSION
CC109078.1 GI:29978133
KEYWORDS
GSS.
SOURCE
Aedes aegypti (yellow fever mosquito)
ORGANISM
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Aedes; Stegomyia.
1 (bases 1 to 779)
Loftus, B., Shetty, J., Knudson, D. and Severson, D.
BAC end sequencing of Aedes aegypti
Unpublished (2003)
Other_GSSs: NDL.50B23.SP6
Contact: Brendan Loftus
Department of Eukaryotic Genomics
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-3543
Fax: 301-838-0208
Email: enta@tigr.org
Library was provided by David Severson
Seq primer: T7
Class: BAC ends.
Location/Qualifiers
1..779
/organism="Aedes aegypti"
/mol_type="genomic DNA"
/strain="liverpool"
/db_xref="taxon:7159"
/clone="NDL.50B23"
/clone_lib="Notre Dame Liverpool"
/notes="Vector: pECBAC1; Site 1: Hind III; The library was prepared from whole body tissue of newly hatched L1 larvae by David Severson at the University of Notre Dame and Hongbin Zhang"

Query Match 91.1%; Score 16.4; DB 28; Length 799;
Best Local Similarity 94.4%; Pred. No. 1.1e+04;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TGCACCGGTGCACGGGGG 18

Library was provided by David Severson
Seq primer: T7
Class: BAC ends.
Location/Qualifiers
1..779
/organism="Aedes aegypti"
/mol_type="genomic DNA"
/strain="liverpool"
/db_xref="taxon:7159"
/clone="NDL.50B23"
/clone_lib="Notre Dame Liverpool"
/notes="Vector: pECBAC1; Site 1: Hind III; The library was prepared from whole body tissue of newly hatched L1 larvae by David Severson at the University of Notre Dame and Hongbin Zhang"

Query Match 91.1%; Score 16.4; DB 28; Length 779;
Best Local Similarity 94.4%; Pred. No. 1.1e+04;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TGCACCGGTGCACGGGGG 18
|||||
DB 306 TGCACCGGTGCACGGGGG 289
|||||

RESULT 14
CC133230/c
LOCUS
DEFINITION
NDL.50B22.T7 Notre Dame Liverpool Aedes aegypti genomic clone
ACCESSION
CC133230
VERSION
CC133230.1 GI:30002285
KEYWORDS
GSS.
SOURCE
Aedes aegypti (yellow fever mosquito)
ORGANISM
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Aedes; Stegomyia.
1 (bases 1 to 799)
Loftus, B., Shetty, J., Knudson, D. and Severson, D.
BAC end sequencing of Aedes aegypti
Unpublished (2003)
Other_GSSs: NDL.50B22.SP6
Contact: Brendan Loftus
Department of Eukaryotic Genomics
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-3543
Fax: 301-838-0208
Email: enta@tigr.org
Library was provided by David Severson
Seq primer: T7
Class: BAC ends.
Location/Qualifiers
1..799
/organism="Aedes aegypti"
/mol_type="genomic DNA"
/strain="liverpool"
/db_xref="taxon:7159"
/clone="NDL.50B22"
/clone_lib="Notre Dame Liverpool"
/notes="Vector: pECBAC1; Site 1: Hind III; The library was prepared from whole body tissue of newly hatched L1 larvae by David Severson at the University of Notre Dame and Hongbin Zhang"

Query Match 91.1%; Score 16.4; DB 28; Length 799;
Best Local Similarity 94.4%; Pred. No. 1.1e+04;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TGCACCGGTGCACGGGGG 18

RESULT 15
CK151795/c
LOCUS
DEFINITION FGAS034520 Triticum aestivum FGAS: Talt3 Triticum aestivum cDNA,
mRNA sequence.

ACCESSION CK151795
VERSION
KEYWORDS
SOURCE
ORGANISM

CK151795.1 GI:38970179
EST.
Triticum aestivum (bread wheat)
Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Poideae; Triticeae; Triticum.

1 (bases 1 to 866)
Allard,F., Crosby,W.L., Danyluk,J., Budes,F., Frick,M., Gaudet,D.,
Genswein,B., Graf,R., Gulick,P., Hrycan,L.D., Laroche,A.,
Links,M.G., McCarthy,E.L., Monroy,A., Muzak,I., Nilsson,D.,
Peniket,C., Roach,J.L. and Sarhan,F.
Functional Genomics of Abiotic Stress In Wheat and Canola Crops
Unpublished (2003)

JOURNAL
COMMENT
Contact: Mm L Crosby
Bioinformatics
University of Saskatchewan, Department of Computer Science
1C101 Engineering Building, 57 Campus Drive, Saskatoon,
Saskatchewan, S7N 5A9, Canada

Tel: 306 966 1769
Fax: 306 966 2033
Email: fgas_estecs.usask.ca
This sequence is the direct result of the base calling software
Phred (default parameters). It is the raw base calls. To aid in the
identification of the high quality insert the software Lucy
(default parameters) has been run on this sequence. Lucy identified
the region [123,504].
Plate: Talt328, row: K, column: 02.

FEATURES
source
location/Qualifiers
1..866
/organism="Triticum aestivum"
/mol_type="mRNA"
/cultivar="Wheat line CI 14106"
/db_xref="taxon:4565"
/lab_host="DHS alpha"
/clone_lib="Triticum aestivum FGAS: Talt3"
/note="Organ: Crown; Vector: pGEM-T; SSH (suppression
subtractive hybridization) cDNA library from genotype
CI14106 cold hardened at 2 C for 21 days and 49 days
(equal amount of cDNA pooled together before subtraction,
tester) and subtracted against genotype Norstar cold
hardened at 2 C for 1 day (24 h)(driver). Nitro-pyrole
anchored oligo-dt priming and non-directional cloning."

ORIGIN
Query Match 91.1%; Score 16.4; DB 14; Length 866;
Best Local Similarity 94.4%; Pred. No. 1.1e+04;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TGCACCGGTGCAGGGGG 18
DB 780 TGCACCGGTGCAGGGGG 763

Search completed: July 2, 2004, 13:32:56
JOB time : 1351.14 secs

OM nucleic - nucleic search, using sw model

Run on: July 2, 2004, 07:36:05 ; Search time 563.317 Seconds
(without alignments)
1231.080 Million cell updates/sec

Title: US-10-068-160-15
Perfect score: 16
Sequence: 1 gggcatgcattggggg 16

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenBank.*

- 1: gb_ba.*
- 2: gb_hg.*
- 3: gb_in.*
- 4: gb_ov.*
- 5: gb_ov.*
- 6: gb_pat.*
- 7: gb_ph.*
- 8: gb_pl.*
- 9: gb_pr.*
- 10: gb_ro.*
- 11: gb_sts.*
- 12: gb_sy.*
- 13: gb_un.*
- 14: gb_vi.*
- 15: gb_ba.*
- 16: em_fun.*
- 17: em_hum.*
- 18: em_in.*
- 19: em_ma.*
- 20: em_ma.*
- 21: em_ov.*
- 22: em_ov.*
- 23: em_pat.*
- 24: em_ph.*
- 25: em_pl.*
- 26: em_ro.*
- 27: em_sts.*
- 28: em_un.*
- 29: em_vi.*
- 30: em_hg_hum.*
- 31: em_hg_inv.*
- 32: em_hg_inv.*
- 33: em_hg_mus.*
- 34: em_hg_pln.*
- 35: em_hg_rtd.*
- 36: em_hg_mam.*
- 37: em_hg_vrt.*
- 38: em_sy.*
- 39: em_hgo_hum.*
- 40: em_hgo_mus.*
- 41: em_hgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
C 1	16	100.0	55655	2	AC120183	AC120183 Mus muscu
C 2	16	100.0	149773	2	AC118209	AC118209 Mus muscu
C 3	16	100.0	154143	2	AC131924	AC131924 Mus muscu
C 4	16	100.0	157263	2	AY178791	AY178791 Canis fam
C 5	16	100.0	158920	2	AC135955	AC135955 Canis fam
C 6	16	100.0	155077	10	AC084382	AC084382 Mus muscu
C 7	16	100.0	183540	2	AC139123	AC139123 Canis fam
C 8	16	100.0	186129	2	AC131987	AC131987 Mus muscu
C 9	16	100.0	192462	9	CNS01RHC	AL161669 Human chr
C 10	16	100.0	222510	2	AC123656	AC123656 Mus muscu
C 11	16	100.0	227805	2	AC147160	AC147160 Mus muscu
C 12	16	100.0	234548	2	AC095635	AC095635 Rattus no
C 13	16	100.0	345420	2	AC131337	AC131337 Mus muscu
C 14	15	93.8	657	6	AX251652	AX251652 Sequence
C 15	15	93.8	867	11	EV013283	EV013283 S212P8739
C 16	15	93.8	2000	6	AX656277	AX656277 Sequence
C 17	15	93.8	2808	8	ITU51741	US1741 Ipomoea tri
C 18	15	93.8	3387	8	AF032369	AF032369 Cochliobo
C 19	15	93.8	3504	8	AF032368	AF032368 Cochliobo
C 20	15	93.8	4349	8	NSETSPR	X76056 N. sylvestr
C 21	15	93.8	5272	8	BSMAT2GEN	X95814 B. sacchari
C 22	15	93.8	17687	1	AE001038	AE001038 Archaeogl
C 23	15	93.8	64168	2	AC079003	AC079003 Homo sapi
C 24	15	93.8	95280	9	AC073133	AC073133 Homo sapi
C 25	15	93.8	107947	8	NCB7N14	AL669986 Neurospor
C 26	15	93.8	108645	2	AL359538	AL359538 Human DNA
C 27	15	93.8	112416	2	AP000482	AP000482 Homo sapi
C 28	15	93.8	112763	2	AC145324	AC145324 Oryza sat
C 29	15	93.8	120832	2	AP001068	AP001068 Homo sapi
C 30	15	93.8	121590	9	HS314N7	AL773602 Homo sapi
C 31	15	93.8	132875	9	AC112907	AC112907 Homo sapi
C 32	15	93.8	133299	8	OSJN00098	AL606658 Oryza sat
C 33	15	93.8	145739	8	OSJN00157	AL662957 Oryza sat
C 34	15	93.8	148845	9	AP001067	AP001067 Homo sapi
C 35	15	93.8	150889	9	AC106881	AC106881 Homo sapi
C 36	15	93.8	155430	9	AL136160	AL136160 Human DNA
C 37	15	93.8	157263	2	AY178791	AY178791 Canis fam
C 38	15	93.8	157347	2	AP001882	AP001882 Homo sapi
C 39	15	93.8	164725	9	AC092938	AC092938 Homo sapi
C 40	15	93.8	168064	2	AC019160	AC019160 Homo sapi
C 41	15	93.8	175550	2	AC009863	AC009863 Homo sapi
C 42	15	93.8	175837	2	AC022045	AC022045 Homo sapi
C 43	15	93.8	176155	2	AC012149	AC012149 Homo sapi
C 44	15	93.8	177417	2	AC133160	AC133160 Mus muscu
C 45	15	93.8	178975	2	AC023222	AC023222 Homo sapi

ALIGNMENTS

RESULT 1
AC120183/c
LOCUS
DEFINITION Mus musculus clone RP24-116K23, LOW-PASS SEQUENCE SAMPLING.
ACCESSION AC120183
VERSION AC120183.1 GI:20429532
KEYWORDS HTG; HTGS PHASEO.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
REFERENCE 1 (bases 1 to 65655)
AUTHORS Birren, B., Linton, L., Nusbaum, C. and Lander, E.
TITLE Mus musculus, clone RP24-116K23
JOURNAL Unpublished

AC120183 65655 bp DNA linear HTG 03-MAY-2002
Mus musculus clone RP24-116K23, LOW-PASS SEQUENCE SAMPLING.

REFERENCE
AUTHORS

2 (bases 1 to 65655)
 Birren, B., Linton, J., Nusbaum, C., Lander, E., Ali, A., Allen, N.,
 Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavsky, L.,
 Boukhalter, B., Brown, A., Camarata, J., Campopiano, A., Chang, J.,
 Chazaro, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A.,
 Cook, A., Cooke, P., DeArelano, K., Dewar, K., Diaz, J. S., Dodge, S.,
 Fero, S., Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyna, S.,
 Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N.,
 Hagos, B., Horton, J., Hulme, W., Iliev, I., Johnson, R., Jones, C.,
 Kama, A., Karatas, A., Kells, C., Lakocue, K., Lamazares, R.,
 Landers, T., Lehotzky, J., Levine, R., Lindblad-Toh, K., Liu, G.,
 Maclean, C., MacDonald, P., Major, J., Marquis, N., Matthews, C.,
 McCarthy, M., McEwan, P., McKernan, K., Meldrum, J., Meneses, L.,
 Miho, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R.,
 Norby, C., Norman, C. H., O'Connor, T., O'Donnell, P., O'Neil, D.,
 Oliver, J., Peterson, K., Phukhang, P., Pierre, N., Pollara, V.,
 Raymond, C., Retta, R., Ribback, M., Riley, R., Rise, C., Rogov, P.,
 Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupbach, R.,
 Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N.,
 Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J.,
 Topham, K., Travers, M., Travis, N., Triglio, J., Vassiliev, H.,
 Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G.,
 Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.
 Direct Submission
 Submitted (03-MAY-2002) Whitehead Institute/MIT Center for Genome
 Research, 320 Charles Street, Cambridge, MA 02141, USA
 All repeats were identified using RepeatMasker:
 Smit, A. P. A. & Green, P. (1996-1997)
 http://ftp.genome.washington.edu/RM/RepeatMasker.html
 ----- Genome Center
 Center: Whitehead Institute/ MIT Center for Genome Research
 Center code: WIBR
 Web site: http://www-seq.wi.mit.edu
 Contact: sequence_submissions@genome.wi.mit.edu
 ----- Project Information
 Center project name: L25878
 Center clone name: 116_K_23

TITLE
JOURNAL
COMMENT

9715 10423: contig of 709 bp in length
 10424 10523: gap of 100 bp
 10524 12443: contig of 720 bp in length
 12443 13443: gap of 100 bp
 13443 14443: contig of 727 bp in length
 14443 15443: gap of 100 bp
 15443 16443: contig of 726 bp in length
 16443 17443: gap of 100 bp
 17443 18443: contig of 710 bp in length
 18443 19443: gap of 100 bp
 19443 20443: contig of 691 bp in length
 20443 21443: gap of 100 bp
 21443 22443: contig of 722 bp in length
 22443 23443: gap of 100 bp
 23443 24443: contig of 726 bp in length
 24443 25443: gap of 100 bp
 25443 26443: contig of 735 bp in length
 26443 27443: gap of 100 bp
 27443 28443: contig of 721 bp in length
 28443 29443: gap of 100 bp
 29443 30443: contig of 720 bp in length
 30443 31443: gap of 100 bp
 31443 32443: contig of 719 bp in length
 32443 33443: gap of 100 bp
 33443 34443: contig of 727 bp in length
 34443 35443: gap of 100 bp
 35443 36443: contig of 716 bp in length
 36443 37443: gap of 100 bp
 37443 38443: contig of 716 bp in length
 38443 39443: gap of 100 bp
 39443 40443: contig of 706 bp in length
 40443 41443: gap of 100 bp
 41443 42443: contig of 724 bp in length
 42443 43443: gap of 100 bp
 43443 44443: contig of 715 bp in length
 44443 45443: gap of 100 bp
 45443 46443: contig of 722 bp in length
 46443 47443: gap of 100 bp
 47443 48443: contig of 708 bp in length
 48443 49443: gap of 100 bp
 49443 50443: contig of 728 bp in length
 50443 51443: gap of 100 bp
 51443 52443: contig of 721 bp in length
 52443 53443: gap of 100 bp
 53443 54443: contig of 716 bp in length
 54443 55443: gap of 100 bp
 55443 56443: contig of 730 bp in length
 56443 57443: gap of 100 bp
 57443 58443: contig of 709 bp in length
 58443 59443: gap of 100 bp
 59443 60443: contig of 706 bp in length
 60443 61443: gap of 100 bp
 61443 62443: contig of 709 bp in length
 62443 63443: gap of 100 bp
 63443 64443: contig of 706 bp in length
 64443 65443: gap of 100 bp
 65443 66443: contig of 724 bp in length
 66443 67443: gap of 100 bp
 67443 68443: contig of 715 bp in length
 68443 69443: gap of 100 bp
 69443 70443: contig of 722 bp in length
 70443 71443: gap of 100 bp
 71443 72443: contig of 708 bp in length
 72443 73443: gap of 100 bp
 73443 74443: contig of 728 bp in length
 74443 75443: gap of 100 bp
 75443 76443: contig of 721 bp in length
 76443 77443: gap of 100 bp
 77443 78443: contig of 716 bp in length
 78443 79443: gap of 100 bp
 79443 80443: contig of 730 bp in length
 80443 81443: gap of 100 bp
 81443 82443: contig of 702 bp in length
 82443 83443: gap of 100 bp
 83443 84443: contig of 709 bp in length
 84443 85443: gap of 100 bp
 85443 86443: contig of 716 bp in length
 86443 87443: gap of 100 bp
 87443 88443: contig of 716 bp in length
 88443 89443: gap of 100 bp
 89443 90443: contig of 716 bp in length
 90443 91443: gap of 100 bp
 91443 92443: contig of 716 bp in length
 92443 93443: gap of 100 bp
 93443 94443: contig of 716 bp in length
 94443 95443: gap of 100 bp
 95443 96443: contig of 716 bp in length
 96443 97443: gap of 100 bp
 97443 98443: contig of 716 bp in length
 98443 99443: gap of 100 bp
 99443 100443: contig of 716 bp in length
 100443 101443: gap of 100 bp
 101443 102443: contig of 716 bp in length
 102443 103443: gap of 100 bp
 103443 104443: contig of 716 bp in length
 104443 105443: gap of 100 bp
 105443 106443: contig of 716 bp in length
 106443 107443: gap of 100 bp
 107443 108443: contig of 716 bp in length
 108443 109443: gap of 100 bp
 109443 110443: contig of 716 bp in length
 110443 111443: gap of 100 bp
 111443 112443: contig of 716 bp in length
 112443 113443: gap of 100 bp
 113443 114443: contig of 716 bp in length
 114443 115443: gap of 100 bp
 115443 116443: contig of 716 bp in length
 116443 117443: gap of 100 bp
 117443 118443: contig of 716 bp in length
 118443 119443: gap of 100 bp
 119443 120443: contig of 716 bp in length
 120443 121443: gap of 100 bp
 121443 122443: contig of 716 bp in length
 122443 123443: gap of 100 bp
 123443 124443: contig of 716 bp in length
 124443 125443: gap of 100 bp
 125443 126443: contig of 716 bp in length
 126443 127443: gap of 100 bp
 127443 128443: contig of 716 bp in length
 128443 129443: gap of 100 bp
 129443 130443: contig of 716 bp in length
 130443 131443: gap of 100 bp
 131443 132443: contig of 716 bp in length
 132443 133443: gap of 100 bp
 133443 134443: contig of 716 bp in length
 134443 135443: gap of 100 bp
 135443 136443: contig of 716 bp in length
 136443 137443: gap of 100 bp
 137443 138443: contig of 716 bp in length
 138443 139443: gap of 100 bp
 139443 140443: contig of 716 bp in length
 140443 141443: gap of 100 bp
 141443 142443: contig of 716 bp in length
 142443 143443: gap of 100 bp
 143443 144443: contig of 716 bp in length
 144443 145443: gap of 100 bp
 145443 146443: contig of 716 bp in length
 146443 147443: gap of 100 bp
 147443 148443: contig of 716 bp in length
 148443 149443: gap of 100 bp
 149443 150443: contig of 716 bp in length
 150443 151443: gap of 100 bp
 151443 152443: contig of 716 bp in length
 152443 153443: gap of 100 bp
 153443 154443: contig of 716 bp in length
 154443 155443: gap of 100 bp
 155443 156443: contig of 716 bp in length
 156443 157443: gap of 100 bp
 157443 158443: contig of 716 bp in length
 158443 159443: gap of 100 bp
 159443 160443: contig of 716 bp in length
 160443 161443: gap of 100 bp
 161443 162443: contig of 716 bp in length
 162443 163443: gap of 100 bp
 163443 164443: contig of 716 bp in length
 164443 165443: gap of 100 bp
 165443 166443: contig of 716 bp in length
 166443 167443: gap of 100 bp
 167443 168443: contig of 716 bp in length
 168443 169443: gap of 100 bp
 169443 170443: contig of 716 bp in length
 170443 171443: gap of 100 bp
 171443 172443: contig of 716 bp in length
 172443 173443: gap of 100 bp
 173443 174443: contig of 716 bp in length
 174443 175443: gap of 100 bp
 175443 176443: contig of 716 bp in length
 176443 177443: gap of 100 bp
 177443 178443: contig of 716 bp in length
 178443 179443: gap of 100 bp
 179443 180443: contig of 716 bp in length
 180443 181443: gap of 100 bp
 181443 182443: contig of 716 bp in length
 182443 183443: gap of 100 bp
 183443 184443: contig of 716 bp in length
 184443 185443: gap of 100 bp
 185443 186443: contig of 716 bp in length
 186443 187443: gap of 100 bp
 187443 188443: contig of 716 bp in length
 188443 189443: gap of 100 bp
 189443 190443: contig of 716 bp in length
 190443 191443: gap of 100 bp
 191443 192443: contig of 716 bp in length
 192443 193443: gap of 100 bp
 193443 194443: contig of 716 bp in length
 194443 195443: gap of 100 bp
 195443 196443: contig of 716 bp in length
 196443 197443: gap of 100 bp
 197443 198443: contig of 716 bp in length
 198443 199443: gap of 100 bp
 199443 200443: contig of 716 bp in length
 200443 201443: gap of 100 bp
 201443 202443: contig of 716 bp in length
 202443 203443: gap of 100 bp
 203443 204443: contig of 716 bp in length
 204443 205443: gap of 100 bp
 205443 206443: contig of 716 bp in length
 206443 207443: gap of 100 bp
 207443 208443: contig of 716 bp in length
 208443 209443: gap of 100 bp
 209443 210443: contig of 716 bp in length
 210443 211443: gap of 100 bp
 211443 212443: contig of 716 bp in length
 212443 213443: gap of 100 bp
 213443 214443: contig of 716 bp in length
 214443 215443: gap of 100 bp
 215443 216443: contig of 716 bp in length
 216443 217443: gap of 100 bp
 217443 218443: contig of 716 bp in length
 218443 219443: gap of 100 bp
 219443 220443: contig of 716 bp in length
 220443 221443: gap of 100 bp
 221443 222443: contig of 716 bp in length
 222443 223443: gap of 100 bp
 223443 224443: contig of 716 bp in length
 224443 225443: gap of 100 bp
 225443 226443: contig of 716 bp in length
 226443 227443: gap of 100 bp
 227443 228443: contig of 716 bp in length
 228443 229443: gap of 100 bp
 229443 230443: contig of 716 bp in length
 230443 231443: gap of 100 bp
 231443 232443: contig of 716 bp in length
 232443 233443: gap of 100 bp
 233443 234443: contig of 716 bp in length
 234443 235443: gap of 100 bp
 235443 236443: contig of 716 bp in length
 236443 237443: gap of 100 bp
 237443 238443: contig of 716 bp in length
 238443 239443: gap of 100 bp
 239443 240443: contig of 716 bp in length
 240443 241443: gap of 100 bp
 241443 242443: contig of 716 bp in length
 242443 243443: gap of 100 bp
 243443 244443: contig of 716 bp in length
 244443 245443: gap of 100 bp
 245443 246443: contig of 716 bp in length
 246443 247443: gap of 100 bp
 247443 248443: contig of 716 bp in length
 248443 249443: gap of 100 bp
 249443 250443: contig of 716 bp in length
 250443 251443: gap of 100 bp
 251443 252443: contig of 716 bp in length
 252443 253443: gap of 100 bp
 253443 254443: contig of 716 bp in length
 254443 255443: gap of 100 bp
 255443 256443: contig of 716 bp in length
 256443 257443: gap of 100 bp
 257443 258443: contig of 716 bp in length
 258443 259443: gap of 100 bp
 259443 260443: contig of 716 bp in length
 260443 261443: gap of 100 bp
 261443 262443: contig of 716 bp in length
 262443 263443: gap of 100 bp
 263443 264443: contig of 716 bp in length
 264443 265443: gap of 100 bp
 265443 266443: contig of 716 bp in length
 266443 267443: gap of 100 bp
 267443 268443: contig of 716 bp in length
 268443 269443: gap of 100 bp
 269443 270443: contig of 716 bp in length
 270443 271443: gap of 100 bp
 271443 272443: contig of 716 bp in length
 272443 273443: gap of 100 bp
 273443 274443: contig of 716 bp in length
 274443 275443: gap of 100 bp
 275443 276443: contig of 716 bp in length
 276443 277443: gap of 100 bp
 277443 278443: contig of 716 bp in length
 278443 279443: gap of 100 bp
 279443 280443: contig of 716 bp in length
 280443 281443: gap of 100 bp
 281443 282443: contig of 716 bp in length
 282443 283443: gap of 100 bp
 283443 284443: contig of 716 bp in length
 284443 285443: gap of 100 bp
 285443 286443: contig of 716 bp in length
 286443 287443: gap of 100 bp
 287443 288443: contig of 716 bp in length
 288443 289443: gap of 100 bp
 289443 290443: contig of 716 bp in length
 290443 291443: gap of 100 bp
 291443 292443: contig of 716 bp in length
 292443 293443: gap of 100 bp
 293443 294443: contig of 716 bp in length
 294443 295443: gap of 100 bp
 295443 296443: contig of 716 bp in length
 296443 297443: gap of 100 bp
 297443 298443: contig of 716 bp in length
 298443 299443: gap of 100 bp
 299443 300443: contig of 716 bp in length
 300443 301443: gap of 100 bp
 301443 302443: contig of 716 bp in length
 302443 303443: gap of 100 bp
 303443 304443: contig of 716 bp in length
 304443 305443: gap of 100 bp
 305443 306443: contig of 716 bp in length
 306443 307443: gap of 100 bp
 307443 308443: contig of 716 bp in length
 308443 309443: gap of 100 bp
 309443 310443: contig of 716 bp in length
 310443 311443: gap of 100 bp
 311443 312443: contig of 716 bp in length
 312443 313443: gap of 100 bp
 313443 314443: contig of 716 bp in length
 314443 315443: gap of 100 bp
 315443 316443: contig of 716 bp in length
 316443 317443: gap of 100 bp
 317443 318443: contig of 716 bp in length
 318443 319443: gap of 100 bp
 319443 320443: contig of 716 bp in length
 320443 321443: gap of 100 bp
 321443 322443: contig of 716 bp in length
 322443 323443: gap of 100 bp
 323443 324443: contig of 716 bp in length
 324443 325443: gap of 100 bp
 325443 326443: contig of 716 bp in length
 326443 327443: gap of 100 bp
 327443 328443: contig of 716 bp in length
 328443 329443: gap of 100 bp
 329443 330443: contig of 716 bp in length
 330443 331443: gap of 100 bp
 331443 332443: contig of 716 bp in length
 332443 333443: gap of 100 bp
 333443 334443: contig of 716 bp in length
 334443 335443: gap of 100 bp
 335443 336443: contig of 716 bp in length
 336443 337443: gap of 100 bp
 337443 338443: contig of 716 bp in length
 338443 339443: gap of 100 bp
 339443 340443: contig of 716 bp in length
 340443 341443: gap of 100 bp
 341443 342443: contig of 716 bp in length
 342443 343443: gap of 100 bp
 343443 344443: contig of 716 bp in length
 344443 345443: gap of 100 bp
 345443 346443: contig of 716 bp in length
 346443 347443: gap of 100 bp
 347443 348443: contig of 716 bp in length
 348443 349443: gap of 100 bp
 349443 350443: contig of 716 bp in length
 350443 351443: gap of 100 bp
 351443 352443: contig of 716 bp in length
 352443 353443: gap of 100 bp
 353443 354443: contig of 716 bp in length
 354443 355443: gap of 100 bp
 355443 356443: contig of 716 bp in length
 356443 357443: gap of 100 bp
 357443 358443: contig of 716 bp in length
 358443 359443: gap of 100 bp
 359443 360443: contig of 716 bp in length
 360443 361443: gap of 100 bp
 361443 362443: contig of 716 bp in length
 362443 363443: gap of 100 bp
 363443 364443: contig of 716 bp in length
 364443 365443: gap of 100 bp
 365443 366443: contig of 716 bp in length
 366443 367443: gap of 100 bp
 367443 368443: contig of 716 bp in length
 368443 369443: gap of 100 bp
 369443 370443: contig of 716 bp in length
 370443 371443: gap of 100 bp
 371443 372443: contig of 716 bp in length
 372443 373443: gap of 100 bp
 373443 374443: contig of 716 bp in length
 374443 375443: gap of 100 bp
 375443 376443: contig of 716 bp in length
 376443 377443: gap of 100 bp
 377443 378443: contig of 716 bp in length
 378443 379443: gap of 100 bp
 379443 380443: contig of 716 bp in length
 380443 381443: gap of 100 bp
 381443 382443: contig of 716 bp in length
 382443 383443: gap of 100 bp
 383443 384443: contig of 716 bp in length
 384443 385443: gap of 100 bp
 385443 386443: contig of 716 bp in length
 386443 387443: gap of 100 bp
 387443 388443: contig of 716 bp in length
 388443 389443: gap of 100 bp
 389443 390443: contig of 716 bp in length
 390443 391443: gap of 100 bp
 391443 392443: contig of 716 bp in length
 392443 393443: gap of 100 bp
 393443 394443: contig of 716 bp in length
 394443 395443: gap of 100 bp
 395443 396443: contig of 716 bp in length
 396443 397443: gap of 100 bp
 397443 398443: contig of 716 bp in length
 398443 399443: gap of 100 bp
 399443 400443: contig of 716 bp in length
 400443 401443: gap of 100 bp
 401443 402443: contig of 716 bp in length
 402443 403443: gap of 100 bp
 403443 404443: contig of 716 bp in length
 404443 405443: gap of 100 bp
 405443 406443: contig of 716 bp in length
 406443 407443: gap of 100 bp
 407443 408443: contig of 716 bp in length
 408443 409443: gap of 100 bp
 409443 410443: contig of 716 bp in length
 410443 411443: gap of 100 bp
 411443 412443: contig of 716 bp in length
 412443 413443: gap of 100 bp
 413443 414443: contig of 716 bp in length
 414443 415443: gap of 100 bp
 415443 416443: contig of 716 bp in length
 416443 417443: gap of 100 bp
 417443 418443: contig of 716 bp in length
 418443 419443: gap of 100 bp
 419443 420443: contig of 716 bp in length
 420443 421443: gap of 100 bp
 421443 422443: contig of 716 bp in length
 422443 423443: gap of 100 bp
 423443 424443: contig of 716 bp in length
 424443 425443: gap of 100 bp
 425443 426443: contig of 716 bp in length
 426443 42744

39704: gap of 100 bp
39705: contig of 719 bp in length
40423: gap of 100 bp
40424: contig of 729 bp in length
41252: gap of 100 bp
41353: contig of 716 bp in length
42069: gap of 100 bp
42168: contig of 720 bp in length
42889: gap of 100 bp
42988: contig of 714 bp in length
43702: gap of 100 bp
43802: contig of 737 bp in length
44539: gap of 100 bp
44639: contig of 726 bp in length
45365: gap of 100 bp
45465: contig of 726 bp in length
46191: gap of 100 bp
46291: contig of 593 bp in length
46984: gap of 100 bp
47800: contig of 716 bp in length
47900: gap of 100 bp
48615: contig of 715 bp in length
48715: gap of 100 bp
49305: contig of 590 bp in length
49405: gap of 100 bp
50139: contig of 714 bp in length
50219: gap of 100 bp
50932: contig of 713 bp in length
51032: gap of 100 bp
51766: contig of 734 bp in length
51866: gap of 100 bp
52584: contig of 718 bp in length
52684: gap of 100 bp
53392: contig of 708 bp in length
53492: gap of 100 bp
54209: contig of 717 bp in length
54309: gap of 100 bp
55026: contig of 717 bp in length
55126: gap of 100 bp
55834: contig of 708 bp in length
55934: gap of 100 bp

Query Match 100.0%; Score 16; DB 2; Length 65655;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGCATGCGTGGGGG 16
DB 29249 GGGCATGCGTGGGGG 29234

RESULT 2
AC118209/c
LOCUS AC118209.3 GI:29150444
DEFINITION HTG; HTGS PHASE1; HTGS DRAFT.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 149773)
AUTHORS Birren, B., Nusbaum, C. and Lander, E.
TITLE Mus musculus, clone RP24-566J22
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 149773)
AUTHORS Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N.,
Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavskiy, L.,
Boukhgalter, B., Brown, A., Camarata, J., Campopiano, A., Chang, J.,
Chazaro, B., Choepel, Y., Collangelo, M., Collins, S., Collymore, A.,
Cook, A., Cooke, P., Dearellano, K., Dewar, K., Diaz, J.S., Dodge, S.,

Paro, S., Ferreira, P., Fitzhugh, W., Gage, D., Galagan, J., Gardyna, S.,
Ginge, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N.,
Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C.,
Kamat, A., Karatas, A., Kells, C., Larocque, K., Lamazares, R.,
Landers, T., Lehoczy, J., Levine, R., Lindblad-Toh, K., Liu, G.,
Maclean, C., Macdonald, P., Major, J., Marguis, N., Matthews, C.,
McCarthy, M., McEwan, P., McKernan, K., Meldrum, J., Menes, L.,
Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R.,
Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neill, D.,
Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V.,
Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P.,
Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupack, R.,
Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N.,
Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J.,
Topham, K., Travers, M., Travis, N., Trigilio, J., Vassiliev, H.,
Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G.,
Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

Direct Submission
Submitted (14-APR-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
3 (bases 1 to 149773)
Birren, B., Nusbaum, C., Lander, E., Abouelleil, A., Allen, N.,
Anderson, S., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T.,
Boguslavskiy, L., Boukhgalter, B., Camarata, J., Chang, J., Choepel, Y.,
Collymore, A., Cook, A., Cooke, P., Corum, B., Dearellano, K., Faro, S.,
Diaz, J.S., Dodge, S., Dooley, K., Dorris, L., Erickson, J., Faro, S.,
Ferreira, P., Fitzgerald, M., Gage, D., Galagan, J., Gardyna, S.,
Graham, L., Grand-Pierre, N., Hafez, N., Hagopian, D., Hagos, B.,
Hall, J., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C.,
Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R.,
Lindblad-Toh, K., Liu, G., Lui, A., Mabbitt, R., Maclean, C.,
Macdonald, P., Major, J., Manning, J., Matthews, C., McCarthy, M.,
Meldrum, J., Menes, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J.,
Nguyen, C., Nicol, R., Norbu, C., O'Connor, T., O'Donnell, P.,
O'Neill, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N.,
Rachupka, A., Ramasamy, U., Raymond, C., Retta, R., Rise, C., Rogov, P.,
Roman, J., Schauer, S., Schupack, R., Seaman, S., Severy, P., Smith, C.,
Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubbs, M.,
Talamas, J., Tesfaye, S., Theodore, J., Topham, K., Travers, M.,
Vassiliev, H., Venkataraman, V.S., Viel, R., Vo, A., Wilson, B., Wu, X.,
Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: <http://www-seq.wi.mit.edu>
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L21328
Center clone name: 566_J22
----- Summary Statistics
Sequencing vector: Plasmid; n/a; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 14886 bases at least Q40
Consensus quality: 149124 bases at least Q30
Consensus quality: 149185 bases at least Q20
Insert size: 151000; agarose-ff
Quality coverage: 149273; sum-of-contigs
Quality coverage: 12.5 in Q20 bases; agarose-ff
Quality coverage: 12.7 in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently
* consists of 6 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.

REFERENCE
JOURNAL
TITLE
AUTHORS
COMMENT

* This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.

1 27796: contig of 27796 bp in length
 27797 27896: gap of 100 bp
 27897 33321: contig of 5425 bp in length
 33322 33421: gap of 100 bp
 33422 45908: contig of 12487 bp in length
 45909 46008: gap of 100 bp
 46009 85248: contig of 39237 bp in length
 85249 85346: gap of 100 bp
 85346 130509: contig of 45164 bp in length
 130510 130609: gap of 100 bp
 130610 149773: contig of 19164 bp in length.

FEATURES

Location/Qualifiers
 1. 149773
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /db_xref="taxon:10090"
 /clone="RP24-566J22"
 /clone_lib="RPCI-24 Male Mouse BAC"

misc_feature
 1. 27796
 /note="assembly_fragment
 clone_end:SP6
 vector_side:left"

misc_feature
 27897..33321
 /note="assembly_fragment"

misc_feature
 33422..45908
 /note="assembly_fragment"

misc_feature
 46009..85245
 /note="assembly_fragment"

misc_feature
 85346..130509
 /note="assembly_fragment"

misc_feature
 130610..149773
 /note="assembly_fragment
 clone_end:T7
 vector_side:right"

ORIGIN

Query Match 100.0%; Score 16; DB 2; Length 149773;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGCATGCGGGGG 16

Db 91261 GGGCATGCGGGGG 91246

RESULT 3
 AC131924
 LOCUS AC131924 154143 bp DNA linear HTG 12-MAR-2003
 DEFINITION Mus musculus clone RP24-227A11, WORKING DRAFT SEQUENCE, 9 unordered
 pieces.
 ACCESSION AC131924
 VERSION HTG; HTGS PHASE1; HTGS DRAFT.
 KEYWORDS Mus musculus (house mouse)
 SOURCE Mus musculus

ORGANISM
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 154143)
 Birren,B., Nusbaum,C. and Lander,E.
 Mus musculus, clone RP24-227A11
 Unpublished

REFERENCE

AUTHORS

TITLE

JOURNAL

AUTHORS

2 (bases 1 to 154143)
 Birren,B., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S.,
 Barna,N., Bastien,V., Bloom,T., Boguslavsky,L., Boukhgalter,B.,
 Camarata,J., Chang,J., Chazaro,B., Choepel,J., Collymore,A.,
 Cook,A., Cooke,P., DeArelano,K., Dewar,K., Diaz,J.S., Dodge,S.,
 Faro,S., Ferreira,P., Fitzgerald,M., Gage,D., Galagan,J.,
 Gardyna,S., Gord,S., Graham,L., Grand-Pierre,N., Hagos,B.,
 Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C., Kamat,A.,
 Karatas,A., Kells,C., Landers,T., Levine,R., Lindblad-Toh,K.,

Liu,G., MacLean,C., Macdonald,P., Major,J., Matthews,C.,
 McCarthy,M., Meldrim,J., Meneus,L., Mihova,T., Mlenga,V.,
 Murphy,T., Naylor,J., Nguyen,C., Nicol,B., Norbu,C., Norman,C.H.,
 O'Connor,T., O'Donnell,P., O'Neil,D., Oliver,J., Peterson,K.,
 Phunkhang,P., Pierre,N., Raymond,C., Retta,R., Risse,C., Rogov,P.,
 Roman,J., Roy,A., Schauer,S., Schuback,R., Seaman,S., Severy,P.,
 Smith,C., Spencer,B., Stange-Thomann,N., Stojanovic,N., Talamas,J.,
 Testaye,S., Theodore,J., Topham,K., Travers,M., Vassiliev,H.,
 Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Young,G., Zainoun,J.,
 Zembek,L., Zimmer,A. and Zody,M.
 Direct Submission
 Submitted (27-AUG-2002) Whitehead Institute/MIT Center for Genome
 Research, 320 Charles Street, Cambridge, MA 02141, USA
 3 (bases 1 to 154143)

REFERENCE

AUTHORS

TITLE

JOURNAL

AUTHORS

TITLE

JOURNAL

AUTHORS

TITLE

JOURNAL

AUTHORS

TITLE

JOURNAL

AUTHORS

TITLE

JOURNAL

AUTHORS

TITLE

JOURNAL

AUTHORS

TITLE

JOURNAL

AUTHORS

TITLE

JOURNAL

AUTHORS

TITLE

JOURNAL

AUTHORS

TITLE

JOURNAL

AUTHORS

TITLE

JOURNAL

AUTHORS

TITLE

JOURNAL

AUTHORS

TITLE

JOURNAL

AUTHORS

TITLE

JOURNAL

AUTHORS

TITLE

JOURNAL

AUTHORS

TITLE

JOURNAL

AUTHORS

TITLE

JOURNAL

AUTHORS

TITLE

JOURNAL

AUTHORS

TITLE

JOURNAL

AUTHORS

TITLE

JOURNAL

AUTHORS

TITLE

JOURNAL

AUTHORS

```

* 3022 10861: contig of 7840 bp in length
* 10862 10961: gap of 100 bp
* 10862 21716: contig of 10755 bp in length
* 21717 21816: gap of 100 bp
* 34324 34324: contig of 12508 bp in length
* 34325 34424: gap of 100 bp
* 34425 46524: contig of 12100 bp in length
* 46525 46624: gap of 100 bp
* 70364 70364: contig of 23740 bp in length
* 70365 70464: gap of 100 bp
* 100316 100316: contig of 29852 bp in length
* 100317 100416: gap of 100 bp
* 100417 154143: contig of 53727 bp in length.

```

FEATURES

Location/Qualifiers

```

1..154143
  /organism="Mus musculus"
  /mol_type="genomic DNA"
  /db_xref="taxon:10090"
  /clone="RP24-227A11"
  /clone_lib="RPCI-24 Male Mouse BAC"

misc_feature
  1..560
    /note="assembly_fragment"
    clone_end:SP6
    vector_side:left"

misc_feature
  661..72921
    /note="assembly_fragment"

misc_feature
  3022..10861
    /note="assembly_fragment"

misc_feature
  10962..21716
    /note="assembly_fragment"

misc_feature
  21817..34324
    /note="assembly_fragment"

misc_feature
  34425..46524
    /note="assembly_fragment"

misc_feature
  46625..70364
    /note="assembly_fragment"

misc_feature
  70465..100316
    /note="assembly_fragment"

misc_feature
  100417..154143
    /note="assembly_fragment"
    clone_end:T7
    vector_side:right"

```

ORIGIN

```

Query Match      100.0%; Score 16; DB 2; Length 154143;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 GGGCAGTCATGGCGG 16
Db      66741 GGGCAGTCATGGCGG 66756

```

```

RESULT 4
LOCUS      AY178791      157263 bp      DNA      linear      HTG 12-MAR-2003
DEFINITION      Canis familiaris chromosome CFA9, *** SEQUENCING IN PROGRESS ***,
55 unordered pieces.
ACCESSION      AY178791
VERSION      AY178791.1 GI:25990197
KEYWORDS      HTG; HTGS PHASE1.
SOURCE      Canis familiaris (dog)
ORGANISM      Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
1 (bases 1 to 157263)
REFERENCE
AUTHORS      Sidjanin,D.J., Miller,B., Kijas,J., McElwee,J., Pillardy,J.,
Malek,J., Pai,G., Feldblyum,T., Fraser,C., Acland,G. and Aguirre,G.
TITLE      Radiation hybrid map, physical map, and low-pass genomic sequence
of the canine pred region on CFA9 and comparative mapping with the
synetic region on human chromosome 17
JOURNAL      Genomics 81 (2), 138-148 (2003)
MEDLINE      22508185

```

PUBMED
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

```

12620391
2 (bases 1 to 157263)
Sidjanin,D.J., Miller,B., Kijas,J., McElwee,J., Pillardy,J.,
Malek,J., Pai,G., Feldblyum,T., Fraser,C., Acland,G. and Aguirre,G.
Direct Submission
Submitted (14-NOV-2002) James A. Baker Institute for Animal Health,
Cornell University, Hungerford Hill Rd., Ithaca, NY 14853, USA
* NOTE: This is a 'working draft' sequence. It currently
* consists of 55 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*
* 953: contig of 953 bp in length
* 954 1053: gap of unknown length
* 1054 2019: contig of 966 bp in length
* 2020 2119: gap of unknown length
* 2120 3233: contig of 1114 bp in length
* 3234 3333: gap of unknown length
* 3334 4288: contig of 955 bp in length
* 4289 4388: gap of unknown length
* 4389 5712: contig of 1324 bp in length
* 5713 5812: gap of unknown length
* 5813 6807: contig of 995 bp in length
* 6808 6907: gap of unknown length
* 6909 8116: contig of 1209 bp in length
* 8117 8216: gap of unknown length
* 8217 9050: contig of 834 bp in length
* 9051 9150: gap of unknown length
* 9151 10098: contig of 948 bp in length
* 10099 10198: gap of unknown length
* 10199 11341: contig of 1143 bp in length
* 11342 11441: gap of unknown length
* 11442 12317: contig of 875 bp in length
* 12317 12417: gap of unknown length
* 12417 13578: contig of 1162 bp in length
* 13579 13678: gap of unknown length
* 13679 14986: contig of 1308 bp in length
* 14987 15086: gap of unknown length
* 15087 16474: contig of 1388 bp in length
* 16475 16574: gap of unknown length
* 16575 17437: contig of 863 bp in length
* 17438 17537: gap of unknown length
* 17538 18264: contig of 1727 bp in length
* 18265 19365: gap of unknown length
* 19366 21032: contig of 1668 bp in length
* 21033 21132: gap of unknown length
* 21133 22044: contig of 912 bp in length
* 22045 22144: gap of unknown length
* 22145 23953: contig of 1809 bp in length
* 23954 24053: gap of unknown length
* 24054 24784: contig of 731 bp in length
* 24785 24884: gap of unknown length
* 24885 25808: contig of 924 bp in length
* 25809 25909: gap of unknown length
* 25910 27662: contig of 1754 bp in length
* 27663 29363: contig of 1601 bp in length
* 29364 29464: gap of unknown length
* 29465 30704: contig of 1241 bp in length
* 30705 31655: contig of 851 bp in length
* 31656 34159: gap of unknown length
* 34160 34259: gap of unknown length
* 34260 36278: contig of 2019 bp in length
* 36279 36378: gap of unknown length
* 36379 38287: contig of 1909 bp in length
* 38288 38388: gap of unknown length
* 38389 40069: contig of 1682 bp in length
* 40070 40169: gap of unknown length

```

* 40170 42358: contig of 2189 bp in length
* 42359 42458: gap of unknown length
* 42459 44189: contig of 1737 bp in length
* 44190 44295: gap of unknown length
* 44296 47477: contig of 3182 bp in length
* 47478 47577: gap of unknown length
* 47578 49430: contig of 1853 bp in length
* 49431 49530: gap of unknown length
* 49531 52362: contig of 2832 bp in length
* 52363 52462: gap of unknown length
* 52463 55254: contig of 2792 bp in length
* 55255 55354: gap of unknown length
* 55355 59067: contig of 3713 bp in length
* 59068 59167: gap of unknown length
* 59168 61978: contig of 2811 bp in length
* 61979 62078: gap of unknown length
* 62079 65069: contig of 2991 bp in length
* 65070 65169: gap of unknown length
* 65170 66196: contig of 1027 bp in length
* 66197 66296: gap of unknown length
* 66297 70294: contig of 3998 bp in length
* 70295 70394: gap of unknown length
* 70395 73934: contig of 3440 bp in length
* 73935 77001: contig of 3067 bp in length
* 77002 80514: gap of unknown length
* 80515 80614: gap of unknown length
* 80616 84163: contig of 3549 bp in length
* 84164 84263: gap of unknown length
* 84264 88075: contig of 3812 bp in length
* 88076 88175: gap of unknown length
* 88176 92611: contig of 4436 bp in length
* 92612 92711: gap of unknown length
* 92712 97497: contig of 4786 bp in length
* 97498 97597: gap of unknown length
* 97598 101150: contig of 3553 bp in length
* 101151 101250: gap of unknown length
* 101251 106678: contig of 5428 bp in length
* 106679 106778: gap of unknown length
* 106779 114133: contig of 7355 bp in length
* 114134 114233: gap of unknown length
* 114234 121354: contig of 7121 bp in length
* 121355 121454: gap of unknown length
* 121455 128106: contig of 6552 bp in length
* 128107 128206: gap of unknown length
* 128207 136825: contig of 8619 bp in length
* 136826 136925: gap of unknown length
* 136926 145360: contig of 8435 bp in length
* 145361 145460: gap of unknown length
* 145461 157263: contig of 11803 bp in length.

FEATURES
Location/Qualifiers
1..157263
/organism="Canis familiaris"
/mol_type="genomic DNA"
/db_xref="taxon:9615"
/chromosome="CFA9"

ORIGIN

Query Match 100.0%; Score 16; DB 2; Length 157263;
Best Local Similarity 100.0%; Pred. NC. 1.1e-02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGCATGTCATGGGGG 16
Db 31156 GGGCATGTCATGGGGG 31171

RESULT 5
AC135955 158920 bp DNA linear HTG 14-NOV-2002
LOCUS
DEFINITION
Canis familiaris clone RP81-65H2, WORKING DRAFT SEQUENCE, 3 ordered
pieces.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

AC135955
AC135955.2 GI:24960942
HTG; HTGS PHASE2; HTGS DRAFT.
Canis familiaris (dog)
Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
1 (bases 1 to 158920)
Akheri N., Antonellis A., Ayele K., Beckstrom-Sternberg S.M.,
Benjamin B., Blakesley R.W., Bouffard G.G., Brinkley C., Brooks S.,
Carriaga K., Coleman B., Engle J., Granite S., Guan X., Gupta J.,
Haghighi P., Han J., Hansen N., Ho S.-L., Idol J.R., Karling E.,
Laric P., Lee-Lin S.-Q., Legaspi R., Maduro Q.L., Maduro V.B.,
Marquies E.H., Masiello C., Maskeri B., McDowell J.,
Paquirigan C., Pearson R., Portnoy M.E., Prasad A.,
Reddix-Dugue N., Schandler K., Schueler M.G., Sison C.,
Stantrypop S., Thomas J.W., Thomas P.J., Touchman J.W., Vogt J.L.,
Wetherby K.D., Wiggins D., Young A. and Green E.D.
NISC Comparative Sequencing Initiative
Unpublished
2 (bases 1 to 158920)
Green E.D.
Direct Submission
Submitted (25-OCT-2002) NIH Intramural Sequencing Center, 8717
Groveomont Circle, Gaithersburg, MD 20877, USA
3 (bases 1 to 158920)
Green E.D.
Direct Submission
Submitted (14-NOV-2002) NIH Intramural Sequencing Center, 8717
Groveomont Circle, Gaithersburg, MD 20877, USA
On Nov 14, 2002 this sequence version replaced gi:24371373.
----- Genome Center
Center: NIH Intramural Sequencing Center
Center code: NISC
Web site: http://www.nisc.nih.gov
Contact: nisc.zoo@nhgri.nih.gov
----- Project Information
Center project name: Cwu
Center clone name: 065H02

The sequence data in this record represents an 'enhanced' version of a Phase 2 submission. Specifically, the indicated order and orientation of each sequence contig has been established using one or more of the following: read-pair data from individual subclones, overlaps with neighboring clones, alignment with available reference sequence (e.g., human), and/or confirmation by PCR testing. In addition, the sequence assembly is based on at least 8X average coverage in Q20 bases and has been reviewed to rule out gross misassemblies, the low-quality ends of sequence contigs have been trimmed away, and each base is associated with a Phrap-derived quality score.

----- Summary Statistics
Sequencing vector: Plasmid; n/a; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 158022 bases at least Q40
Consensus quality: 158465 bases at least Q30
Consensus quality: 158648 bases at least Q20
Insert size: 138000; agarose-fp
Insert size: 138720; sum-of-contigs
Quality coverage: 11.42x in Q20 bases; agarose-fp
Quality coverage: 9.93x in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently consists of 3 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have been provided by the submitter.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.


```

* 1 37538: contig of 37538 bp in length
* 37539 37638: gap of unknown length
* 37639 136759: contig of 99121 bp in length
* 136760 136859: gap of unknown length
* 136860 158920: contig of 22061 bp in length.

```

FEATURES

```

source
1..158920
/organism="Canis familiaris"
/mol_type="genomic DNA"
/db_xref="taxon:9615"
/clone="RP81-65H2"
/clone_lib="RP81"
1..37538
/note="assembly_fragment"
clone_end:SP6
vector_side:left"
misc_feature
37639..136759
/note="assembly_fragment"
misc_feature
136860..158920
/note="assembly_fragment"
clone_end:T7
vector_side:right"

```

ORIGIN

```

Query Match 100.0%; Score 16; DB 2; Length 158920;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 1 GGGCATGCGGGGGG 16
|||||

```

```

Db 20177 GGGCATGCGGGGGG 20192
|||||

```

RESULT 6

```

AC084382 AC084382 165077 bp DNA linear ROD 21-JUN-2002
LOCUS Mus musculus clone RP23-5K17, complete sequence.
DEFINITION AC084382
ACCESSION AC084382.1 GI:15778814
VERSION
KEYWORDS HTG.
SOURCE Mus musculus (house mouse)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

```

```

REFERENCE
1 (bases 1 to 165077)
AUTHORS McPherson,J.D. and Waterston,R.H.
TITLE The sequence of Mus musculus clone
JOURNAL Unpublished
2 (bases 1 to 165077)
AUTHORS McPherson,J.D.
DIRECT SUBMISSION
Submitted (26-SEP-2001) Genetics, Genome Sequencing Center, 4444
Forest Park Parkway, St. Louis, Missouri 63108, USA
3 (bases 1 to 165077)
AUTHORS McPherson,J.D. and Waterston,R.H.
DIRECT SUBMISSION
Submitted (21-JUN-2002) Genome Sequencing Center, 4444 Forest Park
Parkway, St. Louis, MO 63108, USA

```

COMMENT

```

----- Genome Center -----
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site:http://genome.wustl.edu/gsc/index.shtml
Contact: submissions@wustl.wustl.edu
----- Project Information -----
Center project name: M.BA0005K17
-----
Location/Qualifiers
1..165077
/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
/clone="RP23-5K17"

```

FEATURES

```

source
1..165077
/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
/clone="RP23-5K17"

```

ORIGIN

```

Query Match 100.0%; Score 16; DB 10; Length 165077;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy 1 GGGCATGCGGGGGG 16
|||||

```

```

Db 29008 GGGCATGCGGGGGG 29023
|||||

```

RESULT 7

```

AC139123 AC139123 183540 bp DNA linear HTG 05-FEB-2003
LOCUS Canis familiaris clone RP81-340C22, WORKING DRAFT SEQUENCE, 10
DEFINITION AC139123
ACCESSION AC139123
VERSION AC139123.2 GI:28209437
KEYWORDS HTG; HTGS PHASR2; HTGS_DRAFT.
SOURCE Canis familiaris (dog)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.

```

```

REFERENCE
1 (bases 1 to 183540)
AUTHORS Akhter,N., Antonellis,A., Ayele,K., Beckstrom-Sternberg,S.M.,
Benjamin,B., Blakesley,R.W., Bouffard,G.G., Brinkley,C., Brooks,S.,
Carliga,K., Coleman,B., Engle,J., Granite,S., Guan,X., Gupta,J.,
Haghighi,P., Han,J., Hansen,N., Ho,S.-L., Idol,J.R., Karlius,E.,
Leric,P., Lee-Lin,S.-Q., Legaspi,R., Maduro,Q.L., Maduro,V.B.,
Margulies,E.H., Masiello,C., Maskeri,B., McDowell,J.,
Paguirigan,C., Pearson,R., Portnoy,M.E., Prasad,A.,
Raddix-Dugue,N., Schandler,K., Schueler,M.G., Sison,C.,
Stantripop,S., Thomas,J.W., Thomas,P.J., Touchman,J.W., Vogt,J.L.,
Wetherby,K.D., Wiggins,L., Young,A. and Green,E.D.
NISC Comparative Sequencing Initiative
Unpublished
2 (bases 1 to 183540)
Green,E.D.
DIRECT SUBMISSION
Submitted (24-JAN-2003) NIH Intramural Sequencing Center, 8717
Grovemont Circle, Gaithersburg, MD 20877, USA
3 (bases 1 to 183540)
Green,E.D.
DIRECT SUBMISSION
Submitted (05-FEB-2003) NIH Intramural Sequencing Center, 8717
Grovemont Circle, Gaithersburg, MD 20877, USA
On Feb 5, 2003 this sequence version replaced gi:27884878.
----- Genome Center
Center: NIH Intramural Sequencing Center
Center code: NISC
Web site: http://www.nisc.nih.gov
Contact: nisc.zoogen@nih.gov
----- Project Information
Center project name: eav
Center clone name: 340C22

```

The sequence data in this record represents an 'enhanced' version of a Phase 2 submission. Specifically, the indicated order and orientation of each sequence contig has been established using one or more of the following: read-pair data from individual subclones, overlaps with neighboring clones, alignment with available reference sequence (e.g., human), and/or confirmation by PCR testing. In addition, the sequence assembly is based on at least 8X average coverage in Q20 bases and has been reviewed to rule out gross misassemblies, the low-quality ends of sequence contigs have been trimmed away, and each base is associated with a Phrap-derived quality score.

```

----- Summary Statistics
Sequencing vector: plasmid; n/a; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 181869 bases at least Q40

```

Consensus quality: 182282 bases at least Q30
 Consensus quality: 182531 bases at least Q20
 Insert size: 174000; agarose-fp
 Insert size: 182640; sum-of-contigs
 Quality coverage: 11.73x in Q20 bases; agarose-fp
 Quality coverage: 11.17x in Q20 bases; sum-of-contigs

NOTE: This is a 'working draft' sequence. It currently consists of 10 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have been provided by the submitter.

This sequence will be replaced by the finished sequence as soon as it is available and by the accession number will be preserved.

1 1319: contig of 1319 bp in length
 1320 1419: gap of unknown length
 1420 6511: contig of 5092 bp in length
 6512 6611: gap of unknown length
 6612 17980: contig of 11369 bp in length
 17981 18080: gap of unknown length
 18081 61539: contig of 43459 bp in length
 61540 61639: gap of unknown length
 61640 101551: contig of 39912 bp in length
 101552 101651: gap of unknown length
 101652 116778: contig of 15127 bp in length
 116779 116878: gap of unknown length
 116879 156712: contig of 39834 bp in length
 156713 156812: gap of unknown length
 156813 166395: contig of 9483 bp in length
 166396 166395: gap of unknown length
 166396 168306: contig of 2511 bp in length
 168307 169006: gap of unknown length
 169007 183540: contig of 14534 bp in length.
 169007 Location/Qualifiers

FEATURES

source
 1..183540
 /organism="Canis familiaris"
 /mol_type="genomic DNA"
 /db_xref="taxon:9615"
 /clone="RP81-340C32"
 /clone_lib="RP81"
 1..138606
 /note="clone overlaps with GenBank Accession Number AC135955 clone RP81-65H2 (center project name cwn)"
 misc_feature
 1..1319
 /note="assembly_fragment"
 clone_end:T7
 vector_side:left
 1420..6511
 /note="assembly_fragment"
 6612..17980
 /note="assembly_fragment"
 18081..61539
 /note="assembly_fragment"
 61640..101551
 /note="assembly_fragment"
 101652..116778
 /note="assembly_fragment"
 116879..156712
 /note="assembly_fragment"
 156813..166295
 /note="assembly_fragment"
 166396..168906
 /note="assembly_fragment"
 169007..183540
 /note="assembly_fragment"
 clone_end:SP6
 vector_side:right

ORIGIN

Query Match 100.0%; Score 16; DB 2; Length 183540;
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GGGCATGCAATGGGGG 16
 |||||
 Db 1020 GGGCATGCAATGGGGG 1035

RESULT 8

AC131987 186129 bp DNA linear HTG 27-MAR-2003
 AC131987/c
 LOCUS Mus musculus clone RP24-184L10, WORKING DRAFT SEQUENCE, 8 unordered pieces.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

AC131987.3 GI:29294243
 HTG; HTGS PHASE1; HTGS DRAFT; HTGS_FULLTOP.
 Mus musculus (house mouse)

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: <http://www.seq.wi.mit.edu>
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L27107
Center clone name: 184 L 10
----- Summary Statistics
Sequencing vector: Plasmid; n/a; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 183983 bases at least Q40
Consensus quality: 184631 bases at least Q30
Consensus quality: 185040 bases at least Q20
Insert size: 168000; agarose-fp
Insert size: 185429; sum-of-contigs
Quality coverage: 11.1 in Q20 bases; agarose-fp
Quality coverage: 10.1 in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently
* consists of 8 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*
* 1 1963: contig of 1963 bp in length
* 1964 2063: gap of 100 bp
* 2064 7095: contig of 5032 bp in length
* 7096 7196: gap of 100 bp
* 7196 20081: contig of 12886 bp in length
* 20082 20181: gap of 100 bp
* 20182 32509: contig of 12328 bp in length
* 32510 32609: gap of 100 bp
* 32610 45123: contig of 12514 bp in length
* 45124 45223: gap of 100 bp
* 45224 73181: contig of 27958 bp in length
* 73182 73281: gap of 100 bp
* 73282 167035: contig of 93754 bp in length
* 167036 167135: gap of 100 bp
* 167136 186129: contig of 18994 bp in length.
----- Location/Qualifiers
source
1..186129
/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
/clone_lib="RP24-184L10"
/clone_lib="RP24-184L10"
/clone_lib="RP24-184L10"
1..1963
/note="assembly_fragment
clone_end:SP6
vector_side:left"
misc_feature
2064..7095
/note="assembly_fragment"
misc_feature
7196..20081
/note="assembly_fragment"
misc_feature
20182..32509
/note="assembly_fragment"
misc_feature
32610..45123
/note="assembly_fragment"
misc_feature
45224..73181
/note="assembly_fragment"
misc_feature
73282..167035
/note="assembly_fragment"
misc_feature
167136..186129
/note="assembly_fragment
clone_end:T7
vector_side:right"

Query Match 100.0%; Score 16; DB 2; Length 186129;

Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGGCATGTCATGGGGG 16
|||||
DB 173050 GGGCATGTCATGGGGG 173035

RESULT 9
CNS01RHC 192462 bp DNA linear PRI 03-MAY-2001
LOCUS Human chromosome 14 DNA sequence BAC R-736N17 of library RPCI-11
DEFINITION from chromosome 14 of Homo sapiens (Human), complete sequence.
ACCESSION AL161669
VERSION AL161669.5 GI:13990665
KEYWORDS HTG.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 192462)
Heilig, R., Petit, J. L., Vico, V., Dasilva, C., Robert, C., Wincker, P.,
Brottier, P., Cattolico, L., Barbe, V., Pelletier, E., Artiguenave, F.,
Levy, M., Eckenberg, R., Bruls, T., Deberardinis, V., Cruaud, C.,
Gyapay, G., Saurin, W. and Weissenbach, J.
Sequencing of the human chromosome 14
Unpublished
REFERENCE 2 (bases 1 to 192462)
Genoscope.
Direct Submission
Submitted (02-MAY-2001) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)
- Web : www.genoscope.cns.fr
On May 8, 2001 this sequence version replaced gi:11611164.
----- Genom Center
Center: Genoscope / Centre National de Sequencage
Center code: GS
Web site: <http://www.genoscope.cns.fr/>
Contact: Seqref@genoscope.cns.fr

The following BAC sequence is oriented from the T7 to the SP6 end.
Upstream BAC (overlapping the T7 end) : R-45P15 (AC=AL138976)
Downstream BAC (overlapping the SP6 end) : C-2538G10
----- Summary Statistics
Assembly program: Phrap; version 2.0
Quality coverage: 10.43x in Q20 bases; sum-of-contigs

Overall quality chart :
Range : bases
0 :
1 - 9 :
10 - 19 : 4
20 - 29 : 9
30 - 39 : 151
40 - 49 : 2414
50 - 59 : 6200
60 - 69 : 8214
70 - 79 : 18797
80 - 89 : 54419
90 - 99 : 102254
Percentage of bases with a quality value >= 40 : 99 %

Location/Qualifiers
1..192462
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="14"
/clone_lib="RP24-184L10"
/clone_lib="RP24-184L10"
27321..27545
/note="matching EMBL:G04572

FEATURES
source
STS

AUTHORS

Birren, B., Nusbaum, C., Lander, E., Abouelleil, A., Allen, N., Anderson, S., Arachchi, H.M., Barna, N., Bastien, V., Bloom, T., Boguslavskiy, L., Boukhgalter, B., Camarata, J., Chang, J., Choepel, Y., Collymore, A., Cook, A., Cooke, P., Dorris, L., Erickson, K., Faro, S., Diaz, J.S., Dodge, S., Dooley, K., Dorris, L., Erickson, K., Faro, S., Ferreira, P., Fitzgerald, M., Gage, D., Galagan, J., Gardyna, S., Graham, L., Grand-Pierre, N., Hafez, N., Hagopian, D., Hagos, B., Hall, J., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., Liu, A., Mabbitt, R., Maclean, C., Macdonald, P., Major, J., Manning, J., Matthews, C., McCarthy, M., Melnick, J., Meneus, L., Mihova, T., Mieng, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Rachupka, A., Ramasamy, U., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Schauer, S., Schuback, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubbs, M., Talamas, J., Testaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Venkataraman, V.S., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

TITLE

JOURNAL

COMMENT

Submitted (27-MAR-2003) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
On Mar 27, 2003 this sequence version replaced gi:28626869.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

Center: Whitehead Institute/ MIT Center for Genome Research

Center code: WIBR

Web site: <http://www-seq.wi.mit.edu>

Contact: sequence_submissions@genome.wi.mit.edu

Project Information

Center project name: L26354

Center clone name: 188 M.21

Summary Statistics

Sequencing vector: Plasmid; n/a; 100% of reads

Chemistry: Dye-terminator Big Dye; 100% of reads

Assembly program: Phrap; version 0.960731

Consensus quality: 221635 bases at least Q40

Consensus quality: 221908 bases at least Q30

Consensus quality: 221986 bases at least Q20

Insert size: 200000; agarose-fp

Quality coverage: 10.7 in Q20 bases; agarose-fp

Quality coverage: 9.6 in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently consists of 6 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

* 1 2031: contig of 2031 bp in length
* 2032 2131: gap of 100 bp
* 2132 15244: contig of 13113 bp in length
* 15245 15344: gap of 100 bp
* 15345 37649: contig of 22305 bp in length
* 37650 37749: gap of 100 bp
* 37750 148102: contig of 110353 bp in length
* 148103 148203: gap of 100 bp
* 148203 190361: contig of 42159 bp in length
* 190362 190461: gap of 100 bp
* 190462 222510: contig of 32049 bp in length.

FEATURES

source

1. 222510
/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
/clone="RP23-188M21"
/clone_lib="RPC1-23 Female Mouse BAC"

AUTHORS

RHdb:RH53929
RHdb:RH3791
dbSTS:STS22999
Identified using the e-PCR software (G. Schuler)
103114. .103373
/note="matching EMBL:M92357
RHdb:RH17752
dbSTS:STS14628
Identified using the e-PCR software (G. Schuler)
129886. .130095
/note="matching EMBL:G32911
RHdb:RH67603
dbSTS:STS47530
Identified using the e-PCR software (G. Schuler)
130030. .130216
/note="matching EMBL:H60047
RHdb:RH78715
dbSTS:STS55456
Identified using the e-PCR software (G. Schuler)

ORIGIN

Query Match 100.0%; Score 16; DB 9; Length 192462;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GGCGCATGCGGGGG 16
|||||
Db 99243 GGCGCATGCGGGGG 99258

RESULT 10

AC123656

LOCUS

AC123656 222510 bp DNA linear HTG 27-MAR-2003
Mus musculus clone RP23-188M21, WORKING DRAFT SEQUENCE, 6 unordered pieces.

ACCESSION

AC123656

HTG; HTGS_PHASE1; HTGS_DRAFT.

KEYWORDS

Mus musculus

SOURCE

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE

1 (bases 1 to 222510)

Birren, B., Nusbaum, C. and Lander, E.

Unpublished

2 (bases 1 to 222510)

Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barna, N., Bastien, V., Bloom, T., Boguslavskiy, L., Boukhgalter, B., Brown, A., Camarata, J., Campopiano, A., Chang, J., Chararo, B., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, A., Cooke, P., Dearellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., Fitzgerald, M., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., LaRocque, K., Lamazares, R., Landers, T., Lehoczy, J., Levine, R., Lindblad-Toh, K., Liu, G., Maclean, C., Macdonald, P., Major, J., Marquis, N., Matthews, C., McCarthy, M., McEwan, P., McKernan, K., Melnick, J., Meneus, L., Mihova, T., Mieng, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schuback, R., Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Straus, N., Subramanian, A., Talamas, J., Testaye, S., Theodore, J., Topham, K., Travers, M., Travis, N., Trigilio, J., Viel, R., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

TITLE

JOURNAL

Submitted (01-JUN-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

REFERENCE

3 (bases 1 to 222510)

```
misc_feature 1. .2031
              /note="assembly_fragment"
misc_feature 2132. .15244
              /note="assembly_fragment"
misc_feature 15345. .37649
              /note="assembly_fragment"
misc_feature 37750. .148102
              /note="assembly_fragment"
misc_feature 148203. .190361
              /note="assembly_fragment"
misc_feature 190462. .222510
              /note="assembly_fragment
              clone_end:T7
              vector_side:right"

ORIGIN
Query Match      100.0%; Score 16; DB 2; Length 222510;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGCATGCATGGGGG 16
    |||||
Db 32129 GGGCATGCATGGGGG 32144

RESULT 11
AC147160/c
LOCUS          227805 bp      DNA      linear      HTG 04-NOV-2003
DEFINITION     Mus musculus chromosome UNK clone RP24-336A22, WORKING DRAFT
ACCESSION      AC147160
VERSION        AC147160.1 GI:38154247
KEYWORDS       HTG; HTGS, PHASE1; HTGS, DRAFT; HTGS, FULLTOP.
SOURCE         Mus musculus (house mouse)
ORGANISM       Mus musculus
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE      1 (bases 1 to 227805)
AUTHORS        Wilson,R.K.
TITLES         The sequence of Mus musculus clone
               Unpublished
REFERENCE      2 (bases 1 to 227805)
AUTHORS        Wilson,R.K.
TITLES         Direct Submission
JOURNAL         Submitted (04-NOV-2003) Genome Sequencing Center, 4444 Forest Park
               Parkway, St. Louis, MO 63108, USA

COMMENT
----- Genome Center -----
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site:http://genome.wustl.edu
Contact: submission@watson.wustl.edu
----- Project Information -----
Center project name: M_BB0336A22
----- Summary Statistics -----
Sequencing vector: M13; 0%
Sequencing vector: Plasmid; 100%
Chemistry: Dye-primer ET; 0% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 221580 bases at least Q40
Consensus quality: 222826 bases at least Q30
Consensus quality: 223563 bases at least Q20

* NOTE: This is a 'working draft' sequence. It currently
* consists of 15 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
```

```
1272: contig of 1272 bp in length
1372: gap of unknown length
2460: contig of 1088 bp in length
2560: gap of unknown length
3814: contig of 1254 bp in length
3914: gap of unknown length
7235: contig of 3321 bp in length
7335: gap of unknown length
11348: contig of 4013 bp in length
11448: gap of unknown length
20254: contig of 8806 bp in length
20355: gap of unknown length
26122: contig of 5768 bp in length
26223: gap of unknown length
39123: contig of 12901 bp in length
39223: gap of unknown length
56051: contig of 16828 bp in length
56151: gap of unknown length
74804: contig of 18653 bp in length
74905: gap of unknown length
96699: contig of 21795 bp in length
96700: gap of unknown length
121347: contig of 24548 bp in length
121447: gap of unknown length
149969: contig of 28522 bp in length
150069: gap of unknown length
183071: contig of 33002 bp in length
183171: gap of unknown length
183172: 227805; contig of 44634 bp in length.

FEATURES
          location/Qualifiers
          source
1. .227805
   /organism="Mus musculus"
   /mol_type="genomic DNA"
   /db_xref="taxon:10090"
   /chromosome="UNK"
   /clone="RP24-336A22"
misc_feature 1. .1272
              /note="assembly_name:Contig41"
misc_feature 1373. .2460
              /note="assembly_name:Contig43"
misc_feature 2561. .3814
              /note="assembly_name:Contig45"
misc_feature 3915. .7235
              /note="assembly_name:Contig47"
misc_feature 7336. .11348
              /note="assembly_name:Contig48"
misc_feature 11449. .20254
              /note="assembly_name:Contig49"
misc_feature 20355. .26122
              /note="assembly_name:Contig50"
misc_feature 26223. .39123
              /note="assembly_name:Contig51"
misc_feature 39224. .56051
              /note="assembly_name:Contig52"
misc_feature 56152. .74804
              /note="assembly_name:Contig53"
misc_feature 74905. .96699
              /note="assembly_name:Contig54"
misc_feature 96800. .121347
              /note="assembly_name:Contig55"
misc_feature 121448. .149969
              /note="assembly_name:Contig56"
misc_feature 150070. .183071
              /note="assembly_name:Contig57"
misc_feature 183172. .227805
              /note="assembly_name:Contig58"

ORIGIN
Query Match      100.0%; Score 16; DB 2; Length 227805;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGCATGCATGGGGG 16
```

Db 50847 GGGCATGCATGGGGG 50832

|||||

RESULT 12
AC095635
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

AC095635 234548 bp DNA linear HTG 09-MAY-2003
Rattus norvegicus clone CH230-8K1, WORKING DRAFT SEQUENCE, 2
unorderded pieces.
AC095635.6 GI:30467118
HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTDP.
Rattus norvegicus (Norway rat)
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus
1 (bases 1 to 234548)

REFERENCE
AUTHORS
Murray, D., Marie, Metzger, M., Lee, A., Abranson, S., Adams, C., Alder, J.,
Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D.,
Anyalebechi, V., Ayoyagi, A., Ayodeji, M., Baca, E., Baden, H.,
Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, P.,
Biswal, N., Blair, J., Blankenburg, K., Blyth, P., Brown, M.,
Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, B.,
Cardenas, V., Carter, K., Cavazos, I., Ceasar, R., Center, A.,
Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J.,
Cleaveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L.,
Davila, M., Davis, C., Davy-Cazroll, L., De Anda, C., Dederich, D.,
Delgado, O., Denson, S., Deramo, C., Ding, Y., Din, H., Divya, K.,
Draper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Eaves, K.,
Egan, A., Escoto, M., Eugene, C., Evans, C.A., Falls, T., Fan, G.,
Fernandez, S., Finley, M., Flagg, N., Forbes, L., Foster, M., Foster, P.,
Fraser, C.M., Gabisa, A., Ganta, R., Garcia, A., Garner, T., Garza, M.,
Georgiev, S., Geer, K., Gill, R., Grady, M., Guerra, I., Guera, W.,
Gunnarathne, P., Haaland, W., Hamill, C., Hamilton, C., Hamilton, K.,
Harvey, Y., Havlak, P., Hawes, A., Henderson, N., Hernandez, J.,
Hernandez, R., Hines, S., Hladun, S.L., Hodgson, A., Hogues, M.,
Hollins, B., Howells, S., Hui, J., Hume, J., Idlebird, D., Jackson, A.,
Jackson, L., Jacob, L., Jiang, H., Johnson, B., Johnson, R., Jolivet, A.,
Karpatis, S., Kelly, S., Kelly, S., Khan, Z., King, L., Kovar, C.,
Kowis, C., Kraft, C.L., Lebow, H., Levan, J., Lewis, L., Li, Z., Liu, J.,
Liu, J., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J.,
Lorenshewa, L., Louisege, H., Izado, R.J., Lu, X., Ma, J.,
Maheshwari, M., Mahindartne, M., Mahmoud, M., Malloy, K., Mangum, A.,
Mangum, B., Mapa, P., Martin, K., Martin, R., Martinez, E.,
Mawhney, S., McLeod, M.P., McNeill, T.Z., Meenen, E.,
Milosavljevic, A., Miner, G., Minja, E., Montemayor, J., Moore, S.,
Morgan, M., Morris, K., Morris, S., Munidasa, M., Murphy, M., Nair, L.,
Nankervis, C., Neal, D., Newton, N., Nguyen, N., Norris, S.,
Nwackelme, O., Okwono, G., Olairpungoon, A., Pal, S., Parks, K.,
Pasternak, S., Paul, H., Perez, A., Perez, L., Pfannkuch, C.,
Plopper, P., Poindexter, A., Popovic, D., Primus, E., Pu, L.-L.,
Puazo, M., Quiroz, J., Rachlin, E., Reeves, K., Regier, M.A., Reigh, R.,
Reilly, B., Reilly, M., Ren, Y., Reuter, M., Richards, S., Riggs, F.,
Rivers, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S.J.,
Sanders, W., Savery, G., Scherer, S., Scott, G., Shatsman, S., Shen, H.,
Shetty, J., Shvartsbeyn, A., Sison, I., Sitter, C.D., Smajs, D.,
Sneed, A., Sodergren, E., Song, X.-Z., Sorelle, R., Sosa, J.,
Steinle, M., Strong, R., Sutton, A., Svatek, A., Tabor, P., Taylor, C.,
Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Usmani, K.,
Valas, R., Vera, V., Villanasa, D., Waldron, L., Walker, B., Wang, J.,
Wang, Q., Wang, S., Warren, J., Warren, R., Wei, X., White, F.,
Williams, G., Willson, R., Wlecyk, R., Woodson, H., Worley, K.,
Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V.,
Yu, F., Zhang, J., Zhou, J., Zhou, X., Zhao, S., Zhao, S., Dunn, D., von
Niederhausern, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O.,
Weinstock, G. and Gibbs, R.A.
Direct Submission
Unpublished
2 (bases 1 to 234548)
Worley, K.C.
REFERENCE
AUTHORS
TITLE
JOURNAL

of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 234548)
Rat Genome Sequencing Consortium.
Submitted (09-MAY-2003) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On May 9, 2003 this sequence version replaced gi:24817791.
The sequence in this assembly is a combination of BAC based reads
and whole genome shotgun sequencing reads assembled using Atlas
(http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described
in the feature table below represents a scaffold in the Atlas
assembly (a 'contig-scaffold'). Within each contig-scaffold,
individual sequence contigs are ordered and oriented, and separated
by sized gaps filled with Ns to the estimated size. The sequence
may extend beyond the ends of the clone and there may be sequence
contigs within a contig-scaffold that consist entirely of whole
genome shotgun sequence reads. Both end sequences and whole genome
shotgun sequence only contigs will be indicated in the feature
table.

----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: GCWM
Center clone name: CH230-8K1
----- Summary Statistics
Assembly program: Atlas
Consensus quality: 22438 bases at least Q40
Consensus quality: 224642 bases at least Q30
Consensus quality: 225972 bases at least Q20
Estimated insert size: 232080; sum-of-contigs estimation
Quality coverage: 7x in Q20 bases; sum-of-contigs estimation

* NOTE: Estimated insert size may differ from sequence length
(see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
consists of 2 contigs. The true order of the pieces
is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as
runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
as soon as it is available and the accession number will
be preserved

* 1 232993: contig of 232993 bp in length
* 232994 233093: gap of unknown length
* 233094 234548: contig of 1455 bp in length.

FEATURES
source
1. 234548
/organism="Rattus norvegicus"
/mol_type="genomic DNA"
/db_xref="taxon:10116"
/clone="CH230-8K1"
1. 1711
/note="wgs_contig"

misc_feature
100.0%; Score 16; DB 2; Length 234548;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

ORIGIN
Query Match
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GGGCATGCATGGGGG 16
|||||
Db 114301 GGGCATGCATGGGGG 114316

RESULT 13
AC131337
LOCUS
DEFINITION
Submitted (17-SEP-2001) Human Genome Sequencing Center, Department

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

AC131337
GI:30017797
HTG, HTGS, PHASE1, HTGS, DRAFT.
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 345420)
Birren,B., Nusbaum,C. and Lander,B.
Mus musculus, clone RP23-480E1
Unpublished
2 (bases 1 to 345420)

REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS

Birren,B., Nusbaum,C., Lander,B., Ali,A., Allen,N., Anderson,S.,
Barna,N., Bastien,V., Bloom,T., Boguslavsky,L., Boukhalter,B.,
Camarata,J., Chang,J., Charao,B., Choepel,Y., Collymore,A.,
Cook,A., Cooke,P., DeArillano,K., Dewar,K., Diaz,J.S., Dodge,S.,
Faro,S., Ferreira,P., Fitzgerald,M., Gage,D., Galagan,J.,
Gardyna,S., Gord,S., Graham,L., Grand-Pierre,N., Hagos,B.,
Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C., Kamat,A.,
Karatas,A., Kells,C., Landers,T., Levine,R., Lindblad-Toh,K.,
Liu,G., MacLean,C., Macdonald,P., Major,J., Matthews,C.,
McCarthy,M., Meldrim,J., Meneus,L., Mihova,T., Mlenga,V.,
Murphy,T., Naylor,J., Nguyen,C., Nicol,R., Norbu,C., Norman,C.H.,
O'Connor,T., O'Donnell,P., O'Neil,D., Oliver,J., Peterson,K.,
Phunkhang,P., Pierre,N., Raymond,C., Retta,R., Rise,C., Rogov,P.,
Roman,J., Roy,A., Schauer,S., Schuback,R., Seaman,S., Severy,P.,
Smith,C., Spencer,B., Stange-Thomann,N., Stojanovic,N., Talamas,J.,
Tesfaye,S., Theodore,J., Topham,K., Travers,M., Vassiliev,H.,
Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Young,G., Zainoun,J.,
Zembek,L., Zimmer,A. and Zody,M.

TITLE
JOURNAL
REFERENCE
AUTHORS

Direct Submission
Submitted (20-AUG-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
3 (bases 1 to 345420)
Birren,B., Nusbaum,C., Lander,B., Abouelleil,A., Allen,N.,
Anderson,S., Arachchi,H.M., Barna,N., Bastien,V., Bloom,T.,
Boguslavsky,L., Boukhalter,B., Camarata,J., Chang,J., Choepel,Y.,
Collymore,A., Cook,A., Cooke,P., Corum,B., DeArillano,K.,
Diaz,J.S., Dodge,S., Dooley,K., Dorris,L., Erickson,J., Faro,S.,
Ferreira,P., Fitzgerald,M., Gage,D., Galagan,J., Gardyna,S.,
Graham,L., Grand-Pierre,N., Hafez,N., Hagopian,D., Hagos,B.,
Hall,J., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C.,
Kamat,A., Karatas,A., Kells,C., Landers,T., Levine,R.,
Lindblad-Toh,K., Liu,G., Lui,A., Mabbitt,R., MacLean,C.,
Macdonald,P., Major,J., Manning,J., Matthews,C., McCarthy,M.,
Meldrim,J., Meneus,L., Mihova,T., Mlenga,V., Murphy,T., Naylor,J.,
Nguyen,C., Nicol,R., Norbu,C., O'Connor,T., O'Donnell,P.,
O'Neil,D., Oliver,J., Peterson,K., Phunkhang,P., Pierre,N.,
Rachupka,A., Ramasany,U., Raymond,C., Retta,R., Rise,C., Rogov,P.,
Roman,J., Schauer,S., Schuback,R., Seaman,S., Severy,P., Smith,C.,
Spencer,B., Stange-Thomann,N., Stojanovic,N., Stubbs,M.,
Talamas,J., Tesfaye,S., Theodore,J., Topham,K., Travers,M.,
Vassiliev,H., Venkataraman,V.S., Viel,R., Vo,A., Wilson,B., Wu,X.,
Wyman,D., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.

TITLE
JOURNAL
COMMENT

Direct Submission
Submitted (23-APR-2003) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Apr 17, 2003 this sequence version replaced gi:28626850.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submission@genome.wi.mit.edu
----- Project Information
Center project name: L26504
Center clone name: 480_E1

* NOTE: This is a 'working draft' sequence. It currently
* consists of 17 contigs. The true order of the pieces

* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

1 1221: contig of 1221 bp in length
* 1222: gap of 100 bp
* 1322: contig of 1419 bp in length
* 2740: gap of 100 bp
* 2840: contig of 1511 bp in length
* 2841: gap of 100 bp
* 4352: contig of 2780 bp in length
* 4452: gap of 100 bp
* 7232: contig of 6249 bp in length
* 7332: gap of 100 bp
* 13580: contig of 5544 bp in length
* 13680: gap of 100 bp
* 19224: contig of 100 bp
* 19225: gap of 100 bp
* 24245: contig of 4921 bp in length
* 24246: gap of 100 bp
* 24346: contig of 8959 bp in length
* 33045: gap of 100 bp
* 33046: contig of 10555 bp in length
* 33405: gap of 100 bp
* 43959: contig of 20133 bp in length
* 44059: gap of 100 bp
* 64192: contig of 100 bp
* 64193: gap of 100 bp
* 140234: contig of 75941 bp in length
* 140233: gap of 100 bp
* 140234: contig of 26604 bp in length
* 166938: gap of 100 bp
* 167038: contig of 35527 bp in length
* 202564: gap of 100 bp
* 202565: contig of 33201 bp in length
* 235865: gap of 100 bp
* 235966: contig of 46274 bp in length
* 282240: gap of 100 bp
* 282340: contig of 42901 bp in length
* 325341: gap of 100 bp
* 325341: contig of 20080 bp in length.

FEATURES
source

1. 345420
/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
/clone="RP23-480E1"
/clone_lib="RP23-480E1"
1. 1221
/note="assembly_fragment"
1322..2740
/note="assembly_fragment"
2841..4351
/note="assembly_fragment"
4452..7231
/note="assembly_fragment"
7332..13580
/note="assembly_fragment"
13681..19224
/note="assembly_fragment"
19225..24245
/note="assembly_fragment"
24246..33044
/note="assembly_fragment"
33405..43959
/note="assembly_fragment"
44060..64192
/note="assembly_fragment"
64293..140233
/note="assembly_fragment"
140334..166937
/note="assembly_fragment"
167038..202564
/note="assembly_fragment"
202665..235865


```

misc_feature      /note="assembly_fragment"
235966..282239
/note="assembly_fragment"
282340..325240
/note="assembly_fragment"
325341..345420
/note="assembly_fragment"
clone_end:T7
vector_side:right"

```

ORIGIN

```

Query Match      100.0%; Score 16; DB 2; Length 345420;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```
QY      1 GGGCATGCGATGGGGG 16
      |||||

```

```
Db      160990 GGGCATGCGATGGGGG 161005
      |||||

```

RESULT 14

```

LOCUS      AX251652/c      657 bp      DNA      linear      PAT 05-OCT-2001
DEFINITION      Sequence 47 from Patent WO0168849.
ACCESSION      AX251652
VERSION      AX251652.1 GI:15985065
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

```

REFERENCE

```

AUTHORS      Wood, L.S., Vogeli, G., Karnovsky, A.M., Ruble, C.L., Linske-O, L.I.,
Wang, J. and Liu, D.
TITLE      Human ion channels
JOURNAL      Patent: WO 0168849-A 47 20-SEP-2001;
Pharmacia & Upjohn Company (US)

```

FEATURES

```

source
1..657
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

```

ORIGIN

```

Query Match      93.8%; Score 15; DB 6; Length 657;
Best Local Similarity 100.0%; Pred. No. 7e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```
QY      1 GGGCATGCGATGGGGG 15
      |||||

```

```
Db      550 GGGCATGCGATGGGGG 536
      |||||

```

RESULT 15

```

LOCUS      BV013263/c      867 bp      DNA      linear      STS 30-MAY-2003
DEFINITION      S212P6739F510.T0 CZECHII/Ei Mus musculus STS genomic, sequence
tagged site.
ACCESSION      BV013263
VERSION      BV013263.1 GI:31097158
KEYWORDS
SOURCE      Mus musculus (house mouse)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

```

REFERENCE

```

AUTHORS      Wade, C.M., Kulbokas, E.J. III, Kirby, A.W., Zody, M.C., Mullikin, J.C.,
Lander, E.S., Lindblad-Toh, K., and Daly, M.J.
TITLE      The mosaic structure of variation in the laboratory mouse genome
JOURNAL      Nature 420 (6915), 574-578 (2002)
MEDLINE      22354684
PUBMED      12466852
COMMENT

```

Contact: Kerstin Lindblad-Toh
Whitehead Institute for Biomedical Research, Center for Genome
Research
320 Charles Street, Cambridge, MA 02141, USA
Tel: 6175521477
Fax: 6175580903
Email: kersli@genome.wi.mit.edu
Primer A: None
Primer B: None
STS size: 867

Protocol:

WGS-discovery: Paired-end low-coverage whole genome shotgun reads
were generated from 125S1/SvimJ, C3H/HeJ, and BALB/cByJ. The WGS
reads were placed uniquely on the MGS C57BL/6J assembly and SNP
detection was carried out by SSAHA-SNP. 225,000 reads were
annotated

as STGs and 81,000 SNPs were annotated with alleles from C57BL/6J
and the strain from which the particular read came. The validation
rate for these SNPs was estimated at approximately 98%.

FEATURES

source

```

1..867
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="CZECHII/Ei"
/db_xref="taxon:10090"
/map="- 1 28-802 47402426-47401650"
/clone_lib="CZECHII/Ei"
<1..867

```

STS

ORIGIN

```

Query Match      93.8%; Score 15; DB 11; Length 867;
Best Local Similarity 100.0%; Pred. No. 6.9e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```
QY      1 GGGCATGCGATGGGGG 15
      |||||

```

```
Db      99 GGGCATGCGATGGGGG 85
      |||||

```

Search completed: July 2, 2004, 10:08:03

Job time : 568.317 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 2, 2004, 06:05:50 ; Search time 119.902 Seconds
(without alignments)
566.887 Million cell updates/sec

Title: US-10-068-160-15

Perfect score: 16

Sequence: 1 gggcatgcatgggggg 16

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_23Jan04:*

- 1: Geneseqn1980s:*
- 2: Geneseqn1990s:*
- 3: Geneseqn2000s:*
- 4: Geneseqn2001as:*
- 5: Geneseqn2001bs:*
- 6: Geneseqn2002s:*
- 7: Geneseqn2003as:*
- 8: Geneseqn2003bs:*
- 9: Geneseqn2003cs:*
- 10: Geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	15	93.8	657	4	AAD17168 Human ion
C 2	15	93.8	657	7	ACD01553 CDNA clon
C 3	15	93.8	657	9	AD29244 Novel hum
C 4	15	93.8	2000	7	ADA72822 Rice gene
C 5	14.4	90.0	51	4	AAL31444 Human SNP
C 6	14.4	90.0	390	6	ABL78599 Human ova
C 7	14.4	90.0	408	2	AAQ22507
C 8	14.4	90.0	408	2	AAQ22508
C 9	14.4	90.0	408	2	AAQ22510
C 10	14.4	90.0	408	2	AAQ22506
C 11	14.4	90.0	462	8	ACH19351 Human adu
C 12	14.4	90.0	475	8	ACH33855 Human end
C 13	14.4	90.0	675	2	AAV33946 Gibbon in
C 14	14.4	90.0	865	1	AAH80502 Sequence
C 15	14.4	90.0	909	1	AAH92339 Single st
C 16	14.4	90.0	1653	6	ABQ54810 Human ova
C 17	14.4	90.0	1652	2	AAH784711 Human Snc
C 18	14.4	90.0	2001	6	AAH94988 Human DNA
C 19	14.4	90.0	2109	7	ACD19383 CDNA enco
C 20	14.4	90.0	2529	6	ABL69709 Prostate
C 21	14.4	90.0	2529	6	ABT10905 Human bre
C 22	14.4	90.0	2529	8	ADB70327 Keratin 5
C 23	14.4	90.0	2529	9	ADB75393 Prostate

ALIGNMENTS

RESULT 1

AAD17168/c

ID AAD17168 standard; CDNA; 657 BP.

XX AAD17168;

AC AAD17168;

XX 29-NOV-2001 (first entry)

XX Human ion channel-91 (ion91) CDNA.

XX Human; ion channel-91; ion91; antiinflammatory; immunosuppressive; analgesic; norepinephrine; antidiuretic; antipressant; cardiac; cytosolic; antiviral; human immunodeficiency virus; HIV; anorectic; antiviral; thyroid disorder; thyrotoxicosis; myxoedema; renal failure; Crohn's disease; rheumatoid arthritis; autoimmune disorder; pain; stroke; psychotic disorder; neurological disorder; anxiety; dyskinesia; Huntington's disease; degenerative disorder; Parkinson's disease; schizophrenia; Alzheimer's disease; cardiovascular disease; cancer; metabolic disorder; anorexia; obesity; mental disorder; ss.

OS Homo sapiens.

XX Key

XX Location/Qualifiers

XX 141..455

XX /*tag= a

XX /product= "Human ion91 protein"

XX /transl_except= {pos:333..341, aa:Ser-Pro}

XX /note= "This translational exception comprises an in-

XX frame stop codon insertion; CDS does not include start

XX and stop codon"

XX /partial

XX WO200168849-A2.

XX 20-SEP-2001.

XX 09-MAR-2001; 2001WO-US007503.

XX 10-MAR-2000; 2000US-0188400P.

XX 10-MAR-2000; 2000US-0188517P.

XX 10-MAR-2000; 2000US-0188518P.

XX 10-MAR-2000; 2000US-0188519P.

XX 05-JUL-2000; 2000US-0215815P.

XX 06-JUL-2000; 2000US-0216481P.

XX (PMA) PHARMACIA & UPJOHN CO.

XX Wood LS, Vogel G, Karnovsky AM, Ruble CL, Linske-O'Connell LI;
 PI Wang J, Liu D;
 XX WPI; 2001-565795/63.
 DR P-PSDB; AAE10116.
 XX
 XX New ion channel polynucleotides and polypeptides, useful for
 PT identification of ion channel modulators and treatment of mental
 PT disorders, infections, cancer and autoimmune diseases.
 XX
 XX Claim 3; Page 99; 188pp; English.
 CC The patent discloses novel human ion channel polypeptides and their
 CC corresponding polynucleotides. The ion channel sequences and their
 CC modulators are used for the treatment of viral infections (e.g. human
 CC immunodeficiency virus (HIV)), thyroid disorders (e.g., Crohn's
 CC myxoedema), renal failure, inflammatory conditions (e.g., Crohn's
 CC disease), rheumatoid arthritis, autoimmune disorders, pain, stroke,
 CC psychotic and neurological disorders (e.g. anxiety, depression and
 CC schizophrenia), dyskinesias (e.g. Huntington's disease), degenerative
 CC disorders (e.g., Parkinson's disease, Alzheimer's disease), cardio-
 CC vascular diseases, cancer, metabolic disorders (e.g. anorexia, obesity)
 CC and mental disorders. The present sequence is a cDNA encoding human ion
 CC channel-91 (ion91) protein
 XX
 SQ Sequence 657 BP; 134 A; 217 C; 175 G; 131 T; 0 U; 0 Other;
 Query Match 93.8%; Score 15; DB 4; Length 657;
 Best Local Similarity 100.0%; Pred. No. 4.5e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GGGCATGCATGGGGG 15
 Db 550 GGGCATGCATGGGGG 536
 RESULT 2
 AC001553/c
 ID AC001553 standard; cDNA; 657 BP.
 AC AC001553;
 XX
 DT 29-JUL-2003 (first entry)
 XX
 DE cDNA clone Ion91 encoding human ion channel.
 XX
 XX Human; ion channel; immune response; RFLP; genetic mapping;
 KW restriction fragment length polymorphism; viral infection;
 KW inflammatory condition; Crohn's disease; homeostasis; cancer;
 KW rheumatoid arthritis; autoimmune disorder; CNS disorder; dementia;
 KW central nervous system disorder; Huntington's disease; virucide;
 KW degenerative disorder; Parkinson's disease; Alzheimer's disease;
 KW cardiovascular disease; myocardial infarction; hormonal disorder;
 KW transcription factor; antiinflammatory; antirheumatic; antiarthritic;
 KW immunosuppressive; neurotropic; anticonvulsant; antiparkinsonian;
 KW neuroprotective; cardiant; gene; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO2003023014-A2.
 XX
 PD 20-MAR-2003.
 XX
 XX 12-SEP-2002; 2002WO-US029087.
 XX
 PR 12-SEP-2001; 2001US-0318733P.
 PR 13-AUG-2002; 2002US-0403254P.
 XX
 XX (PHAA) PHARMACIA & UPJOHN CO.
 PA
 XX
 XX Robert S., Benjamin CW, Karnovsky AM, Ruble CL;
 PI
 XX

DR WPI: 2003-313250/30.
 DR P-PSDB; AB097377.
 XX
 PT Novel human ion channel polypeptide, useful for inducing an immune
 PT response in a mammal and for treating disease or conditions related to
 PT central nervous system and cancer.
 PT
 PS Example 1; Page 103; 146pp; English.
 XX
 CC The present invention relates to the isolation of novel human ion channel
 CC polypeptides, and the polynucleotide sequences encoding them. The human
 CC ion channel polypeptides are useful for inducing an immune response in a
 CC mammal, and for identifying a compound which binds to and/or modulates
 CC the ion channel. The polynucleotide sequences encoding human ion channel
 CC polypeptides are useful for screening restriction fragment length
 CC polymorphisms (RFLPs) associated with certain disorders, and for genetic
 CC mapping. The human ion channel polypeptide and polynucleotide sequences
 CC are useful in the treatment of diseases or conditions such as viral
 CC infections, inflammatory conditions (e.g. Crohn's disease), diseases
 CC related to homeostasis, rheumatoid arthritis, autoimmune disorders,
 CC central nervous system (CNS) disorders (e.g. dementia, Huntington's
 CC disease), degenerative disorders (e.g. Parkinson's and Alzheimer's
 CC disease), cardiovascular diseases (e.g. myocardial infarction), cancer,
 CC and hormonal disorders. The polynucleotide sequences are useful to design
 CC novel transcription factors for modulating the expression of human ion
 CC polypeptides in native cells, and cells transformed or transfected with
 CC them. The present sequence represents a cDNA clone encoding a human ion
 CC channel polypeptide
 XX
 SQ Sequence 657 BP; 134 A; 217 C; 175 G; 131 T; 0 U; 0 Other;
 Query Match 93.8%; Score 15; DB 7; Length 657;
 Best Local Similarity 100.0%; Pred. No. 4.5e+02;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GGGCATGCATGGGGG 15
 Db 550 GGGCATGCATGGGGG 536
 RESULT 3
 ADE29244/c
 ID ADE29244 standard; cDNA; 657 BP.
 XX
 AC ADE29244;
 XX
 DT 29-JAN-2004 (first entry)
 XX
 DE Novel human ion channel ion-91 cDNA.
 XX
 XX neurotropic; neuroprotective; neuroleptic; immunosuppressive; cardiant;
 KW antiarteriosclerotic; antiinflammatory; antidepressant; antiarthritic;
 KW ophthalmological; cycostatic; hypertensive; hypotensive; vasotropic;
 KW antimigraine; analgesic; antiparkinsonian; thrombolytic; antithyroid;
 KW ion channel; ion-x; brain disorder; mental disorder; schizophrenia;
 KW depression; anxiety; attention deficit hyperactivity disorder; migraine;
 KW stroke; neurodegenerative disease; Alzheimer's disease;
 KW Parkinson's disease; glaucoma; macular degeneration;
 KW cardiovascular disease; ischaemia; congestive heart failure; arrhythmia;
 KW high blood pressure; restenosis; thyroid disorder; renal failure;
 KW inflammatory condition; autoimmune disorder; rheumatoid arthritis;
 KW movement disorder; central nervous system disorder; infection;
 KW eating disorder; cardiovascular disorder; thrombosis; atherosclerosis;
 KW proliferative disorder; cancer; hormonal disorder; sexual dysfunction;
 KW gene; ss.
 XX
 OS Homo sapiens.
 XX
 PN US2003190714-A1.
 XX
 PD 09-OCT-2003.
 XX
 XX 09-MAR-2001; 2001US-00302668.
 PF

XX 10-MAR-2000; 2000US-0188400P.
PR 10-MAR-2000; 2000US-0188484P.
PR 10-MAR-2000; 2000US-0188517P.
PR 10-MAR-2000; 2000US-0188518P.
PR 10-MAR-2000; 2000US-0188519P.
PR 05-JUL-2000; 2000US-0215815P.
PR 06-JUL-2000; 2000US-0216481P.
XX (ROBE/) ROBERTS S L.
PA (BENG/) BENJAMIN C W.
PA (KARN/) KARNOVSKY A M.
PA (RUBL/) RUBLE C L.
PA (LINS/) LINSKE-O'CONNELL L I.
PA (WANG/) WANG.
PA (LIUD/) LIU D.
XX
PI Robert SL, Benjamin CW, Karnovsky AM, Ruble CL;
PI Linske-O'connell LI, Wang J, Liu D;
XX
DR WPI; 2003-875311/81.
DR P-PSDB; ADB29295.
XX
XX New nucleic acid sequences encoding ion channels are useful to detect and
PT treat human diseases and conditions, particularly of the brain,
PT especially mental disorders.
XX
PS Claim 4; SEQ ID NO 47; 105pp; English.
XX
CC The invention describes an isolated nucleic acid comprising a sequence
CC encoding at least a portion of an ion channel (ion-x). The invention is
CC useful to detect and treat diseases and conditions of the brain,
CC particularly mental disorders, including schizophrenia, depression,
CC anxiety, attention deficit hyperactivity disorder, migraine, stroke, and
CC neurodegenerative diseases such as Alzheimer's disease, Parkinson's
CC disease, glaucoma and macular degeneration, cardiovascular diseases such
CC as ischaemia, congestive heart failure, arrhythmia, high blood pressure
CC and restenosis. The invention may also be used to detect or treat thyroid
CC disorders, renal failure, inflammatory conditions, autoimmune disorders
CC including rheumatoid arthritis, movement disorders, central nervous
CC system disorders, infections, eating disorders, cardiovascular disorders
CC including thrombosis and atherosclerosis, and proliferative disorders such
CC as cancers, hormonal disorders and sexual dysfunction. This sequence
CC encodes a novel ion channel.
XX
SQ Sequence 657 BP; 134 A; 217 C; 175 G; 131 T; 0 U; 0 Other;
Query Match 93.8%; Score 15; DB 9; Length 657;
Best Local Similarity 100.0%; Pred. No. 4.5e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGGCATGCGTGGGG 15
DB 550 GGGCATGCGTGGGG 536
RESULT 4
ADA72822/c
ID ADA72822 standard; DNA; 2000 BP.
XX
AC ADA72822;
XX
DT 20-NOV-2003 (first entry)
XX
DE Rice gene, SEQ ID 6147.
XX
KW Plant; bacterial infection; fungal infection; viral infection; rice;
KW gene; ds.
XX
OS Oryza sativa.
XX
PN WO2003000898-A1.
XX

PD 03-JAN-2003.
XX
PF 22-JUN-2001; 2001WO-IB001105.
XX
PR 22-JUN-2001; 2001WO-IB001105.
XX
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
XX
PI Chang H, Chen W, Cooper B, Glazebrook J, Goff SA, Hou Y;
PI Katagiri F, Qian S, Tao Y, Whitham S, Xie Z, Zhu T, Zou G;
XX
DR WPI; 2003-175290/17.
XX
PT Identifying at least one gene involved in plant resistance or response to
PT pathogenic infection for conferring resistance or tolerance to a plant to
PT bacterial, fungal or viral infection by determining or detecting plant
PT gene expression.
XX
PS Claim 27; SEQ ID NO 6147; 899pp; English.
XX
CC The present invention relates to a method (M1) for identifying genes
CC involved in plant resistance or response to pathogenic infection. M1
CC comprises identifying a gene whose expression is significantly altered in
CC the incompatible interaction of plant gene expression relative to
CC expression of the gene in an uninfected plant, in a mutant plant that
CC does not express a gene associated with response to pathogenic infection,
CC or in a corresponding incompatible or compatible interaction. (M1) is
CC useful for conferring resistance to resistance or tolerance to a plant to
CC bacterial, fungal or viral infection. The present sequence was used to
CC illustrate the invention.
XX
SQ Sequence 2000 BP; 527 A; 468 C; 501 G; 503 T; 0 U; 1 Other;
Query Match 93.8%; Score 15; DB 7; Length 2000;
Best Local Similarity 100.0%; Pred. No. 4.8e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGGCATGCGTGGGG 15
DB 1856 GGGCATGCGTGGGG 1842
RESULT 5
AAL31444
ID AAL31444 standard; DNA; 51 BP.
XX
AC AAL31444;
XX
DT 24-JAN-2002 (first entry)
XX
DE Human SNP oligonucleotide #4652.
XX
KW Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;
KW neuroprotective; antimicrobial; gene therapy; vaccine; amylase; cancer;
KW amyloid protein; angiotensin; apoptosis related protein; cadherin;
KW cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
KW complement related protein; cytochrome; kinesin; cytokine; interferon;
KW interleukin; G-protein coupled receptor; thioesterase; inflammation;
KW multifactorial disease; autoimmune disease; infection;
KW nervous system disease; ss.
XX
OS Homo sapiens.
XX
PN WO200147944-A2.
XX
PD 05-JUL-2001.
XX
PF 28-DEC-2000; 2000WO-US035498.
XX
PR 28-DEC-1999; 99US-0173419P.
PR 27-DEC-2000; 2000US-00173419.
XX
PA (CURA-) CURAGEN CORP.
XX

XX Shimkets RA, Leach M;
 XX WPI; 2001-465210/50.
 XX Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,
 PT oncogenes and histones, useful for diagnosing and treating, e.g. cancer,
 PT autoimmune diseases and infections.
 XX Claim 1; Page 2724; 4143pp; English.
 XX The present invention relates to oligonucleotides encoding polymorphic
 CC variants of proteins related to amylases, amyloid proteins, angiotensin,
 CC apoptosis related proteins, cadherin, cyclin, polymerase, oncogenes,
 CC histones, kinases, colony stimulating factors, complement related
 CC proteins, cytochromes, kinesins, cytokines, interferons, interleukins, G-
 CC protein coupled receptors and cholesteraes. The present sequence is one
 CC such oligonucleotide. The oligonucleotides and the peptides encoded by
 CC them may be used in the prevention, diagnosis and treatment of diseases
 CC associated with inappropriate expression of the proteins listed above.
 CC Disorders that may be prevented, diagnosed and/or treated include
 CC multifactorial diseases with a genetic component, such as autoimmune
 CC diseases (e.g. rheumatoid arthritis, multiple sclerosis, diabetes,
 CC systemic lupus erythematosus and Grave's disease), inflammation, cancer
 CC (e.g. cancers of the bladder, brain, breast, colon and kidney,
 CC leukaemia), diseases of the nervous system and an infection of pathogenic
 CC organisms
 XX SQ Sequence 51 BP; 13 A; 7 C; 29 G; 2 T; 0 U; 0 Other;
 Query Match 90.0%; Score 14.4; DB 4; Length 51;
 Best Local Similarity 93.8%; Pred. No. 7.8e+02;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 GGGCATGCATGGGGG 16
 DB 34 GGGCAGGCATGGGGG 49
 RESULT 6
 ID ABL78599 standard; cDNA; 390 BP.
 XX ABL78599;
 XX 17-MAY-2002 (first entry)
 XX Human ovarian cancer related cDNA clone SEQ ID NO:1577.
 XX Human; ovarian cancer; ovarian tumour; cytostatic; gene; ss.
 XX Homo sapiens.
 XX WO200192581-A2.
 XX 06-DEC-2001.
 XX 29-MAY-2001; 2001WO-US017756.
 XX 26-MAY-2000; 2000US-0207484P.
 XX (CORI-) CORIXA CORP.
 XX Algate PA, Harlocker SL, Jones R;
 XX WPI; 2002-122075/16.
 XX Composition for therapy and diagnosis of ovarian cancer comprising
 PT polypeptide of a ovarian tumor polypeptide, polynucleotide encoding
 PT polypeptide, antibody specific to polypeptide or T cell expressing
 PT polypeptide.
 XX Claim 1; SEQ ID NO 1577; 489pp; English.

XX The present invention describes a composition (I) comprising: carriers
 CC and immunostimulants; and a polypeptide (II) of a ovarian tumour
 CC polypeptide encoded by a polynucleotide (III) having a cDNA sequence (S1)
 CC from the 10912 nucleotide sequences as given in ABL77023 to ABL87934,
 CC (III) encoding (II) having a sequence (S2), a T cell population of (II),
 CC or antigen presenting cells that express (II). (I) has cytostatic
 CC activity. An oligonucleotide (IV) that hybridises to (S1) can be used for
 CC detecting ovarian cancer in a patient's biological sample preferably
 CC serum or ovarian tissue. The method comprises contacting a biological
 CC sample from a patient with (IV), detecting the amount of polynucleotide
 CC hybridising to (IV) and comparing the amount to a predetermined cutoff
 CC value and thereby detecting ovarian cancer in the patient, where the
 CC amount of polynucleotide hybridising to (IV) is detected preferably by
 CC polymerase chain reaction (PCR). (I) comprising (III) and/or (II) is
 CC useful for stimulating and/or expanding T cells specific for an ovarian
 CC tumour protein comprising contacting T cells with (III) or (II). (III) is
 CC useful in design and preparation of ribozyme molecules for inhibiting
 CC expression of the tumour polypeptides and proteins in tumour cells; and
 CC to isolate a full length gene from a suitable library e.g., a tumour cDNA
 CC library using well known techniques
 XX SQ Sequence 390 BP; 83 A; 144 C; 95 G; 64 T; 0 U; 4 Other;
 Query Match 90.0%; Score 14.4; DB 6; Length 390;
 Best Local Similarity 93.8%; Pred. No. 8.8e+02;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 GGGCATGCATGGGGG 16
 DB 229 GGGCATGCATGGGGG 244
 RESULT 7
 ID AAQ22507/c
 XX AAQ22507 standard; DNA; 408 BP.
 XX AC
 XX AAQ22507;
 XX 04-SEP-1992 (first entry)
 XX Lys64, Pro83, Met88 Arg99 hIL-35 coding sequence.
 XX Human; interleukin-3; bone marrow transplant; graft; platelet;
 XX hIL-35 derivative.
 XX Homo sapiens.
 XX JP04063595-A.
 XX 28-FEB-1992.
 XX 19-OCT-1990; 90JP-00279108.
 XX 03-APR-1990; 90JP-00087468.
 XX (KIRI) KIRIN BREWERY KK.
 XX WPI; 1992-120155/15.
 XX P-PSDB; AAR22819.
 XX Human interleukin 3 deriv. and its prepn. - for supplementing bone marrow
 PT transplantation and increasing platelet count.
 XX Disclosure; Fig 7; 21pp; Japanese.
 XX This sequence codes for a derivative of human IL-3 having amino acids
 CC Arg, Leu and His at positions 64, 83, 88 and 99, respectively,
 CC substituted by Lys, Pro, Met and Arg. The derivative has a higher
 CC activity than native IL-3. See AAR22813-4, AAQ22503-Q22510 and AAQ22513
 XX Sequence 408 BP; 129 A; 105 C; 87 G; 87 T; 0 U; 0 Other;

```

Query Match          90.0%; Score 14.4; DB 2; Length 408;
Best Local Similarity 93.8%; Pred. No. 8.8e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 GGGCATGCATGGGGGG 16
DB      261 GGGCAGGCATGGGGGG 246

RESULT 8
AAQ22508/c
ID AAQ22508 standard; DNA; 408 BP.
XX AC
XX AC AAQ22508;
XX AC
XX DT
XX DT 04-SEP-1992 (first entry)
XX DE
XX DE K64, P83, M88, K113, E122, M127, E132, S134 hIL-3 coding sequence.
XX KW Human; interleukin-3; bone marrow transplant; graft; platelet;
XX KW hIL-36 derivative; ss.
XX OS
XX OS Homo sapiens.
XX XX
XX PN JP04063595-A.
XX XX
XX PD 28-FEB-1992.
XX PF
XX PF 19-OCT-1990; 90JP-0079108.
XX PR
XX PR 03-APR-1990; 90JP-00087468.
XX PA
XX PA (KIRI } KIRIN BREWERY KK.
XX XX
XX DR WPI; 1992-120155/15.
XX DR P-PSDE; AAR22820.
XX PT
XX PT Human interleukin 3 deriv. and its prepn. - for supplementing bone marrow
XX PT transplantation and increasing platelet count.
XX PS
XX PS Disclosure; Fig 8; 21pp; Japanese.
XX CC
XX CC This sequence codes for a derivative of human IL-3 in which Arg, Leu,
XX CC Leu, Thr, Ala, Thr, Ala and Phe at positions 64, 83, 88, 113, 122, 127,
XX CC 132 and 134 have been substituted. The derivative has a higher activity
XX CC than native IL-3. See AAR22813-4, AAQ22503-Q22510 and AAQ22513
XX SQ
XX SQ Sequence 408 BP; 133 A; 102 C; 86 G; 87 T; 0 U; 0 Other;

Query Match          90.0%; Score 14.4; DB 2; Length 408;
Best Local Similarity 93.8%; Pred. No. 8.8e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 GGGCATGCATGGGGGG 16
DB      261 GGGCAGGCATGGGGGG 246

RESULT 9
AAQ22510/c
ID AAQ22510 standard; DNA; 408 BP.
XX AC
XX AC AAQ22510;
XX AC
XX DT
XX DT 04-SEP-1992 (first entry)
XX DE
XX DE Insert from plasmid pCGS8 used to construct hIL-3 derivs.
XX KW Human; interleukin-3; bone marrow transplant; graft; platelet;
XX KW sticky end; ds.
XX OS
XX OS Homo sapiens.

```

SQ Sequence 408 BP; 130 A; 105 C; 86 G; 87 T; 0 U; 0 Other;
 Query Match 90.0%; Score 14.4; DB 2; Length 408;
 Best Local Similarity 93.8%; Pred. No. 8.8e+02;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGGCATGCATGGGGG 16
 DB 261 GGGCAGCATGGGGG 246

RESULT 11
 ACH19351/c
 ID ACH19351 standard; cDNA; 462 BP.
 XX AC ACH19351;
 XX DT 13-OCT-2003 (first entry)
 XX DE Human adult lung cDNA #354.
 XX KW Human; ss; sequencing by hybridisation; SBH; expressed sequence tag; EST;
 XX KW Genome mapping; biodiversity; genetic disorder.
 XX OS Homo sapiens.
 XX PN US2003073623-A1.
 XX PD 17-APR-2003.
 XX PF 30-JUL-2001; 2001US-00918995.
 XX PR 30-JUL-2001; 2001US-00918995.
 XX PA (DRMA/) DRMANAC R T.
 XX PA (LABA/) LABAT I.
 XX PA (STAC/) STACHE-CRAIN B.
 XX PA (DICK/) DICKSON M C.
 XX PA (JONE/) JONES L W.
 XX PI Drmanac RT, Labat I, Stache-Crain B, Dickson MC, Jones LW;
 XX WPI; 2003-615964/58.
 XX New polynucleotide sequences obtained from various cDNA libraries, useful
 PT as hybridization probes, as oligomers for PCR, for chromosome and gene
 PT mapping, in the recombinant production of protein, or in generating
 PT antisense DNA or RNA.
 XX Claim 1; SEQ ID NO 6563; 44pp; English.
 XX The invention relates to an isolated polynucleotide comprising any one of
 CC 38043 cDNA sequences, appearing as ACH12789-ACH50831, whose sequence was
 CC determined by the technique of SBH (sequencing by hybridisation). Also
 CC included is a purified polypeptide comprising a sequence corresponding to
 CC a reading frame of the novel polynucleotide. The nucleic acid sequences
 CC are useful in diagnostics as expressed sequence tags (EST) for
 CC identifying expressed genes or for physical mapping of the human genome,
 CC in forensics, in assessing biodiversity, or in identifying mutations
 CC responsible for genetic disorders and other traits. The nucleotide
 CC sequences are also useful as hybridisation probes, as oligomers for PCR,
 CC for chromosome and gene mapping, in the recombinant production of
 CC protein, or in generating antibodies specific for it. The present polypeptide
 CC is useful for generating antibodies specific for it. The present sequence
 CC is one of the 38043 isolated cDNA/EST sequences. Note: The sequence data
 CC for this patent did not form part of the printed specification, but was
 CC obtained in electronic format directly from USPTO at
 CC seqdata.uspto.gov/sequence.html?docID=20030073623
 XX SQ Sequence 462 BP; 89 A; 157 C; 141 G; 71 T; 0 U; 4 Other;
 Query Match 90.0%; Score 14.4; DB 8; Length 462;
 Best Local Similarity 93.8%; Pred. No. 8.8e+02;

Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGGCATGCATGGGGG 16
 DB 275 GGGCATCCATGGGGG 260

RESULT 12
 ACH33855/c
 ID ACH33855 standard; cDNA; 475 BP.
 XX AC ACH33855;
 XX DT 13-OCT-2003 (first entry)
 XX DE Human endothelial cell cDNA #1988.
 XX KW Human; ss; sequencing by hybridisation; SBH; expressed sequence tag; EST;
 XX KW Genome mapping; biodiversity; genetic disorder.
 XX OS Homo sapiens.
 XX PN US2003073623-A1.
 XX PD 17-APR-2003.
 XX PF 30-JUL-2001; 2001US-00918995.
 XX PR 30-JUL-2001; 2001US-00918995.
 XX PA (DRMA/) DRMANAC R T.
 XX PA (LABA/) LABAT I.
 XX PA (STAC/) STACHE-CRAIN B.
 XX PA (DICK/) DICKSON M C.
 XX PA (JONE/) JONES L W.
 XX PI Drmanac RT, Labat I, Stache-Crain B, Dickson MC, Jones LW;
 XX WPI; 2003-615964/58.
 XX New polynucleotide sequences obtained from various cDNA libraries, useful
 PT as hybridization probes, as oligomers for PCR, for chromosome and gene
 PT mapping, in the recombinant production of protein, or in generating
 PT antisense DNA or RNA.
 XX Claim 1; SEQ ID NO 21067; 44pp; English.
 XX The invention relates to an isolated polynucleotide comprising any one of
 CC 38043 cDNA sequences, appearing as ACH12789-ACH50831, whose sequence was
 CC determined by the technique of SBH (sequencing by hybridisation). Also
 CC included is a purified polypeptide comprising a sequence corresponding to
 CC a reading frame of the novel polynucleotide. The nucleic acid sequences
 CC are useful in diagnostics as expressed sequence tags (EST) for
 CC identifying expressed genes or for physical mapping of the human genome,
 CC in forensics, in assessing biodiversity, or in identifying mutations
 CC responsible for genetic disorders and other traits. The nucleotide
 CC sequences are also useful as hybridisation probes, as oligomers for PCR,
 CC for chromosome and gene mapping, in the recombinant production of
 CC protein, or in generating antibodies specific for it. The present polypeptide
 CC is useful for generating antibodies specific for it. The present sequence
 CC is one of the 38043 isolated cDNA/EST sequences. Note: The sequence data
 CC for this patent did not form part of the printed specification, but was
 CC obtained in electronic format directly from USPTO at
 CC seqdata.uspto.gov/sequence.html?docID=20030073623
 XX SQ Sequence 475 BP; 92 A; 160 C; 119 G; 104 T; 0 U; 0 Other;
 Query Match 90.0%; Score 14.4; DB 8; Length 475;
 Best Local Similarity 93.8%; Pred. No. 8.9e+02;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGGCATGCATGGGGG 16
 DB 275 GGGCATCCATGGGGG 260

```

Db      340 GGGCAGGCATGGGGG 325

RESULT 13
AAV33946/C
ID      AAV33946 standard; cDNA; 675 BP.
XX
XX
AC      AAV33946;
XX
XX      15-FEB-1999 (first entry)
DT
XX      Gibbon interleukin-3 cDNA.
DE
XX      Panconi anaemia complementation group C; PAC; apoptosis; haematopoiesis;
KW      bone marrow; chemotherapy; gene therapy; interleukin-3; gibbon;
KW      His-ILFAC; ds.
XX
XX      Hylobates lar.
OS
XX
XX      Key      Location/Qualifiers
FH      CDS      1..468
FT      /*tag= a
FT
XX
XX      W09851792-A1.
PN
XX
XX      19-NOV-1998.
PD
XX
XX      15-MAY-1998; 98WC-US009975.
PF
XX
XX      15-MAY-1997; 97US-0046546P.
PR
XX
XX      (BGHM ) BRIGHAM & WOMENS HOSPITAL.
PA
XX
XX      Youssoufian H;
PI
XX
XX      WPI; 1999-009774/01.
DR
XX      P-PSDB; AAW68547.
DR
XX
XX      New conjugate of Panconi anaemia molecule and peptide selective for
PT      haematopoietic precursor cells - inhibits apoptosis of these cells, for
PT      treating Panconi anaemia and patients undergoing high-dose chemotherapy
PT      for cancer.
XX
XX      Example 1; Page 48-49; 72pp; English.
PS
XX
XX      This cDNA clone includes a coding region for gibbon interleukin-3 (IL3,
CC      see AAW68546). IL3 selectively binds to receptors on the surface of
CC      haematopoietic progenitor cells (HPC) and is transported into the cells
CC      by endocytosis. The invention provides conjugates, including fusion
CC      proteins, comprising human Panconi anaemia complementation group C (PAC)
CC      protein (see AAW68546) and a targeting molecule such as gibbon IL3.
CC      These conjugates can be expressed e.g. in E. coli host cells utilising
CC      vectors encoding His-tagged IL3-PAC (termed His-ILFAC) fusions. The
CC      conjugate, or a nucleic acid encoding it, can be used to deliver PAC to
CC      an HPC, specifically to inhibit apoptosis, particularly in patients
CC      exposed to high doses of chemotherapy for treatment of non-myeloid
CC      cancers, also to treat Panconi anaemia (by complementation of the genetic
CC      defect). Treatment of HPC is done in vitro, ex vivo (e.g. for recombinant
CC      production of conjugate in cell cultures) or in vivo. Treatment with PAC
CC      may eliminate the need for extensive bone marrow transplants to restore
CC      haematopoiesis after chemotherapy
XX
XX      Sequence 675 BP; 187 A; 192 C; 138 G; 158 T; 0 U; 0 Other;
SQ

Query Match      90.0%; Score 14.4; DB 2; Length 675;
Best Local Similarity 93.8%; Pred. No. 9e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 GGGCATGCATGGGGG 16
      |||||
Db      324 GGGCAGGCATGGGGG 309

RESULT 14
AAW80502/C
ID      AAN80502 standard; cDNA; 865 BP.
XX
XX
AC      AAN80502;
XX
XX      25-MAR-2003 (revised)
DT
XX      06-DEC-1990 (first entry)
DT
XX
XX      Sequence encoding gibbon ape leukemia virus-infected gibbon T-cell line
DE      UCD-144-MLA colony stimulating factor-80 (CSF-80).
DE
XX      Haematopoietic growth factor; lymphokine; interleukin-3; therapy;
KW      diagnosis; ss.
KW
XX      Gibbon.
OS
XX
XX      Key      Location/Qualifiers
FH      CDS      35..91
FT      /*tag= a
FT      /product= "Leader secretory sequence"
FT      mat_peptide 92..493
FT      /*tag= b
XX
XX      W08800598-A.
PN
XX
XX      28-JAN-1988.
PD
XX
XX      13-JUL-1987; 87WO-US001702.
PF
XX
XX      14-JUL-1986; 86US-00885060.
PR
XX      06-AUG-1986; 86US-00893764.
PR
XX      07-OCT-1986; 86US-00916335.
PR
XX      04-MAR-1987; 87US-00021865.
XX
XX      (GEMY ) GENETICS INST INC.
PA
XX
XX      Clark SC, Ciarletta AB, Yang YC;
PI
XX      WPI; 1988-036434/05.
DR
XX      P-PSDB; AAP80502.
DR
XX
XX      Primate IL-3 haematopoietic growth factors - used for treating disease
PT      states due to immune cell or haematopoietic cell deficiency.
XX
XX      Disclosure; ges 7-8; 51pp; English.
PS
XX
XX      Non-coding portions may have a regulatory role in transcription in the
CC      natural host. The 3'-end contains an AT-rich segment including several
CC      repeats of the sequence ATTAA, which is believed to be related to the RNA
CC      message stability. DNA sequence was used as a probe to obtain a 674bp DNA
CC      sequence from a human genomic library (AAN80503). (Updated on 25-MAR-2003
CC      to correct PR field.) (Updated on 25-MAR-2003 to correct PA field.)
XX
XX      Sequence 865 BP; 235 A; 224 C; 179 G; 227 T; 0 U; 0 Other;
SQ

Query Match      90.0%; Score 14.4; DB 1; Length 865;
Best Local Similarity 93.8%; Pred. No. 9.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 GGGCATGCATGGGGG 15
      |||||
Db      349 GGGCAGGCATGGGGG 334

RESULT 15
AAW92339/C
ID      AAN92339 standard; DNA; 909 BP.
XX
XX
AC      AAN92339;
XX
XX      25-MAR-2003 (revised)
DT
XX      16-MAR-1990 (first entry)
DT

```

XX Single stranded DNA sequence for maize locus 288.
DE Rapid RFLP analysis; chromosome; fluorescing molecule; maize loci 288;
KW primers 238B, 238A/238AR, 238AOL1, 238COL1 and 238C1.
XX
OS Maize.
XX
FH Key Location/Qualifiers
FT misc_feature 37..57 /*tag= a
FT misc_feature 103..123 /*tag= b
FT misc_feature 305..324 /*tag= c
FT misc_feature 636..655 /*tag= d
FT misc_feature 882..903 /*tag= e
XX
PN EP317239-A.
XX
XX 24-MAY-1989.
XX
PF 14-NOV-1988; 88EP-00310729.
XX
XX 13-NOV-1987; 87US-00120309.
PR 03-NOV-1988; 88US-00266970.
XX
XX (NATI-) NATIVE PLANTS INC.
XX
XX Heientjaris TG, Lee MS, Shattuck-Bidens D;
XX
XX WPI; 1989-152719/21.
XX
XX Rapid restriction fragment polymorphism analysis, esp. in plant study -
PT using a primer labelled with a fluorescing molecule and an elongating
PT enzyme.
XX
XX Fig 2 & 3; Page ?; 27pp; English.
XX
XX It is the nucleic acid sequence for maize locus 288. The tags indicate
CC the location of primer sequences used in a rapid method of RFLP analysis.
CC In the method each primer is labelled with a fluorescing molecule
CC (chromophore) and hybridised with a restricted target DNA sample in the
CC presence of an oligodeoxyribonucleotide elongating enzyme. Hybridisation
CC is determined by reviewing the gels with a laser and appropriate detector
CC - no southern blotting is necessary. tags A - B = primers 238B, 238A/
CC 238AR/238AOL1, 238COL1 and 238C1 respectively. (Updated on 25-MAR-
CC 2003 to correct PR field.) (Updated on 25-MAR-2003 to correct PI field.)
XX
SQ Sequence 909 BP; 196 A; 233 C; 244 G; 236 T; 0 U; 0 Other;

Query Match 90.0%; Score 14.4; DB 1; Length 909;
Best Local Similarity 93.8%; Pred. No. 9.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGGCATGCATGGGGG 16
|||||||
Db 402 GGGCATGCATGGGGG 387

Search completed: July 2, 2004, 08:31:35
Job time : 121.902 secs

OM nucleic - nucleic search, using sw model

Run on: July 2, 2004, 08:09:30 ; Search time 25,0732 Seconds
(without alignments)
354.132 Million cell updates/sec

Title: US-10-068-160-15

Perfect score: 16

Sequence: 1 gggcatgcattggggggg 16

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA.*
1: /cgm2_6/ptodata/2/ina/5A COMB.seq.*
2: /cgm2_6/ptodata/2/ina/5B COMB.seq.*
3: /cgm2_6/ptodata/2/ina/6A COMB.seq.*
4: /cgm2_6/ptodata/2/ina/6B COMB.seq.*
5: /cgm2_6/ptodata/2/ina/PTUS COMB.seq.*
6: /cgm2_6/ptodata/2/ina/backfiles.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	14.4	90.0	768	4	US-09-252-991A-1689
C 2	14.4	90.0	1662	3	US-08-807-342B-3
C 3	14.4	90.0	3079	4	US-09-643-597-116
C 4	14.4	90.0	3079	4	US-09-480-884A-116
C 5	14.4	90.0	3079	4	US-09-542-635A-116
C 6	14.4	90.0	3079	4	US-09-606-421B-116
C 7	14.4	90.0	3079	4	US-09-221-107-116
C 8	14.4	90.0	3673	4	US-09-266-225D-5
C 9	14.4	90.0	4866	1	US-08-110-158-5
C 10	13.4	83.8	242	4	US-09-397-787-54
C 11	13.4	83.8	481	4	US-09-621-976-10744
C 12	13.4	83.8	684	4	US-09-252-991A-2852
C 13	13.4	83.8	1536	4	US-09-180-109A-3
C 14	13.4	83.8	1930	4	US-09-724-864-9
C 15	13.4	83.8	2000	4	US-09-056-285A-3
C 16	13.4	83.8	2403	4	US-09-023-655-1226
C 17	13.4	83.8	2403	3	US-08-985-908-25
C 18	13.4	83.8	2517	3	US-08-985-908-30
C 19	13.4	83.8	2539	4	US-09-620-312D-454
C 20	13.4	83.8	4368	1	US-08-026-138E-17
C 21	13.4	83.8	4392	1	US-08-026-138E-5
C 22	13.4	83.8	4446	1	US-08-026-138E-6
C 23	13.4	83.8	4808	2	US-08-231-193A-10
C 24	13.4	83.8	4808	2	US-08-486-273A-10
C 25	13.4	83.8	4808	2	US-08-940-086A-10
C 26	13.4	83.8	4808	4	US-08-940-035A-10
C 27	13.4	83.8	4808	4	US-08-935-105A-10

28	13.4	83.8	4808	4	US-09-648-797-10
29	13.4	83.8	4808	4	US-09-386-123-10
30	13.4	83.8	4858	3	US-08-436-332B-9
31	13.4	83.8	6151	4	US-08-217-704C-1
32	13.4	83.8	111282	4	US-09-754-250-3
33	13.4	83.8	319608	4	US-09-539-333D-1
34	13.4	83.8	319608	4	US-09-679-409-1
35	13	81.2	400	4	US-08-956-171E-2996
36	13	81.2	1899	4	US-09-328-352-659
37	13	81.2	3545	3	US-08-480-474-10
38	12.8	80.0	143	4	US-09-025-769B-263
39	12.8	80.0	276	4	US-09-313-294A-1580
40	12.8	80.0	290	4	US-09-702-705-264
41	12.8	80.0	290	4	US-09-736-457-264
42	12.8	80.0	290	4	US-09-614-124B-264
43	12.8	80.0	290	4	US-09-671-325-264
44	12.8	80.0	290	4	US-09-589-184-264
45	12.8	80.0	378	4	US-09-489-039A-4088

ALIGNMENTS

RESULT 1
US-09-252-991A-1689/c
; Sequence 1689, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 1689
; LENGTH: 768
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-1689

Query Match 90.0%; Score 14.4; DB 4; Length 768;
Best Local Similarity 93.8%; Pred. No. 1.3e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGCATGCATGGGGG 16
|||||
Db 352 GGCATTCATGGGGG 337

RESULT 2
US-08-807-342B-3
; Sequence 3, Application US/08807342B
; Patent No. 607686
; GENERAL INFORMATION:
; APPLICANT: Der, Channing
; APPLICANT: O'Bryan, John P.
; APPLICANT: Pawson, Anthony
; TITLE OF INVENTION: No. 607686el SHC Proteins
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Howson and Howson
; STREET: Spring House Corporate Cntr., P.O. Box 457
; CITY: Spring House
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19477
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

OM nucleic - nucleic search, using sw model

Run on: July 2, 2004, 07:38:45 ; Search time 1198.24 Seconds
(without alignments)
398.746 Million cell updates/sec

Title: US-10-068-160-15

Perfect score: 16

Sequence: 1 999catgcatg999999 16

Scoring table: IDENTITY_NUC

Gapop 10.0, Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST.*

1: em_estb.*
2: em_esthm.*
3: em_estin.*
4: em_estm.*
5: em_estov.*
6: em_estpl.*
7: em_estro.*
8: em_hic.*
9: gb_est1.*
10: gb_est2.*
11: gb_hic.*
12: gb_est3.*
13: gb_est4.*
14: gb_est5.*
15: em_estfun.*
16: em_estom.*
17: em_gss_hum.*
18: em_gss_inv.*
19: em_gss_pln.*
20: em_gss_vrt.*
21: em_gss_fun.*
22: em_gss_man.*
23: em_gss_mus.*
24: em_gss_pro.*
25: em_gss_rod.*
26: em_gss_phg.*
27: em_gss_vri.*
28: gb_gss1.*
29: gb_gss2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	16	100.0	178	29	CE070440 tigr-gss-
2	16	100.0	312	9	AA080746 oe56h05.s
3	16	100.0	373	14	CB010201 LB18G01 m
4	16	100.0	399	14	CB010108 LB16E11 m

C	5	16	100.0	422	9	AA798510
C	6	16	100.0	423	9	AA798509
C	7	16	100.0	507	28	BZ317770
C	8	16	100.0	525	28	BZ308462
C	9	16	100.0	526	29	CNS07EQ7
C	10	16	100.0	531	29	CE663190
C	11	16	100.0	551	28	BZ323566
C	12	16	100.0	577	28	BH877725
C	13	16	100.0	645	28	BZ308895
C	14	16	100.0	667	28	BZ371261
C	15	16	100.0	673	28	BZ413880
C	16	16	100.0	674	28	BH881300
C	17	16	100.0	683	9	AW044282
C	18	16	100.0	690	28	BZ966328
C	19	16	100.0	690	28	BZ994883
C	20	16	100.0	696	28	BZ374394
C	21	16	100.0	720	28	BZ416253
C	22	16	100.0	721	28	BZ416263
C	23	16	100.0	769	28	CC400096
C	24	16	100.0	796	28	BZ416255
C	25	16	100.0	797	28	BZ416245
C	26	16	100.0	835	13	BX347138
C	27	16	100.0	836	28	BZ792665
C	28	16	100.0	847	29	CG129135
C	29	16	100.0	859	14	CD384067
C	30	16	100.0	925	13	BX348859
C	31	16	100.0	933	13	BX371748
C	32	16	100.0	938	28	BZ792664
C	33	16	100.0	1065	13	BX338228
C	34	16	100.0	1125	13	BUS11621
C	35	16	100.0	1201	9	ALU523531
C	36	16	100.0	1201	13	BX356439
C	37	15.2	95.0	538	29	CNS04HG3
C	38	15	93.8	217	12	B1898692
C	39	15	93.8	273	14	W23910
C	40	15	93.8	288	14	F22293
C	41	15	93.8	341	14	F20981
C	42	15	93.8	379	12	B1313004
C	43	15	93.8	395	9	AA406068
C	44	15	93.8	424	9	AA496072
C	45	15	93.8	449	10	AW661455

ALIGNMENTS

RESULT 1	CE070440	178 bp	DNA	linear	GSS 24-SBP-2003
LOCUS	tigr-gss-dog-17000322997936	Dog Library	Canis familiaris	genomic,	
DEFINITION	Genomic survey sequence.				
ACCESSION	CE070440				
VERSION	CE070440.1	GI:35131550			
KEYWORDS	GSS.				
SOURCE	Canis familiaris (dog)				
ORGANISM	Canis familiaris				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
AUTHORS	Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.				
	1 (bases 1 to 178)				
	Kirkness, E.F., Hafna, V., Halpern, A.L., Levy, S., Remington, K.,				
	Rusch, D.B., Delcher, A.L., Pop, M., Wang, W., Fraser, C.M. and				
	Venter, J.C.				
TITLE	The dog genome: survey sequencing and comparative analysis				
JOURNAL	Science	301 (5641), 1898-1903 (2003)			
MEDLINE	22875432				
PUBMED	14512627				
COMMENT	Contact: Kirkness EF				
	The Institute for Genomic Research				
	Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,				
	Rockville, MD 20850, USA				
	Tel: 301-838-0200				
	Fax: 301-838-0208				
	Email: ekirknes@tigr.org				

```

FEATURES
  source
    Class: shotgun.
    Location/Qualifiers
      1..178
        /organism="Canis familiaris"
        /mol_type="genomic DNA"
        /strain="Standard Poodle"
        /db_xref="taxon:9615"
        /clone_lib="Dog Library"
        /note="Site 1: BstXI; Libraries were prepared from peripheral blood"

ORIGIN
  Query Match      100.0%; Score 16; DB 29; Length 178;
  Best Local Similarity 100.0%; Pred. No. 3e+03;
  Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGCATGCGTGGGGG 16
    |||||
Db 37 GGGCATGCGTGGGGG 52

RESULT 2
AA808746      312 bp mRNA linear EST 21-APR-1998
LOCUS
DEFINITION
  O656805.s1 NCI_CGAP_Lu5 Homo sapiens cDNA clone IMAGE:1415673 3',
  mRNA sequence.
ACCESSION
  AA808746
KEYWORDS
  EST.
SOURCE
  Homo sapiens (human)
ORGANISM
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
  1 (bases 1 to 312)
  NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
  Tumor Gene Index
JOURNAL
  Unpublished (1997)
COMMENT
  Contact: Robert Strausberg, Ph.D.
  Email: cgaps-remail.nih.gov
  Unknown library type
  Insert Length: 413 Std Error: 0.00
  Seq primer: -40m13 fwd. ET from Amersham.
  Location/Qualifiers
    1..312
      /organism="Homo sapiens"
      /mol_type="mRNA"
      /db_xref="taxon:9606"
      /clone_lib="IMAGE:1415673"
      /tissue_type="carcinoid"
      /lab_hosts="DH10B"
      /clone_lib="NCI CGAP Lu5"
      /note="Organ: lung; Vector: pTT3D-Pac (Pharmacia) with a
      modified polylinker; 1st strand cDNA was prepared from
      neuroendocrine lung carcinoid, and was then primed with a
      Not I - oligo(dT) primer. Double-stranded cDNA was ligated
      to Eco RI adaptors (Pharmacia), digested with Not I and
      cloned into the Not I and Eco RI sites of the modified
      pTT73 vector. Library is normalized. Library was
      constructed by Bento Soares and M. Fatima Bonaldo."

ORIGIN
  Query Match      100.0%; Score 16; DB 9; Length 312;
  Best Local Similarity 100.0%; Pred. No. 3.4e+03;
  Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGCATGCGTGGGGG 16
    |||||
Db 177 GGGCATGCGTGGGGG 192

RESULT 3
CE010201
LOCUS
DEFINITION
  Lb18601 mycelium of Laccaria bicolor grown for ten weeks Laccaria
  bicolor cDNA 5', mRNA sequence.
ACCESSION
  CE010201
KEYWORDS
  EST.
SOURCE
  Laccaria bicolor
ORGANISM
  Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
  Agaricales; Tricholomataceae; Laccaria.
REFERENCE
  1 (bases 1 to 399)
  Peter, M., Courty, P.-E., Kohler, A., Delaruelle, C., Martin, D.,
  Tagu, D., Frey-Kiest, P., Duplessis, S., Chalor, M., Podila, G. and
  Martin, F.
  Analysis of expressed sequence tags from the ectomycorrhizal
  basidiomycetes Laccaria bicolor and Pisolithus microcarpus
  JOURNAL
  New Phytol. 159 (1), 117-129 (2003)
COMMENT
  Contact: Martin FM
  Equipe de Microbiologie Forestiere
  Institut National de la Recherche Agronomique
  Centre INRA de Nancy, 54280 Champenoux, France
  Tel: +33 383 39 40 80
  Fax: +33 383 39 40 69
  Email: fmartin@nancy.inra.fr
  Insert Length: 373 Std Error: 0.00
  Seq primer: Fornat 5' AGCGCGCATGTGCTGTGTGATCCC.
  Location/Qualifiers
    1..373
      /organism="Laccaria bicolor"
      /mol_type="mRNA"
      /cultivar="S238N"
      /db_xref="taxon:29883"
      /dev_stage="ten-weeks-old"
      /clone_lib="mycelium of Laccaria bicolor grown for ten
      weeks"
      /note="Organ: mycelium; Vector: pTriplEx2; Laccaria
      bicolor Maire Orton; cDNA library from mycelium of
      Laccaria bicolor grown for ten weeks on agar-plates
      containing low sugar (1 g/l glucose) Pachlewski medium.
      The cDNA library was constructed from mRNA which was
      isolated from 13ug of total Dnaase digested RNA using the
      SMART cDNA synthesis kit (Clontech, Palo Alto, CA, USA)
      according to the manufacturer's instructions. The
      resulting cDNA was packed into lambda phages using the
      Gigapack III Gold packaging kit (Stratagene, La Jolla,
      CA). The pTriplEx2 phagemid clones in Escherichia coli
      were obtained by using the mass in vivo excision protocol
      according to the manufacturer's instructions (Clontech)."
```

Tagu, D., Frey-Klett, P., Duplessis, S., Chalot, M., Podila, G. and Martin, P.
 Analysis of expressed sequence tags from the ectomycorrhizal basidiomycetes *Laccaria bicolor* and *Pisolithus microcarpus*
 New Phytol. 159 (1), 117-129 (2003)
 Contact: Martin PM
 Equipe de Microbiologie Forestiere
 Institut National de la Recherche Agronomique
 Centre INRA de Nancy, 54280 Champenoux, France
 Tel: +33 383 39 40 80
 Fax: +33 383 39 40 69
 Email: fmartin@nancy.inra.fr
 Insert Length: 399 Std Error: 0.00
 Seq primer: Forwat 5' AAGCGCGCATGTGTGTGTACCC.

Location/Qualifiers

1. 399
 /organism="Laccaria bicolor"
 /mol_type="mRNA"
 /cultivar="5238N"
 /db_xref="taxon:29883"
 /dev_stage="ten-weeks-old"
 /clone_lib="mycelium of Laccaria bicolor grown for ten weeks"

/note="Organ: mycelium; Vector: pTriplEx2; Laccaria bicolor Maire Orton; cDNA library from mycelium of Laccaria bicolor grown for ten weeks on agar-plates containing low sugar (1 g/l glucose) Pachlewski medium. The cDNA library was constructed from mRNA which was isolated from 13ug of total Dnase digested RNA using the SMART cDNA synthesis kit (Clontech, Palo Alto, CA, USA) according to the manufacturer's instructions. The resulting cDNA was packed into lambda phages using the Gigapack III Gold packaging kit (Stratagene, La Jolla, CA). The pTriplEx2 phagemid clones in Escherichia coli were obtained by using the mass in vivo excision protocol according to the manufacturer's instructions (Clontech)."

ORIGIN

Query Match 100.0%; Score 16; DB 14; Length 399;
 Best Local Similarity 100.0%; Pred. No. 3.6e+03;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGCATGTCATGGGGG 16
 |||||
 Db 382 GGGCATGTCATGGGGG 367

RESULT 5
 AA798510/c
 LOCUS
 DEFINITION vx68f08.r1 Stratagene mouse skin (#937313) Mus musculus cDNA clone
 IMAGE:1280391 5', mRNA sequence.

ACCESSION AA798510
 VERSION
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)

ORGANISM

REFERENCE
 AUTHORS
 Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, P., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.

TITLE
 JOURNAL
 COMMENT
 The WashU-HMI Mouse EST Project
 Unpublished (1996)
 Contact: Marra M/Mouse EST Project
 WashU-HMI Mouse EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810

Email: mouseest@watson.wustl.edu
 This clone is available royalty-free through LNL ; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
 MGI:672191

Seq primer: -28ml3 rev1 ET from Amersham.

FEATURES source

Location/Qualifiers
 1. 422
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="C57BL/6"
 /db_xref="taxon:10090"
 /clone="IMAGE:1280391"
 /sex="females"
 /tissue type="whole skin"
 /dev stage="11 weeks old"
 /lab_hosts="SOLR (kanamycin resistant)"
 /clone_lib="Stratagene mouse skin (#937313)"
 /note="Organ: skin; Vector: pBluescript SK-; Site: 1: EcoRI; Site 2: XhoI; Cloned unidirectionally. Primer: Oligo dt. Whole skin from 11 week old C57BL/6 female mice. Average insert size: 1.0 kb; Uni-ZAP XR Vector; -5' adaptor sequence: 5' GAATTCGGCAGAG 3' -3' adaptor sequence: 5' CTCGAGTTTTTTTTTTT 3'"

ORIGIN

Query Match 100.0%; Score 16; DB 9; Length 422;
 Best Local Similarity 100.0%; Pred. No. 3.7e+03;
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGCATGTCATGGGGG 16
 |||||
 Db 377 GGGCATGTCATGGGGG 362

ORIGIN

RESULT 6
 AA798509/c
 LOCUS
 DEFINITION vx8f07.r1 Stratagene mouse skin (#937313) Mus musculus cDNA clone
 IMAGE:1280389 5', mRNA sequence.

ACCESSION AA798509
 VERSION
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)

ORGANISM

REFERENCE
 AUTHORS
 Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, P., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.

TITLE
 JOURNAL
 COMMENT
 The WashU-HMI Mouse EST Project
 Unpublished (1996)
 Contact: Marra M/Mouse EST Project
 WashU-HMI Mouse EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810

ORGANISM

REFERENCE
 AUTHORS
 Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T., Geisel, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M., Schellenberg, K., Steptoe, M., Tan, P., Underwood, K., Moore, B., Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and Waterston, R.

TITLE
 JOURNAL
 COMMENT
 The WashU-HMI Mouse EST Project
 Unpublished (1996)
 Contact: Marra M/Mouse EST Project
 WashU-HMI Mouse EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810

ORGANISM


```

SOURCE
ORGANISM  Anopheles gambiae (African malaria mosquito)
           Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
           Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
           Anopheles.
REFERENCE  1 (bases 1 to 526)
AUTHORS   Genoscope.
TITLE     Direct Submission
JOURNAL   Submitted (01-OCT-2001) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
REFERENCE  2 (bases 1 to 526)
AUTHORS   Roth,C.M., Brey,P.F., Ke,Z. and Collins,F.H.
TITLE     Direct Submission
JOURNAL   Submitted (01-OCT-2001) BEMl, Institut Pasteur, 25, rue du Dr.
Roux, Paris 75015, France
COMMENT   This clone is from an A. gambiae BAC library provided by F.H.
Collins and sequenced by Genoscope in collaboration with the
Laboratory of Biochem. and Biol. Molec. of Insects, Institut
Pasteur.
FEATURES
source    Location/Qualifiers
1..526
/organism="Anopheles gambiae"
/mol_type="genomic DNA"
/strain="PEST"
/db_xref="taxon:7165"
/clone="02L03"
/clone_lib="NotreDamel"
/notes="end : T7"

ORIGIN
Query Match      100.0%; Score 16; DB 29; Length 526;
Best Local Similarity 100.0%; Pred. No. 3.9e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1  GGCGATGTCATGGGGG 16
    |||||
Db   225 GGCGATGTCATGGGGG 210

RESULT 10
CE663190/c
LOCUS      tigr-gss-dog-1700031366808 Dog Library Canis familiaris genomic,
DEFINITION genomic survey sequence.
ACCESSION  CE663190.1 GI:36982058
VERSION    1
KEYWORDS   GSS.
SOURCE     Canis familiaris (dog)
ORGANISM   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE  1 (bases 1 to 531)
AUTHORS   Kirkness,E.F., Bafna,V., Halpern,A.L., Levy,S., Remington,K.,
Rusch,D.B., Deicher,A.L., Pop,M., Wang,M., Fraser,C.M. and
Venter,J.C.
TITLE     The dog genome: survey sequencing and comparative analysis
JOURNAL   Science 301 (5641), 1898-1903 (2003)
MEDLINE   22875432
PUBMED    14512627
COMMENT   Contact: Kirkness EP
The Institute for Genomic Research
Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
Rockville, MD 20850, USA
Tel: 301-838-0200
Fax: 301-838-0208
Email: ekirknes@tigr.org
Class: shotgun.
FEATURES
source    Location/Qualifiers
1..531
/organism="Canis familiaris"
/mol_type="genomic DNA"
/strain="Standard Poodle"

SOURCE
ORGANISM  /db_xref="taxon:9615"
/clone_lib="Dog Library"
/notes="Site 1: BstXI; Libraries were prepared from peripheral blood"

ORIGIN
Query Match      100.0%; Score 16; DB 29; Length 531;
Best Local Similarity 100.0%; Pred. No. 3.9e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1  GGCGATGTCATGGGGG 16
    |||||
Db   125 GGCGATGTCATGGGGG 110

RESULT 11
BZ323566
LOCUS      ia79g11.g1 WGS-ZmayrF (JM107 adapted methyl filtered) Zea mays
DEFINITION genomic clone ia79g11 5', genomic survey sequence.
ACCESSION  BZ323566
VERSION    1
KEYWORDS   GSS.
SOURCE     Zea mays
ORGANISM   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
           Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
           clade; Panicoideae; Andropogoneae; Zea.
REFERENCE  1 (bases 1 to 551)
AUTHORS   Rabinowicz,P.D., O'Shaughnessy,A.L., Ballja,V., Dedhia,N.,
           Katzenburger,F., King,L., Miller,B., Muller,S., Nascimento,L.,
           Zutavern,T., McCombie,W.R. and Martienssen,R.A.
TITLE     Genomic shotgun sequences from Zea mays (methyl-filtered)
JOURNAL   Unpublished (2002)
COMMENT   Contact: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
Fax: 516 367 8874
Email: mcombie@cshl.org
Plate: ia79 row: g column: 11
Seq primer: -21M13UnivRev
Class: shotgun
High quality sequence stop: 551.
FEATURES
source    Location/Qualifiers
1..551
/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="B73"
/db_xref="taxon:4577"
/clone="ia79g11"
/lab_host="JM107 or DH5a"
/clone_lib="WGS-ZmayrF (JM107 adapted methyl filtered)"
/notes="Organ: immature ears; Site 1: Xba I; Site 2: Xba I;
The vector was digested with XbaI and one nucleotide was
added by fill in in the recessive 3' end. The genomic DNA
was nebulized, end repaired, adaptor ligated and size
fractionated using sephadex. The resulting fragments were
between 0.8 and 3 kb and were cloned into the vector
(.x/y reads in M13mpl9, .b/g reads in pUC19). The same
ligation was transformed in either JM107 or DH5a. "

ORIGIN
Query Match      100.0%; Score 16; DB 28; Length 551;
Best Local Similarity 100.0%; Pred. No. 3.9e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  1  GGCGATGTCATGGGGG 16
    |||||
Db   331 GGCGATGTCATGGGGG 346

```

```

RESULT 12
BH877725
LOCUS
DEFINITION
hr54e02.g1 WGS-ZmaysF (JM107 adapted methyl filtered) Zea mays
genomic clone hr54e02 5', genomic survey sequence.
ACCESSION
BH877725
VERSION
BH877725.1 GI:22113622
KEYWORDS
GSS.
SOURCE
Zea mays
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 577)
REFERENCE
AUTHORS
Rabinowicz,P.D., O'Shaughnessy,A.L., Ballija,V., Dedhia,N.,
Katzenburger,F., King,L., Miller,B., Muller,S., Nascimento,L.,
Zutavern,T., McCombie,W.R. and Martienssen,R.A.
Genomic shotgun sequences from Zea mays (methyl-filtered)
Unpublished (2002)
TITLE
JOURNAL
COMMENT
Contact: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
Fax: 516 367 8874
Email: mcombie@cshl.org
Plate: hr54 row: e column: 02
Seq primer: -21M13UnivFwd
Class: shotgun
High quality sequence stop: 577.
FEATURES
source
Location/Qualifiers
1..577
/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="B73"
/db_xref="taxon:4577"
/clone="hr54e02"
/lab_host="JM107 or DH5a"
/clone_lib="WGS-ZmaysF (JM107 adapted methyl filtered)"
/notes="Organ: immature ears; Site_1: Xba I; Site_2: Xba I;
The vector was digested with XbaI and one nucleotide was
added by fill in the recessive 3' end. The genomic DNA
was nebulized, end repaired, adaptor ligated and size
fractionated using sephadex. The resulting fragments were
between 0.8 and 3 kb and were cloned into the vector
(.x/y reads in M13mpl9, b/g reads in pUC19). The same
ligation was transformed in either JM107 or DH5a."
ORIGIN
Query Match 100.0%; Score 16; DB 28; Length 577;
Best Local Similarity 100.0%; Pred. No. 3.9e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGGCATGCATGGGGGG 16
DB 547 GGGCATGCATGGGGGG 562
RESULT 13
BZ308895
LOCUS
DEFINITION
BZ308895
1d76f05.b1 WGS-ZmaysF (JM107 adapted methyl filtered) Zea mays
genomic clone id76f05 5', genomic survey sequence.
ACCESSION
BZ308895
VERSION
BZ308895.1 GI:24669162
KEYWORDS
GSS.
SOURCE
Zea mays
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 645)
REFERENCE
AUTHORS
Rabinowicz,P.D., O'Shaughnessy,A.L., Ballija,V., Dedhia,N.,
Katzenburger,F., King,L., Miller,B., Muller,S., Nascimento,L.,
Zutavern,T., McCombie,W.R. and Martienssen,R.A.
Genomic shotgun sequences from Zea mays (methyl-filtered)
Unpublished (2002)
TITLE
JOURNAL
COMMENT
Contact: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
Fax: 516 367 8874
Email: mcombie@cshl.org
Plate: id76 row: f column: 05
Seq primer: -21M13UnivFwd
Class: shotgun
High quality sequence stop: 645.
FEATURES
source
Location/Qualifiers
1..645
/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="B73"
/db_xref="taxon:4577"
/clone="id76f05"
/lab_host="JM107 or DH5a"
/clone_lib="WGS-ZmaysF (JM107 adapted methyl filtered)"
/notes="Organ: immature ears; Site_1: Xba I; Site_2: Xba I;
The vector was digested with XbaI and one nucleotide was
added by fill in the recessive 3' end. The genomic DNA
was nebulized, end repaired, adaptor ligated and size
fractionated using sephadex. The resulting fragments were
between 0.8 and 3 kb and were cloned into the vector
(.x/y reads in M13mpl9, b/g reads in pUC19). The same
ligation was transformed in either JM107 or DH5a."
ORIGIN
Query Match 100.0%; Score 16; DB 28; Length 645;
Best Local Similarity 100.0%; Pred. No. 4.1e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGGCATGCATGGGGGG 16
DB 470 GGGCATGCATGGGGGG 485
RESULT 14
BZ371261/c
LOCUS
DEFINITION
BZ371261
ie33b08.b1 WGS-ZmaysF (DH5a methyl filtered) Zea mays genomic clone
ie33b08 5', genomic survey sequence.
ACCESSION
BZ371261
VERSION
BZ371261.1 GI:25455161
KEYWORDS
GSS.
SOURCE
Zea mays
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 667)
REFERENCE
AUTHORS
Rabinowicz,P.D., O'Shaughnessy,A.L., Ballija,V., Dedhia,N.,
Katzenburger,F., King,L., Miller,B., Muller,S., Nascimento,L.,
Zutavern,T., McCombie,W.R. and Martienssen,R.A.
Genomic shotgun sequences from Zea mays (methyl-filtered)
Unpublished (2002)
TITLE
JOURNAL
COMMENT
Contact: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
Fax: 516 367 8874
Email: mcombie@cshl.org
Plate: ie33 row: b column: 08
Seq primer: -21M13UnivFwd
Class: shotgun
High quality sequence stop: 667.

```

```

Katzenburger,F., King,L., Miller,B., Muller,S., Nascimento,L.,
Zutavern,T., McCombie,W.R. and Martienssen,R.A.
Genomic shotgun sequences from Zea mays (methyl-filtered)
Unpublished (2002)
Contact: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
Fax: 516 367 8874
Email: mcombie@cshl.org
Plate: id76 row: f column: 05
Seq primer: -21M13UnivFwd
Class: shotgun
High quality sequence stop: 645.
FEATURES
source
Location/Qualifiers
1..645
/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="B73"
/db_xref="taxon:4577"
/clone="id76f05"
/lab_host="JM107 or DH5a"
/clone_lib="WGS-ZmaysF (JM107 adapted methyl filtered)"
/notes="Organ: immature ears; Site_1: Xba I; Site_2: Xba I;
The vector was digested with XbaI and one nucleotide was
added by fill in the recessive 3' end. The genomic DNA
was nebulized, end repaired, adaptor ligated and size
fractionated using sephadex. The resulting fragments were
between 0.8 and 3 kb and were cloned into the vector
(.x/y reads in M13mpl9, b/g reads in pUC19). The same
ligation was transformed in either JM107 or DH5a."
ORIGIN
Query Match 100.0%; Score 16; DB 28; Length 645;
Best Local Similarity 100.0%; Pred. No. 4.1e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGGCATGCATGGGGGG 16
DB 470 GGGCATGCATGGGGGG 485
RESULT 14
BZ371261/c
LOCUS
DEFINITION
BZ371261
ie33b08.b1 WGS-ZmaysF (DH5a methyl filtered) Zea mays genomic clone
ie33b08 5', genomic survey sequence.
ACCESSION
BZ371261
VERSION
BZ371261.1 GI:25455161
KEYWORDS
GSS.
SOURCE
Zea mays
ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 667)
REFERENCE
AUTHORS
Rabinowicz,P.D., O'Shaughnessy,A.L., Ballija,V., Dedhia,N.,
Katzenburger,F., King,L., Miller,B., Muller,S., Nascimento,L.,
Zutavern,T., McCombie,W.R. and Martienssen,R.A.
Genomic shotgun sequences from Zea mays (methyl-filtered)
Unpublished (2002)
TITLE
JOURNAL
COMMENT
Contact: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
Fax: 516 367 8874
Email: mcombie@cshl.org
Plate: ie33 row: b column: 08
Seq primer: -21M13UnivFwd
Class: shotgun
High quality sequence stop: 667.

```

FEATURES

source
Location/Qualifiers
1. .667
/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="B73"
/db_xref="taxon:4577"
/clone="ie33b08"
/lab_host="DH5a"
/clone_lib="WGS-ZmaysF (DH5a methyl filtered)"
/note="Organ: immature ears; Site_1: Xba I; Site_2: Xba I;
The vector was digested with XbaI and one nucleotide was
added by fill in the recessive 3' end. The genomic DNA
was nebulized, end repaired, adaptor ligated and size
fractionated using sephadex. The resulting fragments were
between 0.8 and 3 kb and were cloned into the vector (.x/y
reads in M13mpl9, .b/g reads in pUC19). The same ligation
was transformed into DH5a."

ORIGIN

Query Match 100.0%; Score 16; DB 28; Length 667;
Best Local Similarity 100.0%; Pred. No. 4.1e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGGCATGCGATGGGGG 16
Db 97 GGGCATGCGATGGGGG 82

RESULT 15

B2413880
LOCUS B2413880 673 bp DNA linear GSS 10-DEC-2002
DEFINITION if18e05.g1 WGS-ZmaysF (DH5a methyl filtered) Zea mays genomic clone
if18e05.5', genomic survey sequence.
ACCESSION B2413880
VERSION B2413880.1 GI:26355896
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 673)
Rabinowicz,P.D., O'Shaughnessy,A.L., Ballja,V., Dedhia,N.,
Katzenburger,F., King,L., Miller,B., Muller,S., Nascimento,L.,
Zutavern,T., McCombie,W.R. and Martienssen,R.A.
Genomic shotgun sequences from Zea mays (methyl-filtered)
Unpublished (2002)
Contact: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
Fax: 516 367 8874
Email: mcombie@cshl.org
Plate: if18 row: e column: 05
Seq primer: -21M13UnivRev
Class: shotgun
High quality sequence stop: 673.

FEATURES

source
Location/Qualifiers
1. .673
/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="B73"
/db_xref="taxon:4577"
/clone="if18e05"
/lab_host="DH5a"
/clone_lib="WGS-ZmaysF (DH5a methyl filtered)"
/note="Organ: immature ears; Site_1: Xba I; Site_2: Xba I;
The vector was digested with XbaI and one nucleotide was
added by fill in the recessive 3' end. The genomic DNA
was nebulized, end repaired, adaptor ligated and size
fractionated using sephadex. The resulting fragments were
between 0.8 and 3 kb and were cloned into the vector (.x/y

reads in M13mpl9, .b/g reads in pUC19). The same ligation
was transformed into DH5a."

ORIGIN

Query Match 100.0%; Score 16; DB 28; Length 673;
Best Local Similarity 100.0%; Pred. No. 4.1e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGGCATGCGATGGGGG 16
Db 68 GGGCATGCGATGGGGG 83

Search completed: July 2, 2004, 13:32:59
Job time : 1201.35 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 2, 2004, 08:11:05 ; Search time 123.317 Seconds
(without alignments)
625.926 Million cell updates/sec

Title: US-10-068-160-15
Perfect score: 16
Sequence: 1 gggcatgcatg99999 16

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3163042 seqs, 2412103800 residues

Total number of hits satisfying chosen parameters: 6326084

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

- Database :
- 1: /cgn2_6/prodata/2/pubpna/US07_PUBCOMB.seq.*
 - 2: /cgn2_6/prodata/2/pubpna/PCT_NEW_PUB.seq.*
 - 3: /cgn2_6/prodata/2/pubpna/US06_NEW_PUB.seq.*
 - 4: /cgn2_6/prodata/2/pubpna/US06_PUBCOMB.seq.*
 - 5: /cgn2_6/prodata/2/pubpna/US07_NEW_PUB.seq.*
 - 6: /cgn2_6/prodata/2/pubpna/PCTUS_PUBCOMB.seq.*
 - 7: /cgn2_6/prodata/2/pubpna/US08_NEW_PUB.seq.*
 - 8: /cgn2_6/prodata/2/pubpna/US08_PUBCOMB.seq.*
 - 9: /cgn2_6/prodata/2/pubpna/US09A_PUBCOMB.seq.*
 - 10: /cgn2_6/prodata/2/pubpna/US09B_PUBCOMB.seq.*
 - 11: /cgn2_6/prodata/2/pubpna/US09C_PUBCOMB.seq.*
 - 12: /cgn2_6/prodata/2/pubpna/US09_NEW_PUB.seq.*
 - 13: /cgn2_6/prodata/2/pubpna/US09_NEW_PUB.seq.*
 - 14: /cgn2_6/prodata/2/pubpna/US10A_PUBCOMB.seq.*
 - 15: /cgn2_6/prodata/2/pubpna/US10B_PUBCOMB.seq.*
 - 16: /cgn2_6/prodata/2/pubpna/US10C_PUBCOMB.seq.*
 - 17: /cgn2_6/prodata/2/pubpna/US10_NEW_PUB.seq.*
 - 18: /cgn2_6/prodata/2/pubpna/US60_NEW_PUB.seq.*
 - 19: /cgn2_6/prodata/2/pubpna/US60_PUBCOMB.seq.*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	16	100.0	16	15	US-10-068-160-15
2	16	100.0	16	15	US-10-194-035-119
3	15	93.8	657	10	US-09-802-668-47
4	15	93.8	657	15	US-10-243-475-47
5	15	93.8	82660	13	US-10-087-192-2017
6	14.4	90.0	388	17	US-10-437-963-34086
7	14.4	90.0	390	9	US-09-867-703-1577
8	14.4	90.0	462	10	US-09-518-995-6563
9	14.4	90.0	475	15	US-09-518-995-21067
10	14.4	90.0	518	15	US-10-029-386-12515
11	14.4	90.0	607	13	US-10-027-632-142400
12	14.4	90.0	607	13	US-10-027-632-142401
13	14.4	90.0	607	16	US-10-027-632-142400
14	14.4	90.0	607	16	US-10-027-632-142401

c	15	14.4	90.0	617	17	US-10-437-963-22690	Sequence 22690, A
	16	14.4	90.0	691	13	US-10-027-632-283534	Sequence 283534, A
	17	14.4	90.0	691	16	US-10-027-632-283534	Sequence 283534, A
	18	14.4	90.0	822	13	US-10-027-632-157576	Sequence 157576, A
	19	14.4	90.0	822	16	US-10-027-632-157576	Sequence 157576, A
c	20	14.4	90.0	863	13	US-10-027-632-142398	Sequence 142398, A
	21	14.4	90.0	863	13	US-10-027-632-142398	Sequence 142398, A
c	22	14.4	90.0	863	16	US-10-027-632-142399	Sequence 142399, A
	23	14.4	90.0	863	16	US-10-027-632-142399	Sequence 142399, A
c	24	14.4	90.0	893	13	US-10-425-114-1734	Sequence 1734, Ap
	25	14.4	90.0	959	16	US-10-282-596-94	Sequence 94, Appl
c	26	14.4	90.0	990	9	US-09-880-107-2366	Sequence 2366, Ap
	27	14.4	90.0	1616	13	US-10-027-632-257360	Sequence 257360, A
	28	14.4	90.0	1616	13	US-10-027-632-257361	Sequence 257361, A
	29	14.4	90.0	1616	16	US-10-027-632-257360	Sequence 257360, A
	30	14.4	90.0	1616	16	US-10-027-632-257361	Sequence 257361, A
c	31	14.4	90.0	1653	16	US-10-284-049-690	Sequence 690, App
	32	14.4	90.0	2001	15	US-10-240-965-243	Sequence 243, App
	33	14.4	90.0	2322	13	US-10-027-632-110914	Sequence 110914, A
	34	14.4	90.0	2322	16	US-10-027-632-110914	Sequence 110914, A
c	35	14.4	90.0	2529	9	US-09-969-708-575	Sequence 575, App
	36	14.4	90.0	2529	13	US-10-240-425-1307	Sequence 1307, Ap
	37	14.4	90.0	2529	13	US-10-342-887-485	Sequence 485, App
c	38	14.4	90.0	2529	13	US-10-172-118-485	Sequence 485, App
	39	14.4	90.0	2529	15	US-10-205-823-217	Sequence 217, App
	40	14.4	90.0	2529	16	US-10-236-031B-19	Sequence 19, Appl
c	41	14.4	90.0	3079	9	US-09-735-705-116	Sequence 116, App
	42	14.4	90.0	3079	9	US-09-850-716A-116	Sequence 116, App
c	43	14.4	90.0	3079	9	US-09-897-778-116	Sequence 116, App
	44	14.4	90.0	3079	10	US-09-466-386A-116	Sequence 116, App
c	45	14.4	90.0	3079	13	US-10-007-700-116	Sequence 116, App

ALIGNMENTS

RESULT 1

US-10-068-160-15
; Sequence 15, Application US/10068160
; Publication No. US2003006040A1
; GENERAL INFORMATION:
; APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA, REPRESENTED BY THE
; APPLICANT: SECRETARY, DEPARTMENT OF HEALTH AND HUMAN SERVICES
; APPLICANT: KLINMAN, Dennis
; APPLICANT: ISHII, Ken
; APPLICANT: VERTHELI, Daniela
; TITLE OF INVENTION: OLIGODEOXYNUCLEOTIDE AND ITS USE TO INDUCE AN IMMUNE RESPONSE
; FILE REFERENCE: 4239-61999
; CURRENT APPLICATION NUMBER: US/10/068.160
; CURRENT FILING DATE: 2002-02-05
; PRIOR APPLICATION NUMBER: 60/128,898
; PRIOR FILING DATE: 1999-04-12
; NUMBER OF SEQ ID NOS: 120
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
; LENGTH: 16
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide
US-10-068-160-15

Query Match 100.0%; Score 16; DB 15; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGGCATGTCATGGGGG 16

DB 1 GGGCATGTCATGGGGG 16

RESULT 2

US-10-194-035-119

; Sequence 119, Application US/10194035
; Publication No. US2003014229A1
; GENERAL INFORMATION:
; APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS REPRESENTED BY THE
; SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES
; APPLICANT: KLINMAN, Dennis
; APPLICANT: ISHII, Ken
; APPLICANT: VERTHELYI, Daniela
; TITLE OF INVENTION: OLIGODEOXYNUCLEOTIDE AND ITS USE TO INDUCE AN IMMUNE RESPONSE
; FILE REFERENCE: 4239-63317
; CURRENT APPLICATION NUMBER: US/10/194,035
; PRIOR FILING DATE: 2002-07-12
; PRIOR APPLICATION NUMBER: PCT/US01/01122
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: US 60/176,115
; PRIOR FILING DATE: 2000-01-14
; NUMBER OF SEQ ID NOS: 119
; SOFTWARE: Patentin ver. 2.1
; SEQ ID NO 119
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
US-10-194-035-119

Query Match 100.0%; Score 16; DB 15; Length 16;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGCATGCATGGGGG 16
|||||
DB 1 GGGCATGCATGGGGG 16

RESULT 3

US-09-802-668-47/c
; Sequence 47, Application US/09802668
; Publication No. US20030190714A1
; GENERAL INFORMATION:
; APPLICANT: Wood, Linda
; APPLICANT: Vogeli, Gabriel
; APPLICANT: Karnovsky, Alla
; APPLICANT: Linske-O'Connell, Lisa I.
; APPLICANT: Wang, Jun
; APPLICANT: Liu, Derong
; TITLE OF INVENTION: Human Ion Channels
; FILE REFERENCE: 00069US1
; CURRENT APPLICATION NUMBER: US/09/802,668
; CURRENT FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 60/188,517
; PRIOR FILING DATE: 2000-03-10
; NUMBER OF SEQ ID NOS: 117
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 47
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-802-668-47

Query Match 93.8%; Score 15; DB 10; Length 657;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGCATGCATGGGGG 15
|||||
DB 550 GGGCATGCATGGGGG 536

RESULT 4

US-10-243-475-47/c
; Sequence 47, Application US/10243475
; Publication No. US20030194720A1

; GENERAL INFORMATION:
; APPLICANT: Roberts, Steven L.
; APPLICANT: Benjamin, Christopher W.
; APPLICANT: Karnovsky, Alla M.
; APPLICANT: Ruble, Cara L.
; TITLE OF INVENTION: Human Ion Channels
; FILE REFERENCE: PHEM0039-100
; CURRENT APPLICATION NUMBER: US/10/243,475
; CURRENT FILING DATE: 2003-01-16
; PRIOR APPLICATION NUMBER: 60/403,254
; PRIOR FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: 60/318,733
; PRIOR FILING DATE: 2001-09-12
; NUMBER OF SEQ ID NOS: 138
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 47
; LENGTH: 657
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-243-475-47

Query Match 93.8%; Score 15; DB 15; Length 657;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGCATGCATGGGGG 15
|||||
DB 550 GGGCATGCATGGGGG 536

RESULT 5

US-10-087-192-2017/c
; Sequence 2017, Application US/10087192
; Publication No. US20020182586A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David W.
; APPLICANT: Engelhard, Eric K.
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
; TITLE OF INVENTION: CANCER
; FILE REFERENCE: 529452000122
; CURRENT APPLICATION NUMBER: US/10/087,192
; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 09/747,377
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/798,586
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 2059
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2017
; LENGTH: 82660
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(82660)
; OTHER INFORMATION: n = A,T,C or G
US-10-087-192-2017

Query Match 93.8%; Score 15; DB 13; Length 82660;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGCATGCATGGGGG 15
|||||
DB 49515 GGGCATGCATGGGGG 49501

RESULT 6

US-10-437-963-34086/c
; Sequence 34086, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.

APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 34086
LENGTH: 388
TYPE: DNA
ORGANISM: Oryza sativa
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT4530_38135C.1
US-10-437-963-34086

Query Match 90.0%; Score 14.4; DB 17; Length 388;
Best Local Similarity 93.8%; Pred. No. 6.5e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGGCATGCGTGGGGG 16
|||||
Db 124 GGGCATGCGTGGGGG 109

RESULT 7
US-09-867-701-1577
Sequence 1577, Application US/09867701
Patent No. US2002013237A1
GENERAL INFORMATION:
APPLICANT: Aglate, Paul A.
APPLICANT: Jones, Robert
APPLICANT: Harlocker, Susan L.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
FILE REFERENCE: 210121.497
CURRENT APPLICATION NUMBER: US/09/867,701
CURRENT FILING DATE: 2001-05-29
NUMBER OF SEQ ID NOS: 10912
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1577
LENGTH: 390
TYPE: DNA
ORGANISM: Homo sapien
FEATURE:
NAME/KEY: misc.feature
LOCATION: (1)...(390)
OTHER INFORMATION: n = A,T,C or G
US-09-867-701-1577

Query Match 90.0%; Score 14.4; DB 9; Length 390;
Best Local Similarity 93.8%; Pred. No. 6.5e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGGCATGCGTGGGGG 16
|||||
Db 229 GGGCATGCGTGGGGG 244

RESULT 8
US-09-918-995-6563/c
Sequence 6563, Application US/09918995
Publication No. US20030073623A1
GENERAL INFORMATION:
APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
FILE REFERENCE: 20411-756

CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: US/09/235,076
PRIOR FILING DATE: 1999-01-20
NUMBER OF SEQ ID NOS: 38054
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 6563
LENGTH: 462
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc.feature
LOCATION: (1)...(462)
OTHER INFORMATION: n = A,T,C or G
US-09-918-995-6563

Query Match 90.0%; Score 14.4; DB 10; Length 462;
Best Local Similarity 93.8%; Pred. No. 6.4e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGGCATGCGTGGGGG 16
|||||
Db 275 GGGCATGCGTGGGGG 260

RESULT 9
US-09-918-995-21067/c
Sequence 21067, Application US/09918995
Publication No. US20030073623A1
GENERAL INFORMATION:
APPLICANT: Hyseq, Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
FILE REFERENCE: 20411-756
CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: US/09/235,076
PRIOR FILING DATE: 1999-01-20
NUMBER OF SEQ ID NOS: 38054
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 21067
LENGTH: 475
TYPE: DNA
ORGANISM: Homo sapiens
US-09-918-995-21067

Query Match 90.0%; Score 14.4; DB 10; Length 475;
Best Local Similarity 93.8%; Pred. No. 6.4e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGGCATGCGTGGGGG 16
|||||
Db 340 GGGCATGCGTGGGGG 325

RESULT 10
US-10-029-386-12515/c
Sequence 12515, Application US/10029386
Publication No. US20030194704A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR C
FILE REFERENCE: ASOMICA-X-2
CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT FILING DATE: 2001-12-20
NUMBER OF SEQ ID NOS: 34288
SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
SEQ ID NO 12515
LENGTH: 518
TYPE: DNA

```
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO CHR19.3
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 5.5
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.8
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 4.9
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2.3
; OTHER INFORMATION: SWISSPROT HIT: P09012, EVALUE 1.00e-09
; OTHER INFORMATION: NT HIT: M60784.1, EVALUE 1.00e-111
; OTHER INFORMATION: EST_HUMAN HIT: A518377.1, EVALUE 1.00e-85
US-10-029-386-12515

Query Match          90.0%; Score 14.4; DB 15; Length 518;
Best Local Similarity 93.8%; Pred. No. 6.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGGCATGCATGGGGGG 16
   ||||| ||||| |||||
DB 119 GGGCAGGCATGGGGGG 104

RESULT 11
US-10-027-632-142400
; Sequence 142400, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 142400
; LENGTH: 607
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-142400

Query Match          90.0%; Score 14.4; DB 13; Length 607;
Best Local Similarity 93.8%; Pred. No. 6.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGGCATGCATGGGGGG 16
   ||||| ||||| |||||
DB 403 GAGCATGCATGGGGGG 418

RESULT 12
US-10-027-632-142401
; Sequence 142401, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 142400
; LENGTH: 607
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-142400

Query Match          90.0%; Score 14.4; DB 16; Length 607;
Best Local Similarity 93.8%; Pred. No. 6.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGGCATGCATGGGGGG 16
   ||||| ||||| |||||
DB 403 GAGCATGCATGGGGGG 418

RESULT 13
US-10-027-632-142400
; Sequence 142400, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 142400
; LENGTH: 607
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-142400

Query Match          90.0%; Score 14.4; DB 16; Length 607;
Best Local Similarity 93.8%; Pred. No. 6.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGGCATGCATGGGGGG 16
   ||||| ||||| |||||
DB 403 GAGCATGCATGGGGGG 418
```

RESULT 14

US-10-027-632-142401
; Sequence 142401, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 142401
; LENGTH: 607
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-142401

Query Match 90.0%; Score 14.4; DB 16; Length 607;
Best Local Similarity 93.8%; Pred. No. 6.2e+02;
Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGCGATGCATGGGGG 16
DB 403 GAGCATGCATGGGGG 418

RESULT 15

US-10-437-963-22690/c
; Sequence 22690, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boutharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(33221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 22690
; LENGTH: 617
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(617)
; OTHER INFORMATION: unsure at all n locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_27843C.1
US-10-437-963-22690

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 2, 2004, 07:36:05 ; Search time 633.732 Seconds
(without alignments)
1231.080 Million cell updates/sec

Title: US-10-068-160-16

Perfect score: 18
Sequence: 1 tgcgtcgatgcagggggg 18

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl.*

- 1: gb.ba.*
- 2: gb.htg.*
- 3: gb.in.*
- 4: gb.om.*
- 5: gb.ov.*
- 6: gb.pat.*
- 7: gb.ph.*
- 8: gb.pl.*
- 9: gb.pr.*
- 10: gb.ro.*
- 11: gb.sts.*
- 12: gb.sy.*
- 13: gb.un.*
- 14: gb.vi.*
- 15: em.ba.*
- 16: em.fun.*
- 17: em.hum.*
- 18: em.in.*
- 19: em.mu.*
- 20: em.om.*
- 21: em.or.*
- 22: em.ov.*
- 23: em.pat.*
- 24: em.ph.*
- 25: em.pl.*
- 26: em.ro.*
- 27: em.sts.*
- 28: em.un.*
- 29: em.vi.*
- 30: em.htg.hum.*
- 31: em.htg.in.*
- 32: em.htg.inv.*
- 33: em.htg.other.*
- 34: em.htg.mus.*
- 35: em.htg.pln.*
- 36: em.htg.rod.*
- 37: em.htg.mam.*
- 38: em.htg.vrt.*
- 39: em.sy.*
- 40: em.htgo.hum.*
- 41: em.htgo.mus.*
- 42: em.htgo.other.*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	18	100.0	20	6	AX194440	AX194440 Sequence
2	18	100.0	20	6	AX194481	AX194481 Sequence
3	18	100.0	20	6	AX194482	AX194482 Sequence
4	18	100.0	20	6	AX465390	AX465390 Sequence
5	18	100.0	20	6	AX465431	AX465431 Sequence
6	18	100.0	20	6	AX465432	AX465432 Sequence
7	17	94.4	19	6	AX194483	AX194483 Sequence
8	17	94.4	19	6	AX465433	AX465433 Sequence
9	16.4	91.1	18	6	AX352207	AX352207 Sequence
10	16.4	91.1	18	6	AX352217	AX352217 Sequence
11	16.4	91.1	18	6	AX352255	AX352255 Sequence
12	16.4	91.1	20	6	AX194432	AX194432 Sequence
13	16.4	91.1	20	6	AX194434	AX194434 Sequence
14	16.4	91.1	20	6	AX194437	AX194437 Sequence
15	16.4	91.1	20	6	AX194438	AX194438 Sequence
16	16.4	91.1	20	6	AX194439	AX194439 Sequence
17	16.4	91.1	20	6	AX194441	AX194441 Sequence
18	16.4	91.1	20	6	AX194443	AX194443 Sequence
19	16.4	91.1	20	6	AX194472	AX194472 Sequence
20	16.4	91.1	20	6	AX194502	AX194502 Sequence
21	16.4	91.1	20	6	AX352198	AX352198 Sequence
22	16.4	91.1	20	6	AX352201	AX352201 Sequence
23	16.4	91.1	20	6	AX352206	AX352206 Sequence
24	16.4	91.1	20	6	AX352209	AX352209 Sequence
25	16.4	91.1	20	6	AX352212	AX352212 Sequence
26	16.4	91.1	20	6	AX352216	AX352216 Sequence
27	16.4	91.1	20	6	AX352242	AX352242 Sequence
28	16.4	91.1	20	6	AX352245	AX352245 Sequence
29	16.4	91.1	20	6	AX352250	AX352250 Sequence
30	16.4	91.1	20	6	AX352254	AX352254 Sequence
31	16.4	91.1	20	6	AX465382	AX465382 Sequence
32	16.4	91.1	20	6	AX465384	AX465384 Sequence
33	16.4	91.1	20	6	AX465387	AX465387 Sequence
34	16.4	91.1	20	6	AX465388	AX465388 Sequence
35	16.4	91.1	20	6	AX465389	AX465389 Sequence
36	16.4	91.1	20	6	AX465391	AX465391 Sequence
37	16.4	91.1	20	6	AX465393	AX465393 Sequence
38	16.4	91.1	20	6	AX465422	AX465422 Sequence
39	16.4	91.1	20	6	AX816067	AX816067 Sequence
40	16.4	91.1	22	6	AX352204	AX352204 Sequence
41	16.4	91.1	22	6	AX352248	AX352248 Sequence
42	16.4	91.1	26	6	AX352228	AX352228 Sequence
43	16.4	91.1	26	6	AX352240	AX352240 Sequence
44	16.4	91.1	28	6	AX352219	AX352219 Sequence
45	16.4	91.1	28	6	AX352222	AX352222 Sequence

ALIGNMENTS

RESULT 1	AX194440	AX194440	Sequence 40 from Patent WO0151500.	20 bp	DNA	linear	PAT 28-AUG-2001
LOCUS	AX194440	AX194440	Sequence 40 from Patent WO0151500.	20 bp	DNA	linear	PAT 28-AUG-2001
DEFINITION	AX194440	AX194440	Sequence 40 from Patent WO0151500.	20 bp	DNA	linear	PAT 28-AUG-2001
ACCESSION	AX194440	AX194440	Sequence 40 from Patent WO0151500.	20 bp	DNA	linear	PAT 28-AUG-2001
VERSION	AX194440.1	GI:15385096	Sequence 40 from Patent WO0151500.	20 bp	DNA	linear	PAT 28-AUG-2001
KEYWORDS	AX194440.1	GI:15385096	Sequence 40 from Patent WO0151500.	20 bp	DNA	linear	PAT 28-AUG-2001
SOURCE	AX194440.1	GI:15385096	Sequence 40 from Patent WO0151500.	20 bp	DNA	linear	PAT 28-AUG-2001
ORGANISM	AX194440.1	GI:15385096	Sequence 40 from Patent WO0151500.	20 bp	DNA	linear	PAT 28-AUG-2001
REFERENCE	AX194440.1	GI:15385096	Sequence 40 from Patent WO0151500.	20 bp	DNA	linear	PAT 28-AUG-2001
AUTHORS	AX194440.1	GI:15385096	Sequence 40 from Patent WO0151500.	20 bp	DNA	linear	PAT 28-AUG-2001
TITLE	AX194440.1	GI:15385096	Sequence 40 from Patent WO0151500.	20 bp	DNA	linear	PAT 28-AUG-2001
JOURNAL	AX194440.1	GI:15385096	Sequence 40 from Patent WO0151500.	20 bp	DNA	linear	PAT 28-AUG-2001

Kliman, D., Ishii, K. and Verthelyi, D.
Oligodeoxynucleotide and its use to induce an immune response
Patent: WO 0151500-A 40 19-JUL-2001;
Secretary of the Department of Health and Human Services (US)

Pred. No. is the number of results predicted by chance to have a

FEATURES
source
Location/Qualifiers
1. .20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic DNA"

ORIGIN

Query Match
Best Local Similarity 100.0%; Score 18; DB 6; Length 20;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGCCTCGATGCAGGGGG 18
Db 3 TGCCTCGATGCAGGGGG 20

RESULT 2
AX194481
LOCUS AX194481 20 bp DNA linear PAT 28-AUG-2001
DEFINITION Sequence 81 from Patent WO0151500.
ACCESSION AX194481
VERSION AX194481.1 GI:15385137
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Kliman,D., Ishii,K. and Verthelyi,D.
TITLE Oligodeoxynucleotide and its use to induce an immune response
JOURNAL Patent: WO 0151500-A 81 19-JUL-2001;
Secretary of the Department of Health and Human Services (US)
FEATURES
source
Location/Qualifiers
1. .20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic DNA"

ORIGIN

Query Match
Best Local Similarity 100.0%; Score 18; DB 6; Length 20;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGCCTCGATGCAGGGGG 18
Db 3 TGCCTCGATGCAGGGGG 20

RESULT 3
AX194482
LOCUS AX194482 20 bp DNA linear PAT 28-AUG-2001
DEFINITION Sequence 82 from Patent WO0151500.
ACCESSION AX194482
VERSION AX194482.1 GI:15385138
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Kliman,D., Ishii,K. and Verthelyi,D.
TITLE Oligodeoxynucleotide and its use to induce an immune response
JOURNAL Patent: WO 0151500-A 82 19-JUL-2001;
Secretary of the Department of Health and Human Services (US)
FEATURES
source
Location/Qualifiers
1. .20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic DNA"

ORIGIN

Query Match 100.0%; Score 18; DB 6; Length 20;

Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGCCTCGATGCAGGGGG 18
Db 3 TGCCTCGATGCAGGGGG 20

RESULT 4
AX465390
LOCUS AX465390 20 bp DNA linear PAT 16-JUL-2002
DEFINITION Sequence 58 from Patent WO0211761.
ACCESSION AX465390
VERSION AX465390.1 GI:21899753
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Mond,J.J., Prince,G. and Klinman,D.M.
TITLE Vaccine against RSV
JOURNAL Patent: WO 0211761-A 58 14-FEB-2002;
HENRY M. JACKSON FOUNDATION FOR THE ADVANCEMENT OF MILITARY
MEDICINE (US)
FEATURES
source
Location/Qualifiers
1. .20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic oligonucleotide"

ORIGIN

Query Match 100.0%; Score 18; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGCCTCGATGCAGGGGG 18
Db 3 TGCCTCGATGCAGGGGG 20

RESULT 5
AX465431
LOCUS AX465431 20 bp DNA linear PAT 16-JUL-2002
DEFINITION Sequence 99 from Patent WO0211761.
ACCESSION AX465431
VERSION AX465431.1 GI:21899794
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Mond,J.J., Prince,G. and Klinman,D.M.
TITLE Vaccine against RSV
JOURNAL Patent: WO 0211761-A 99 14-FEB-2002;
HENRY M. JACKSON FOUNDATION FOR THE ADVANCEMENT OF MILITARY
MEDICINE (US)
FEATURES
source
Location/Qualifiers
1. .20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic oligonucleotide"

ORIGIN

Query Match 100.0%; Score 18; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGCCTCGATGCAGGGGG 18
Db 3 TGCCTCGATGCAGGGGG 20

RESULT 6
AX465431
LOCUS AX465431 20 bp DNA linear PAT 16-JUL-2002
DEFINITION Sequence 99 from Patent WO0211761.
ACCESSION AX465431
VERSION AX465431.1 GI:21899794
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.
REFERENCE 1
AUTHORS Mond,J.J., Prince,G. and Klinman,D.M.
TITLE Vaccine against RSV
JOURNAL Patent: WO 0211761-A 99 14-FEB-2002;
HENRY M. JACKSON FOUNDATION FOR THE ADVANCEMENT OF MILITARY
MEDICINE (US)
FEATURES
source
Location/Qualifiers
1. .20
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Synthetic oligonucleotide"

```

RESULT 6
AX465432
LOCUS AX465432 20 bp DNA linear PAT 16-JUL-2002
DEFINITION Sequence 100 from Patent WO0211761.
ACCESSION AX465432
VERSION AX465432.1 GI:21899795
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
          artificial sequences.
REFERENCE
AUTHORS Mond,J.J., Prince,G. and Klinman,D.M.
TITLE Vaccine against RSV
JOURNAL Patent: WO 0211761-A 100 14-FEB-2002;
        HENRY M. JACKSON FOUNDATION FOR THE ADVANCEMENT OF MILITARY
        MEDICINE (US)
FEATURES
  source
    Location/Qualifiers
      1..20
        /organism="synthetic construct"
        /mol_type="unassigned DNA"
        /db_xref="taxon:32630"
        /note="Synthetic oligonucleotide"
ORIGIN
Query Match 100.0%; Score 18; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TCGTCGATGCAGGGGG 18
   |||||
Db 3 TCGTCGATGCAGGGGG 20

RESULT 7
AX194483
LOCUS AX194483 19 bp DNA linear PAT 28-AUG-2001
DEFINITION Sequence 83 from Patent WO0151500.
ACCESSION AX194483
VERSION AX194483.1 GI:15385139
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
          artificial sequences.
REFERENCE
AUTHORS Klinman,D., Ishii,K. and Verthelyi,D.
TITLE Oligodeoxynucleotide and its use to induce an immune response
JOURNAL Patent: WO 0151500-A 83 19-JUL-2001;
        Secretary of the Department of Health and Human Services (US)
FEATURES
  source
    Location/Qualifiers
      1..19
        /organism="synthetic construct"
        /mol_type="unassigned DNA"
        /db_xref="taxon:32630"
        /note="Synthetic DNA"
ORIGIN
Query Match 94.4%; Score 17; DB 6; Length 19;
Best Local Similarity 100.0%; Pred. No. 7.8e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TCGTCGATGCAGGGGG 17
   |||||
Db 3 TCGTCGATGCAGGGGG 19

RESULT 8
AX465433
LOCUS AX465433 19 bp DNA linear PAT 16-JUL-2002
DEFINITION Sequence 101 from Patent WO0211761.
ACCESSION AX465433
VERSION AX465433.1 GI:21899796
KEYWORDS

```

```

SOURCE synthetic construct
ORGANISM synthetic construct
          artificial sequences.
REFERENCE
AUTHORS Mond,J.J., Prince,G. and Klinman,D.M.
TITLE Vaccine against RSV
JOURNAL Patent: WO 0211761-A 101 14-FEB-2002;
        HENRY M. JACKSON FOUNDATION FOR THE ADVANCEMENT OF MILITARY
        MEDICINE (US)
FEATURES
  source
    Location/Qualifiers
      1..19
        /organism="synthetic construct"
        /mol_type="unassigned DNA"
        /db_xref="taxon:32630"
        /note="Synthetic oligonucleotide"
ORIGIN
Query Match 94.4%; Score 17; DB 6; Length 19;
Best Local Similarity 100.0%; Pred. No. 7.8e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TCGTCGATGCAGGGGG 17
   |||||
Db 3 TCGTCGATGCAGGGGG 19

RESULT 9
AX352207
LOCUS AX352207 18 bp DNA linear PAT 06-FEB-2002
DEFINITION Sequence 503 from Patent WO0193902.
ACCESSION AX352207
VERSION AX352207.1 GI:18617490
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
          artificial sequences.
REFERENCE
AUTHORS Mond,J.J., Flora,M. and Klinman,D.M.
TITLE Immunostimulatory rna/dna hybrid molecules
JOURNAL Patent: WO 0193902-A 503 13-DEC-2001;
        Biosynexus Incorporated (US)
FEATURES
  source
    Location/Qualifiers
      1..18
        /organism="synthetic construct"
        /mol_type="unassigned DNA"
        /db_xref="taxon:32630"
        /note="Synthetic HDR"
ORIGIN
Query Match 91.1%; Score 16.4; DB 6; Length 18;
Best Local Similarity 94.4%; Pred. No. 1.6e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 TCGTCGATGCAGGGGG 18
   |||||
Db 1 TGCATCGATGCAGGGGG 18

RESULT 10
AX352217
LOCUS AX352217 18 bp DNA linear PAT 06-FEB-2002
DEFINITION Sequence 513 from Patent WO0193902.
ACCESSION AX352217
VERSION AX352217.1 GI:18617500
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
          artificial sequences.
REFERENCE
AUTHORS Mond,J.J., Flora,M. and Klinman,D.M.
TITLE Immunostimulatory rna/dna hybrid molecules
JOURNAL Patent: WO 0193902-A 513 13-DEC-2001;
        Biosynexus Incorporated (US)

```



```

FEATURES
  source
    Location/Qualifiers
      1..18
        /organism="synthetic construct"
        /mol_type="unassigned DNA"
        /db_xref="taxon:32630"
        /note="Synthetic HDR"

ORIGIN
  Query Match
    Best Local Similarity 91.1%; Score 16.4; DB 6; Length 18;
    Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

  Qy 1 TGCCTCGATGCAGGGGG 18
      ||| ||||| ||||| |||||
  Db 1 TGCATCGATGCAGGGGG 20
      ||| ||||| ||||| |||||

RESULT 11
AX194432
LOCUS
DEFINITION
  Sequence 551 from Patent WO0193902.
ACCESSION
  AX194432
VERSION
  AX194432.1 GI:18617538
KEYWORDS
  .
SOURCE
  synthetic construct
  artificial sequences.
ORGANISM
  .
REFERENCE
  1
  AUTHORS
    Mond, J.J., Flora, M. and Klinman, D.M.
  TITLE
    Immunostimulatory rna/dna hybrid molecules
  JOURNAL
    Patent: WO 0193902-A 551 13-DEC-2001;
    Biosynexus Incorporated (US)
FEATURES
  source
    Location/Qualifiers
      1..18
        /organism="synthetic construct"
        /mol_type="unassigned DNA"
        /db_xref="taxon:32630"
        /note="Synthetic HDR"

ORIGIN
  Query Match
    Best Local Similarity 91.1%; Score 16.4; DB 6; Length 18;
    Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

  Qy 1 TGCCTCGATGCAGGGGG 18
      ||| ||||| ||||| |||||
  Db 1 TGCATCGATGCAGGGGG 18
      ||| ||||| ||||| |||||

RESULT 12
AX194432
LOCUS
DEFINITION
  Sequence 32 from Patent WO0151500.
ACCESSION
  AX194432
VERSION
  AX194432.1 GI:15385088
KEYWORDS
  .
SOURCE
  synthetic construct
  artificial sequences.
ORGANISM
  .
REFERENCE
  1
  AUTHORS
    Klinman, D., Ishii, K. and Verthelyi, D.
  TITLE
    Oligodeoxynucleotide and its use to induce an immune response
  JOURNAL
    Patent: WO 0151500-A 32 19-JUL-2001;
    Secretary of the Department of Health and Human Services (US)
FEATURES
  source
    Location/Qualifiers
      1..20
        /organism="synthetic construct"
        /mol_type="unassigned DNA"
        /db_xref="taxon:32630"
        /note="Synthetic DNA"

ORIGIN
  Query Match
    Best Local Similarity 91.1%; Score 16.4; DB 6; Length 20;
    Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

  Qy 1 TGCCTCGATGCAGGGGG 18
      ||| ||||| ||||| |||||
  Db 1 TGCATCGATGCAGGGGG 20
      ||| ||||| ||||| |||||

RESULT 13
AX194434
LOCUS
DEFINITION
  Sequence 34 from Patent WO0151500.
ACCESSION
  AX194434
VERSION
  AX194434.1 GI:15385090
KEYWORDS
  .
SOURCE
  synthetic construct
  artificial sequences.
ORGANISM
  .
REFERENCE
  1
  AUTHORS
    Klinman, D., Ishii, K. and Verthelyi, D.
  TITLE
    Oligodeoxynucleotide and its use to induce an immune response
  JOURNAL
    Patent: WO 0151500-A 34 19-JUL-2001;
    Secretary of the Department of Health and Human Services (US)
FEATURES
  source
    Location/Qualifiers
      1..20
        /organism="synthetic construct"
        /mol_type="unassigned DNA"
        /db_xref="taxon:32630"
        /note="Synthetic DNA"

ORIGIN
  Query Match
    Best Local Similarity 91.1%; Score 16.4; DB 6; Length 20;
    Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

  Qy 1 TGCCTCGATGCAGGGGG 18
      ||| ||||| ||||| |||||
  Db 1 TGCATCGATGCAGGGGG 20
      ||| ||||| ||||| |||||

RESULT 14
AX194437
LOCUS
DEFINITION
  Sequence 37 from Patent WO0151500.
ACCESSION
  AX194437
VERSION
  AX194437.1 GI:15385093
KEYWORDS
  .
SOURCE
  synthetic construct
  artificial sequences.
ORGANISM
  .
REFERENCE
  1
  AUTHORS
    Klinman, D., Ishii, K. and Verthelyi, D.
  TITLE
    Oligodeoxynucleotide and its use to induce an immune response
  JOURNAL
    Patent: WO 0151500-A 37 19-JUL-2001;
    Secretary of the Department of Health and Human Services (US)
FEATURES
  source
    Location/Qualifiers
      1..20
        /organism="synthetic construct"
        /mol_type="unassigned DNA"
        /db_xref="taxon:32630"
        /note="Synthetic DNA"

ORIGIN
  Query Match
    Best Local Similarity 91.1%; Score 16.4; DB 6; Length 20;
    Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

  Qy 1 TGCCTCGATGCAGGGGG 18
      ||| ||||| ||||| |||||
  Db 1 TGCATCGATGCAGGGGG 20
      ||| ||||| ||||| |||||

RESULT 15
AX194437
LOCUS
DEFINITION
  Sequence 37 from Patent WO0151500.
ACCESSION
  AX194437
VERSION
  AX194437.1 GI:15385093
KEYWORDS
  .
SOURCE
  synthetic construct
  artificial sequences.
ORGANISM
  .
REFERENCE
  1
  AUTHORS
    Klinman, D., Ishii, K. and Verthelyi, D.
  TITLE
    Oligodeoxynucleotide and its use to induce an immune response
  JOURNAL
    Patent: WO 0151500-A 37 19-JUL-2001;
    Secretary of the Department of Health and Human Services (US)
FEATURES
  source
    Location/Qualifiers
      1..20
        /organism="synthetic construct"
        /mol_type="unassigned DNA"
        /db_xref="taxon:32630"
        /note="Synthetic DNA"

ORIGIN
  Query Match
    Best Local Similarity 91.1%; Score 16.4; DB 6; Length 20;
    Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

  Qy 1 TGCCTCGATGCAGGGGG 18
      ||| ||||| ||||| |||||
  Db 1 TGCATCGATGCAGGGGG 20
      ||| ||||| ||||| |||||

```

```

AX194438
LOCUS AX194438 20 bp DNA linear PAT 28-AUG-2001
DEFINITION Sequence 38 from Patent WO0151500.
ACCESSION AX194438
VERSION AX194438.1 GI:15385094
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
          artificial sequences.
REFERENCE
  1 Klinman,D., Ishii,K. and Verthelyi,D.
    Oligodeoxynucleotide and its use to induce an immune response
    Patent: WO 0151500-A 38 19-JUL-2001;
    Secretary of the Department of Health and Human Services (US)
FEATURES
      source
        1..20
          /organism="synthetic construct"
          /mol_type="unassigned DNA"
          /db_xref="taxon:32630"
          /note="Synthetic DNA"
ORIGIN
Query Match 91.1%; Score 16.4; DB 6; Length 20;
Best Local Similarity 94.4%; Fred. No. 1.6e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TCGCTCGATGCAGGGGG 18
   ||| ||||| |||||
Db 3 TGCATCGATGCAGGGGG 20

Search completed: July 2, 2004, 10:08:03
Job time : 633.732 secs

```

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 2, 2004, 07:38:45 ; Search time 1348.02 Seconds
(without alignments)
398.746 Million cell updates/sec

Title: US-10-068-160-16

Perfect score: 18

Sequence: 1 tgcgtcgatcagggggggg 18

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hcc:*
9: gb_est1:*
10: gb_est2:*
11: gb_hcc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_man:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_phg:*
27: em_gss_vrl:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	17	94.4	1026	11	CNS08MNL
2	16.4	91.1	360	9	AA086330
3	16.4	91.1	429	28	BH746584
4	16.4	91.1	1110	29	AG082246

5	16	88.9	489	13	BQ102588
6	16	88.9	705	29	CE730492
7	15.6	86.7	893	13	BA448966
8	15.4	85.6	125	9	AV128107
9	15.4	85.6	320	9	AA662789
10	15.4	85.6	366	10	BE400545
11	15.4	85.6	442	14	CA706144
12	15.4	85.6	470	14	CA693337
13	15.4	85.6	499	9	AU001427
14	15.4	85.6	553	14	CF639409
15	15.4	85.6	565	28	BH797911
16	15.4	85.6	590	12	BJ232664
17	15.4	85.6	621	9	AV398828
18	15.4	85.6	633	14	CA760384
19	15.4	85.6	653	14	CF642132
20	15.4	85.6	740	9	AV401323
21	15.4	85.6	742	12	BG707792
22	15.4	85.6	749	29	AG100828
23	15.4	85.6	759	9	AU002700
24	15.4	85.6	781	29	AG042213
25	15.4	85.6	802	28	BH982312
26	15.4	85.6	807	13	CA101677
27	15.4	85.6	808	10	BF530495
28	15.4	85.6	870	29	CG254815
29	15.4	85.6	877	29	CG238619
30	15.4	85.6	907	29	CG62082
31	15.4	85.6	929	29	CG254827
32	15.4	85.6	931	9	AU091129
33	15.4	85.6	955	10	BF794250
34	15.4	85.6	964	29	CG662091
35	15.4	85.6	972	29	CG615817
36	15.4	85.6	1015	29	CNS054D6
37	15.4	85.6	1055	10	BB869694
38	15.4	85.6	1064	12	BG920455
39	15.4	85.6	1071	13	BZ253418
40	15.4	85.6	1390	13	BQ877978
41	15	83.3	448	29	CG740971
42	15	83.3	449	9	AU173854
43	15	83.3	958	12	BI758635
44	15	83.3	1015	9	AV117227
45	15	83.3	1399	28	BZ579332

ALIGNMENTS

RESULT 1	CNS08MNL	1026 bp	mRNA	linear	HTC 07-JAN-2003
LOCUS	Single read from an extremity of a full-length cDNA clone made from Anopheles gambiae total adult females. 3-PRIME end of clone FK0AA28CA12 of strain 6-9 of Anopheles gambiae (African malaria mosquito).				
DEFINITION	mosquito).				
ACCESSION	BX018781				
VERSION	BX018781.1 GI:27568001				
KEYWORDS	HTC.				
SOURCE	Anopheles gambiae (African malaria mosquito)				
ORGANISM	Anopheles gambiae				
REFERENCE	1 (bases 1 to 1026)				
AUTHORS	Genoscope.				
TITLE	Direct Submission				
JOURNAL	Submitted (06-JAN-2003) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)				
FEATURES	- Web : www.genoscope.cns.fr Location/Qualifiers				
Source	1..1026				
	/organism="Anopheles gambiae"				
	/mol_type="mRNA"				
	/strain="6-9"				
	/db_xref="taxon:7165"				

/clone="FK0AAA28CA12"
/plasmid="pME18S-FL"
/note="end : 3-PRIME"

ORIGIN

Query Match 94.4%; Score 17; DB 11; Length 1026;
Best Local Similarity 100.0%; Pred. No. 4.3e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GCGTCGATCGAGGGGG 18
|||||
Db 205 GCGTCGATCGAGGGGG 221

RESULT 2

AA066330

LOCUS

DEFINITION

mm14606.r1 Stragatene mouse diaphragm (#937303) Mus musculus cDNA
clone IMAGE:521506 5' similar to gb:X03208 Mouse group 1 gene
(MOUSE); mRNA sequence.

ACCESSION

AA066330

VERSION

AA066330.1

GI:1563400

EST.

Mus musculus

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Unpublished (1996)

Contact: Marra M/Mouse EST Project

Washington University School of MedicineP

4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108

Tel: 314 286 1800

Fax: 314 286 1810

Email: mouseest@watson.wustl.edu

This clone is available royalty-free through LNL; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.

MGI:315354

Trace considered overall poor quality

Seq primer: -28ml3 rev1 ET from Amersham

High quality sequence stop: 1.

Location/Qualifiers

1..360

/organism="Mus musculus"

/mol_type="mRNA"

/db_xref="taxon:10090"

/clone="IMAGE:521506"

/issue_type="diaphragm"

/dev_stage="adult"

/lab_host="SOLR (kanamycin resistant)"

/clone_lib="Stratagene mouse diaphragm (#937303)"

/note="Organ: diaphragm; Vector: pBluescript SK-; Site 1:

EcoRI; Site 2: XhoI; Cloned unidirectionally from mRNA

prepared from diaphragm muscle. Primer: Oligo dt. Average

insert size: 1.5 kb. Uni-ZAP XR Vector; -5' adaptor

sequence: 5' GAATTCGACGACG 3' -3' adaptor sequence: 5'

CTCGAGTTTCTTTTCTTTT 3'

ORIGIN

Query Match 91.1%; Score 16.4; DB 9; Length 360;
Best Local Similarity 94.4%; Pred. No. 6.3e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TCGTCGATCGAGGGGG 18
|||||

Db 91 TGTGTCGATCGAGGGGG 108
|||||

RESULT 3

BH746584/c

LOCUS

DEFINITION

Arabis thaliana genomic clone SALK_044872.30.00.x, genomic

survey sequence.

ACCESSION

BH746584

VERSION

BH746584.1

GI:18959699

GSS.

Arabidopsis thaliana (thale cress)

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Unpublished (2001)

Contact: Joseph R. Ecker

Salk Institute Genomic Analysis Laboratory (SIGAL)

The Salk Institute for Biological Studies

10010 N. Torrey Pines Road, La Jolla, CA 92037, USA

Tel: 858 453 4100 x1752

Fax: 858 558 6379

Email: eckersalk.edu

This is single pass sequence recovered from the left border of

TDNA. This sequence lies within an annotated exon of At1g42480.

Class: TDNA tagged.

Location/Qualifiers

1..429

/organism="Arabidopsis thaliana"

/mol_type="genomic DNA"

/strain="Columbia 0"

/db_xref="taxon:3702"

/clone="SALK_044872.30.00.x"

/clone_lib="Arabidopsis thaliana TDNA insertion lines"

/note="PCR was performed on Arabidopsis thaliana lines

each of which contains one or more TDNA insertion

elements. The resultant fragment for each line was

directly sequenced to determine the genomic sequence at

the site of insertion. Details of the protocols used can

be found at http://signal.salk.edu/tdna_protocols.html"

ORIGIN

Query Match 91.1%; Score 16.4; DB 28; Length 429;
Best Local Similarity 94.4%; Pred. No. 6.5e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TCGTCGATCGAGGGGG 18
|||||

Db 414 TCGTCGATCGAGGGGG 397
|||||

RESULT 4

AG082246/c

LOCUS

DEFINITION

Pan troglodytes DNA, clone: PTB-079807.R, genomic survey sequence.

ACCESSION

AG082246

VERSION

AG082246.1

GI:16634048

GSS.

Pan troglodytes (chimpanzee)

ORGANISM

REFERENCE

AUTHORS

TITLE

Pan troglodytes

Sukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.

1

Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,

Tocoki, Y., Watanabe, H. and Sakaki, Y.

BAC end sequences of Library PTB

BH746584 429 bp DNA linear GSS 27-FEB-2002
SALK_044872.30.00.x Arabidopsis thaliana TDNA insertion lines
Arabidopsis thaliana genomic clone SALK_044872.30.00.x, genomic
survey sequence.

BH746584 429 bp DNA linear GSS 27-FEB-2002
SALK_044872.30.00.x Arabidopsis thaliana TDNA insertion lines
Arabidopsis thaliana genomic clone SALK_044872.30.00.x, genomic
survey sequence.

BH746584 429 bp DNA linear GSS 27-FEB-2002
SALK_044872.30.00.x Arabidopsis thaliana TDNA insertion lines
Arabidopsis thaliana genomic clone SALK_044872.30.00.x, genomic
survey sequence.

BH746584 429 bp DNA linear GSS 27-FEB-2002
SALK_044872.30.00.x Arabidopsis thaliana TDNA insertion lines
Arabidopsis thaliana genomic clone SALK_044872.30.00.x, genomic
survey sequence.

BH746584 429 bp DNA linear GSS 27-FEB-2002
SALK_044872.30.00.x Arabidopsis thaliana TDNA insertion lines
Arabidopsis thaliana genomic clone SALK_044872.30.00.x, genomic
survey sequence.

BH746584 429 bp DNA linear GSS 27-FEB-2002
SALK_044872.30.00.x Arabidopsis thaliana TDNA insertion lines
Arabidopsis thaliana genomic clone SALK_044872.30.00.x, genomic
survey sequence.

BH746584 429 bp DNA linear GSS 27-FEB-2002
SALK_044872.30.00.x Arabidopsis thaliana TDNA insertion lines
Arabidopsis thaliana genomic clone SALK_044872.30.00.x, genomic
survey sequence.

BH746584 429 bp DNA linear GSS 27-FEB-2002
SALK_044872.30.00.x Arabidopsis thaliana TDNA insertion lines
Arabidopsis thaliana genomic clone SALK_044872.30.00.x, genomic
survey sequence.

BH746584 429 bp DNA linear GSS 27-FEB-2002
SALK_044872.30.00.x Arabidopsis thaliana TDNA insertion lines
Arabidopsis thaliana genomic clone SALK_044872.30.00.x, genomic
survey sequence.

BH746584 429 bp DNA linear GSS 27-FEB-2002
SALK_044872.30.00.x Arabidopsis thaliana TDNA insertion lines
Arabidopsis thaliana genomic clone SALK_044872.30.00.x, genomic
survey sequence.

BH746584 429 bp DNA linear GSS 27-FEB-2002
SALK_044872.30.00.x Arabidopsis thaliana TDNA insertion lines
Arabidopsis thaliana genomic clone SALK_044872.30.00.x, genomic
survey sequence.

BH746584 429 bp DNA linear GSS 27-FEB-2002
SALK_044872.30.00.x Arabidopsis thaliana TDNA insertion lines
Arabidopsis thaliana genomic clone SALK_044872.30.00.x, genomic
survey sequence.

BH746584 429 bp DNA linear GSS 27-FEB-2002
SALK_044872.30.00.x Arabidopsis thaliana TDNA insertion lines
Arabidopsis thaliana genomic clone SALK_044872.30.00.x, genomic
survey sequence.

BH746584 429 bp DNA linear GSS 27-FEB-2002
SALK_044872.30.00.x Arabidopsis thaliana TDNA insertion lines
Arabidopsis thaliana genomic clone SALK_044872.30.00.x, genomic
survey sequence.

BH746584 429 bp DNA linear GSS 27-FEB-2002
SALK_044872.30.00.x Arabidopsis thaliana TDNA insertion lines
Arabidopsis thaliana genomic clone SALK_044872.30.00.x, genomic
survey sequence.

BH746584 429 bp DNA linear GSS 27-FEB-2002
SALK_044872.30.00.x Arabidopsis thaliana TDNA insertion lines
Arabidopsis thaliana genomic clone SALK_044872.30.00.x, genomic
survey sequence.

BH746584 429 bp DNA linear GSS 27-FEB-2002
SALK_044872.30.00.x Arabidopsis thaliana TDNA insertion lines
Arabidopsis thaliana genomic clone SALK_044872.30.00.x, genomic
survey sequence.

BH746584 429 bp DNA linear GSS 27-FEB-2002
SALK_044872.30.00.x Arabidopsis thaliana TDNA insertion lines
Arabidopsis thaliana genomic clone SALK_044872.30.00.x, genomic
survey sequence.

BH746584 429 bp DNA linear GSS 27-FEB-2002
SALK_044872.30.00.x Arabidopsis thaliana TDNA insertion lines
Arabidopsis thaliana genomic clone SALK_044872.30.00.x, genomic
survey sequence.

BH746584 429 bp DNA linear GSS 27-FEB-2002
SALK_044872.30.00.x Arabidopsis thaliana TDNA insertion lines
Arabidopsis thaliana genomic clone SALK_044872.30.00.x, genomic
survey sequence.

BH746584 429 bp DNA linear GSS 27-FEB-2002
SALK_044872.30.00.x Arabidopsis thaliana TDNA insertion lines
Arabidopsis thaliana genomic clone SALK_044872.30.00.x, genomic
survey sequence.

BH746584 429 bp DNA linear GSS 27-FEB-2002
SALK_044872.30.00.x Arabidopsis thaliana TDNA insertion lines
Arabidopsis thaliana genomic clone SALK_044872.30.00.x, genomic
survey sequence.

BH746584 429 bp DNA linear GSS 27-FEB-2002
SALK_044872.30.00.x Arabidopsis thaliana TDNA insertion lines
Arabidopsis thaliana genomic clone SALK_044872.30.00.x, genomic
survey sequence.

BH746584 429 bp DNA linear GSS 27-FEB-2002
SALK_044872.30.00.x Arabidopsis thaliana TDNA insertion lines
Arabidopsis thaliana genomic clone SALK_044872.30.00.x, genomic
survey sequence.

BH746584 429 bp DNA linear GSS 27-FEB-2002
SALK_044872.30.00.x Arabidopsis thaliana TDNA insertion lines
Arabidopsis thaliana genomic clone SALK_044872.30.00.x, genomic
survey sequence.

```

JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Unpublished
2 (bases 1 to 1110)
Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
Totoki,Y., Watanabe,H. and Sakaki,Y.
Direct Submission
Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-chou,Tsukumi-ku, Yokohama, Kanagawa 230-0045, Japan
(E-mail:chimbases@gsc.riken.go.jp, URL:http://hgp-gsc.riken.go.jp/,
Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC end
was generated during the R&D process and may have higher chance of
clone tracking errors.
PRIMERS
Sequencing: M13Rev
LIBRARY
Vector : PKS145
R.Site 1 : SacI
R.Site 2 : SacI.
Location/Qualifiers
1. .1110
/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
/clone="PTB-079807.R"
/sex="male"
/cell_type="lymphoblast"
/clone_lib="PTB Chimpanzee Male BAC Library"

ORIGIN
Query Match 91.1%; Score 16.4; DB 29; Length 1110;
Best Local Similarity 94.4%; Pred. No. 7.9e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TCGTCGATCGACGGGG 18
|||||
Db 611 TCGTCGCTCGACGGGG 594

RESULT 5
BQ102588 489 bp mRNA linear EST 12-APR-2002
LOCUS MIN172 MIN Nitrogen-replete Schizophyllum library Schizophyllum
DEFINITION commune cDNA 5' similar to stomatin, mRNA sequence.
ACCESSION BQ102588
VERSION BQ102588.1 GI:20144047
SOURCE EST.
ORGANISM Schizophyllum commune
Schizophyllum commune
Schizophyllum commune
Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
Agaricales; Schizophyllaceae; Schizophyllum.
REFERENCE
AUTHORS Jackson,E.N., Abner,J., Honaas,L., Hittinger,C.T., Green,A.,
Lilly,W.W. and Gathman,A.C.
TITLE Expressed sequence tags from Schizophyllum commune nitrogen-replete
and nitrogen-limited libraries, 2002
JOURNAL Unpublished (2002)
COMMENT Contact: Gathman AC
Biology Department
Southeast MO State University
1 University Plaza, Cape Girardeau, MO 63701, USA
Tel: 5736512361
Fax: 5739866433
Email: agathman@semo.edu
Seq primer: T3
POLYA=NO. Location/Qualifiers
1. .489
/organism="Schizophyllum commune"
/mol_type="mRNA"
/strain="4-40"
/db_xref="taxon:5334"
/tissue_type="mycelium"

FEATURES
source
BX448966
LOCUS BX448966 Homo sapiens FETAL LIVER Homo sapiens cDNA clone
DEFINITION CS0DM012YN11 5-PRIME, mRNA sequence.
ACCESSION BX448966
VERSION BX448966.1 GI:31035980
KEYWORDS EST.

/clone_lib="MIN Nitrogen-replete Schizophyllum library"
/note="Vector: lambda Zap; Site 1: EcoRI; Site 2: XhoI;
4-day-old mycelia of Schizophyllum commune were
transferred from minimal (nitrogen-replete) medium to
fresh minimal medium. RNA was extracted twelve hours after
transfer and cDNAs prepared."

ORIGIN
Query Match 88.9%; Score 16; DB 13; Length 489;
Best Local Similarity 100.0%; Pred. No. 9.9e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 CGTCGATCGACGGGG 18
|||||
Db 143 CGTCGATCGACGGGG 158

RESULT 6
CE730492/c
LOCUS CE730492 705 bp DNA linear GSS 30-SEP-2003
DEFINITION tigr-gss-dog-17000315416995 Dog Library Canis familiaris genomic,
genomic survey sequence.
ACCESSION CE730492
VERSION CE730492.1 GI:37070612
KEYWORDS GSS.
SOURCE Canis familiaris (dog)
ORGANISM Canis familiaris
Canis familiaris
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE
AUTHORS Kirkness,E.F., Baina,V., Halpern,A.L., Levy,S., Remington,K.,
Rusch,D.B., Delcher,A.L., Pop,M., Wang,W., Fraser,C.M. and
Venter,J.C.
TITLE The dog genome: survey sequencing and comparative analysis
JOURNAL Science 301 (5641), 1898-1903 (2003)
MEDLINES 22875432
PUBMED 14512627
COMMENT Contact: Kirkness EP
The Institute for Genomic Research
Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
Rockville, MD 20850, USA
Tel: 301-838-0200
Fax: 301-838-0208
Email: ekirknes@tigr.org
Class: shotgun.
Location/Qualifiers
1. .705
/organism="Canis familiaris"
/mol_type="genomic DNA"
/strain="Standard Poodle"
/db_xref="taxon:9615"
/clone_lib="Dog Library"
/note="Site 1: BstXI; Libraries were prepared from
peripheral blood"

FEATURES
source
BX448966
LOCUS BX448966 Homo sapiens FETAL LIVER Homo sapiens cDNA clone
DEFINITION CS0DM012YN11 5-PRIME, mRNA sequence.
ACCESSION BX448966
VERSION BX448966.1 GI:31035980
KEYWORDS EST.

ORIGIN
Query Match 88.9%; Score 16; DB 29; Length 705;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCGTCGATCGACGGGG 16
|||||
Db 297 TCGTCGATCGACGGGG 282

RESULT 7
BX448966
LOCUS BX448966 Homo sapiens FETAL LIVER Homo sapiens cDNA clone
DEFINITION CS0DM012YN11 5-PRIME, mRNA sequence.
ACCESSION BX448966
VERSION BX448966.1 GI:31035980
KEYWORDS EST.

```

SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 893)
 AUTHORS Li, W.B., Gruber, C., Jesse, J. and Polayes, D.
 TITLE Full-length cDNA libraries and normalization
 JOURNAL Unpublished (2001)
 COMMENT Contact: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 EVRY cedex - France
 Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr
 was not normalized. Library was constructed by Life Technologies, a
 division of Invitrogen. Contact : Peng Liang Email :
 fliang@lifetech.com URL : http://fulllength.invitrogen.com/
 Invitrogen Corporation 1600 Faraday Avenue Genoscope sequence ID :
 CS0AM012CG06QPL.

FEATURES source
 Location/Qualifiers
 1..893
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="CS0AM012YN11"
 /tissue_type="FETAL LIVER"
 /dev_stage="fetal"
 /clone_lib="Homo sapiens FETAL LIVER"
 /note="Organ: liver; Vector: pCMVSPORT 6; 1st strand cDNA
 was primed with a NotI-oligo(dT) primer. Five prime end
 enriched, double-strand cDNA was digested with Not I and
 cloned into the Not I and EcoRV sites of the pCMVSPORT 6
 vector. Library was not normalized."

ORIGIN
 Query Match 86.7%; Score 15.6; DB 13; Length 893;
 Best Local Similarity 93.8%; Pred. No. 1.7e+04;
 Matches 15; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 GCGTCGATCGAGGGG 17
 |||||
 Db 59 GCGTCGATCGAGGGG 74

RESULT 8
 AV128107 125 bp mRNA linear EST 01-JUL-1999
 LOCUS AV128107 Mus musculus C57BL/6J 11-day embryo Mus musculus cDNA
 DEFINITION clone 2700054B15, mRNA sequence.

ACCESSION AV128107 GI:5314341
 VERSION AV128107
 KEYWORDS EST.
 SOURCE Mus musculus (house mouse)
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 125)
 AUTHORS Carninci, P., Shibata, K., Ozawa, Y., Konno, H., Itoh, M., Aizawa, K.,
 Akahira, S., Akiyama, J., Fukuda, S., Fukunishi, Y., Funayama, T.,
 Hara, A., Hayatsu, N., Hori, F., Ishikawa, T., Itoh, M., Izawa, M.,
 Kawai, J., Kikuchi, N., Kojima, Y., Matsuyama, T., Naitsuma, H., Oda, H.,
 Owa, C., Sato, K., Shibata, Y., Shigemoto, Y., Shiraki, T., Sogabe, Y.,
 Sugahara, Y., Suzuki, H., Suzuki, H., Tateno, M., Tomaru, Y.,
 Tomimaga, N., Watanabe, S., Yagame, M., Yamamura, T., Yokota, T.,
 Yoshino, M., Muramatsu, M., Okazaki, Y. and Hayashizaki, Y.
 RIKEN Mouse ESTs
 Unpublished (1999)
 CONTACT Chie Owa
 Genomic Science Laboratory
 RIKEN
 3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
 Tel: 81-298-36-9145
 Fax: 81-298-36-9098
 Email: genome-res@rtc.riken.go.jp

Thermostabilization and thermoactivation of thermolabile enzymes by

trehalose and its application for the synthesis of full length cDNA
 (Proc. Natl. Acad. Sci. U.S.A. 95(2):520-524 (1998))
 Transcriptional sequencing: A method for DNA sequencing using RNA
 polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998))
 Please visit our web site (<http://genome.rtc.riken.go.jp>) for
 further details.

FEATURES source
 Location/Qualifiers

1..125
 /organism="Mus musculus"
 /mol_type="mRNA"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="2700054B15"
 /sex="mixed"
 /dev_stage="11-day embryo"
 /clone_lib="Mus musculus C57BL/6J 11-day embryo"

ORIGIN

Query Match 85.6%; Score 15.4; DB 9; Length 125;
 Best Local Similarity 94.1%; Pred. No. 1.4e+04;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GCGTCGATCGAGGGG 18
 |||||
 Db 15 GCGTCGATCGAGGGG 31

RESULT 9

AA662789 320 bp mRNA linear EST 12-NOV-1997
 LOCUS AA662789.1 NCI CGAP Pr22 Homo sapiens cDNA clone IMAGE:1218808 3,
 DEFINITION similar to gb:X12794_cds1 V-ERBA RELATED PROTEIN EAR-2 (HUMAN);
 mRNA sequence.

ACCESSION AA662789 GI:2616780
 VERSION AA662789.1
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 320)
 AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 JOURNAL Unpublished (1997)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael R.
 Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D.
 CDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality
 Seq primer: -40ml3 fwd. ET from Amersham
 High quality sequence stop: 1.

FEATURES source
 Location/Qualifiers

1..320
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:1218808"
 /sex="male"
 /tissue_type="normal prostate"
 /lab_host="DH10B"
 /clone_lib="NCI CGAP Pr22"

/note="Organ: prostate; Vector: pT7T3D-Pac (Pharmacia)
 with a modified polylinker; 1st strand cDNA was prepared
 from normal prostate bulk tissue, and was then primed with
 a Not I - oligo(dT) primer. Double-stranded cDNA was

ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. Library is normalized, and was constructed by Bento Soares and M. Fatima Bonaldo. "

ORIGIN

Query Match 85.6%; Score 15.4; DB 9; Length 320;
Best Local Similarity 94.1%; Pred. No. 1.7e+04;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GCGTCGATGCAGGGGGG 18
||| ||||| ||||| |||||
Db 68 GCGCCGATGCAGGGGGG 52

RESULT 10

BE400545/c
LOCUS 366 bp mRNA linear EST 21-JUL-2000
DEFINITION AWS004.G12F000328 ITEC AWS Wheat Meiotic Stage Library Triticum aestivum cDNA clone AWS004.G12, mRNA sequence.

ACCESSION BE400545
VERSION BE400545.1 GI:9360013
KEYWORDS EST
SOURCE Triticum aestivum (bread wheat)

ORGANISM Triticum aestivum (bread wheat)

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae; Triticum.

1 (bases 1 to 366)

AUTHORS Anderson, O.A., Appels, R., Bailey, P., Blake, T., Close, T., Cloutier, S., Dubcovsky, J., Feuillet, C., Gale, M., Graner, A., Gustafson, P., Hermann, R.G., Holton, T., Jacquemais, J.M., Jia, J., Joudrier, P., Langridge, P., Lazo, G.R., Lin, J.J., McGuire, P., Ogihara, Y., Pecchioni, N., Qualset, C., Schuch, W., Selvaraj, G., Shariflou, M., Sorrells, M., Warburton, M., and Wenzel, G.

TITLE International Triticaceae EST Cooperative (ITEC): Production of Expressed Sequence Tags for Species of the Triticeae

JOURNAL

COMMENT Unpublished (2000)

Contact: Langridge P
Special Research Centre, Basic and Applied Plant Molecular Biology
Waite Campus, University of Adelaide, Glen Osmond SA 5064 AUSTRALIA
Tel: 61 8 8303 7368
Fax: 61 8 8303 7102

Email: plangridge@waite.adelaide.edu.au

International Triticaceae EST Cooperative (ITEC)

<http://wheat.pw.usda.gov/genome>.

FEATURES

source

1..366
Location/Qualifiers
/organism="Triticum aestivum"
/mol_type="mRNA"
/cultivar="Chinese Spring"
/db_xref="taxon:4565"
/clone="AWS004.G12"

/tissue_type="excised florets"
/dev_stage="meiotic stage no later than metaphase I"
/clone_lib="ITEC AWS Wheat Meiotic Stage Library"
/notes="Vector: pSport 1 (Life Technologies cat. no. 18248-013); Site 1: SalI; Library constructed in pSport 1. Directionally cloned using the Superscript Plasmid System for cDNA synthesis and plasmid cloning. M13 Reverse sequencing primer used to obtain 5' sequence data. 1.4 kbp average insert size."

ORIGIN

Query Match 85.6%; Score 15.4; DB 10; Length 366;
Best Local Similarity 94.1%; Pred. No. 1.7e+04;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GCGTCGATGCAGGGGGG 18
||| ||||| ||||| |||||
Db 79 GCGTCGATGCAGGGGGG 63

RESULT 11

CA706144/c
LOCUS

DEFINITION

CA706144

VERSION

KEYWORDS

SOURCE

ORGANISM

CA706144.1 GI:25427937

Triticum aestivum (bread wheat)

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Unpublished (2002)

Contact: Scott V. Tingey

Crop Genetics

E. I. DuPont de Nemours and Company

1 Innovation Way, P.O. Box 6104, Newark, DE 19714-6104, USA

Tel: 302-631-2602

Fax: 302-631-2607

Email: Scott.V.Tingey@USA.dupont.com

Seq primer: M13.

Location/Qualifiers

1..442

/organism="Triticum aestivum"

/mol_type="mRNA"

/db_xref="taxon:4565"

/clone="wdk1c.pk022.b10"

/tissue_type="kernel"

/clone_lib="wdk1c"

/note="Vector: pBluescript SK+; Wheat (Triticum aestivum L.) developing kernel, 3 days after anthesis."

ORIGIN

Query Match 85.6%; Score 15.4; DB 14; Length 442;

Best Local Similarity 94.1%; Pred. No. 1.8e+04;

Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GCGTCGATGCAGGGGGG 18

Db 199 GAGTCGATGCAGGGGGG 183

RESULT 12

CA693337/c

LOCUS

DEFINITION

CA693337

VERSION

KEYWORDS

SOURCE

ORGANISM

CA693337.1 GI:25415123

Triticum aestivum (bread wheat)

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Unpublished (2002)

Contact: Scott V. Tingey

Crop Genetics

E. I. DuPont de Nemours and Company

1 Innovation Way, P.O. Box 6104, Newark, DE 19714-6104, USA

Tel: 302-631-2602

Fax: 302-631-2607

Email: Scott.V.Tingey@USA.dupont.com

Seq primer: M13.

Location/Qualifiers

1..470

/organism="Triticum aestivum"

/mol_type="mRNA"

/db_xref="taxon:4565"

/clone="wim96.pk061.b18"

/tissue_type="kernel"

/note="Vector: pBluescript SK+; Wheat (Triticum aestivum L.) developing kernel, 3 days after anthesis."

ORIGIN

Query Match 85.6%; Score 15.4; DB 14; Length 442;

Best Local Similarity 94.1%; Pred. No. 1.8e+04;

Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GCGTCGATGCAGGGGGG 18

Db 199 GAGTCGATGCAGGGGGG 183

RESULT 12

CA693337/c

LOCUS

DEFINITION

CA693337

VERSION

KEYWORDS

SOURCE

ORGANISM

CA693337.1 GI:25415123

Triticum aestivum (bread wheat)

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Unpublished (2002)

Contact: Scott V. Tingey

Crop Genetics

E. I. DuPont de Nemours and Company

1 Innovation Way, P.O. Box 6104, Newark, DE 19714-6104, USA

Tel: 302-631-2602

Fax: 302-631-2607

Email: Scott.V.Tingey@USA.dupont.com

Seq primer: M13.

Location/Qualifiers

1..470

/organism="Triticum aestivum"

/mol_type="mRNA"

/db_xref="taxon:4565"

/clone="wim96.pk061.b18"

/tissue_type="kernel"

/note="Vector: pBluescript SK+; Wheat (Triticum aestivum L.) developing kernel, 3 days after anthesis."

FEATURES source Location/Qualifiers

1..470

/organism="Triticum aestivum"

/mol_type="mRNA"

/cultivar="Stephens"

/db_xref="taxon:4565"

/clone="wlm96.pk061.b18"

/tissue_type="leaf"

/clone_lib="wlm96"

/note="Vector: pluscript SK+, Site 1: EcoRI; Site 2: XhoI; Wheat (Triticum aestivum L.) seedlings 96 hr after inoculation w/ E. graminis"

ORIGIN

Query Match 85.6%; Score 15.4; DB 14; Length 470;

Best Local Similarity 94.1%; Pred. No. 1.8e+04;

Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GCGTCGATCGAGGGGG 18

Db 136 GCGTCGATCGAGGGGG 120

RESULT 13

AU001427

LOCUS

DEFINITION AU001427 Bombyx mori p50(Daizo) Bombyx mori cDNA clone fbm0407f, mRNA sequence.

ACCESSION AU001427

VERSION AU001427.1 GI:4157671

KEYWORDS EST.

SOURCE Bombyx mori (domestic silkworm)

ORGANISM Bombyx mori

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Bombycoidea; Bombycidae; Bombyx.

REFERENCE 1 (bases 1 to 499)

AUTHORS Mita K., Morimoto, M., Shimada, T., Okano, K. and Maeda, S.

TITLE Establishment of cDNA database of Bombyx mori

JOURNAL Unpublished (1999)

COMMENT Contact: Mita K

Genome Research Group

National Institute of Agrobiological Sciences

Owashi 1-2, Tsukuba, Ibaraki 305-8634, Japan

Email: kmita@nias.affrc.go.jp

PROJECT = CREST project by JST.

FEATURES source Location/Qualifiers

1..499

/organism="Bombyx mori"

/mol_type="mRNA"

/strain="p50(Daizo)"

/db_xref="taxon:7091"

/clone="fbm0407f"

/clone_lib="Bombyx mori p50(Daizo)"

ORIGIN

Query Match 85.6%; Score 15.4; DB 9; Length 499;

Best Local Similarity 94.1%; Pred. No. 1.8e+04;

Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GCGTCGATCGAGGGGG 18

Db 411 GCGTCGATCGAGGGGG 427

RESULT 14

CF639409

LOCUS

DEFINITION D15_D01 Filamentous Forced Diploid Ustilago maydis CDNA 3', mRNA sequence.

ACCESSION CF639409

VERSION CF639409.1 GI:37403984

KEYWORDS EST.

SOURCE Ustilago maydis

ORGANISM Ustilago maydis

Eukaryota; Fungi; Basidiomycota; Ustilaginomycetes; Ustilaginomycetidae; Ustilaginales; Ustilaginaceae; Ustilago.

REFERENCE 1 (bases 1 to 553)

AUTHORS Nugent, K.G., Choffe, K. and Saville, B.J.

TITLE Gene Expression during Ustilago maydis Diploid Filamentous Growth: EST Library Creation and Analyses

JOURNAL Unpublished (2003)

COMMENT Contact: Barry J. Saville

Saville Lab

University of Toronto

3359 Mississauga Road North, Mississauga, ON, L5L 1C6, Canada

Tel: 905 569 4702

Fax: 905 828 3792

Email: bsaville@utoronto.ca

Plate: UTM-UM-D126/7-015-UTM row: 01 column: D

Seq primer: T7 Reverse fs' GAGTATACGACTACTATAGGG 3')

High quality sequence stop: 553.

FEATURES source Location/Qualifiers

1..553

/organism="Ustilago maydis"

/mol_type="mRNA"

/strain="FBD12"

/db_xref="taxon:5270"

/cell_type="Mycelia"

/dev_stage="Filamentous diploid"

/clone_lib="Filamentous Forced Diploid"

/note="Vector: pSPORT; mRNA was extracted from diploid mycelia. A cDNA library was constructed and unidirectionally cloned into pSPORT plasmid, with the use of the Superscript II cDNA Library Construction Kit."

ORIGIN

Query Match 85.6%; Score 15.4; DB 14; Length 553;

Best Local Similarity 94.1%; Pred. No. 1.8e+04;

Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TCGTCGATCGAGGGGG 17

Db 226 TCGTCGATCGAGGGG 242

RESULT 15

BH797911

LOCUS

DEFINITION BH797911.1 565 bp DNA linear GSS 25-APR-2002 1008096D04.xl 1008 - RescueMu Grid I Zea mays genomic, genomic survey sequence.

ACCESSION BH797911

VERSION BH797911.1 GI:20307382

KEYWORDS GSS.

SOURCE Zea mays

ORGANISM Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.

REFERENCE 1 (bases 1 to 565)

AUTHORS Walbot, V.

TITLE Maize genomic sequences found using engineered RescueMu transposon

JOURNAL Unpublished (2001)

COMMENT Contact: Walbot V

Department of Biological Sciences

Stanford University

855 California Ave, Palo Alto, CA 94304, USA

Tel: 650 723 2227

Fax: 650 725 8221

Email: walbot@stanford.edu

Possible ligation site so sequence was trimmed. Post-ligation sequence submitted separately.

Plate: 1008096 row: 26

Class: transposon-tagged.

FEATURES source Location/Qualifiers

1..565


```
/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="mixed background W23/Al88/B73"
/db_xref="taxon:4577"
/tissue_type="leaf"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="1008 - RescueMu Grid I"
/note="Organ: leaf; Vector: RescueMu (engineered from
pBlueScript backbone); Site 1: BamHI; Site 2: BglII;
RescueMu is a 4.9 kb, modified maize Mu transposon
designed to allow plasmid rescue from total genomic DNA.
Mu elements insert preferentially into transcription
units. For more information on RescueMu, go to the web
site www.zmdb.iastate.edu and follow the links for
'RescueMu.' Grid I was grown at Berkeley in 2001. DNA was
extracted from leaf punches, double digested using BamHI
and BglII, and ligated to form circular plasmids. DH10B
cells were transformed and then screened on LB plates with
ampicillin."
```

ORIGIN

```
Query Match      85.6%; Score 15.4; DB 28; Length 565;
Best Local Similarity 94.1%; Pred. No. 1.8e+04;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 TGCCTCGATCGAGGGG 17
      ||| ||||| |||||
Db      521 TGCCTCGATCGAGGGG 537
```

Search completed: July 2, 2004, 13:33:02
Job time : 1351.14 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 2, 2004, 06:05:50 ; Search time 134.89 Seconds

(without alignments)
566.887 Million cell updates/sec

Title: US-10-068-160-16

Perfect score: 18

Sequence: 1 tgcgtcgatgcagggggg 18

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747725

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_29Jan04.*
1: Geneseqn1980s.*
2: Geneseqn1990s.*
3: Geneseqn2000s.*
4: Geneseqn2001as.*
5: Geneseqn2001bs.*
6: Geneseqn2002s.*
7: Geneseqn2003as.*
8: Geneseqn2003bs.*
9: Geneseqn2003cs.*
10: Geneseqn2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	18	100.0	20	4	AAC80662	Immunogen
2	18	100.0	20	4	AAC80661	Immunogen
3	18	100.0	20	4	AAC80620	Immunogen
4	18	100.0	20	4	AAS09631	Immunorea
5	18	100.0	20	4	AAS09590	Immunorea
6	18	100.0	20	4	AAS09632	Immunorea
7	18	100.0	20	6	ABL35510	Immunosti
8	18	100.0	20	6	ABL35510	Immunosti
9	18	100.0	20	6	ABL35510	Immunosti
10	18	100.0	20	7	ACC48298	CpG oligo
11	18	100.0	20	7	ACC48312	CpG oligo
12	18	100.0	20	7	ACC48306	CpG oligo
13	18	100.0	20	7	ACC48319	CpG oligo
14	18	100.0	20	8	ACC83117	D class C
15	18	100.0	20	8	ACC83124	D class C
16	18	100.0	20	9	ADD01050	CpG D oli
17	17	94.4	19	4	AAC80663	Immunogen
18	17	94.4	19	4	AAS09633	Immunorea
19	17	94.4	19	6	ABL35511	Immunosti
20	16.4	91.1	18	6	ABL35587	Immunosti
21	16.4	91.1	18	6	ABL35577	Immunosti
22	16.4	91.1	18	6	ABL35625	Immunosti
23	16.4	91.1	18	9	ADD01052	CpG D oli

ALIGNMENTS

RESULT 1
AAC80662
ID AAC80662 standard; DNA; 20 BP.
XX
AC AAC80662;
XX
DT 14-FEB-2001 (first entry)
XX
DE Immunogenic CpG oligodeoxynucleotide, SEQ ID NO:82.
XX
KW CpG oligodeoxynucleotide; unmethylated; antigen-presenting cell;
KW immunogenic; cytokine release; natural killer cell; NK cell activation;
KW cell-mediated immune response; T-cell response; humoral response;
KW B-cell response; antibody production; immune response induction; vaccine;
KW allergy; asthma; infection; bacterial; viral; fungal; protozoal;
KW parasitic; tuberculosis; AIDS; autoimmune disease; lupus erythematosus;
KW rheumatoid arthritis; multiple sclerosis; solid tumour; cancer;
KW immune deficiency; biological warfare agent; cytostatic; antiarthritic;
KW antimicrobial; antiallergic; protozoicide; tuberculostatic;
KW antiasthmatic; dermatological; phosphorothioate; ss.
XX
OS Synthetic.
XX
PN WO200061151-A2.
XX
PD 19-OCT-2000.
XX
PF 12-APR-2000; 2000WO-US009839.
XX
PR 12-APR-1999; 99US-0128898P.
XX
PA (KLIN/) KLINMAN D.
PA (ISHI/) ISHII K.
PA (VERT/) VERTHELYI D.
PI Klinman D, Ishii K, Verthelyi D;
XX
DR WPI; 2001-006880/01.
XX
PT Novel oligonucleotides useful for the prevention and treatment of
PT allergies, cancer, and autoimmune disorders and for ameliorating symptoms
PT resulting from exposure to a bio-warfare agent.
XX
PS Claim 4; Page 36; 46pp; English.
XX
CC The invention relates to novel immunogenic CpG oligodeoxynucleotides

24	16.4	91.1	20	4	AAC80619	Immunogen
25	16.4	91.1	20	4	AAC80621	Immunogen
26	16.4	91.1	20	4	AAC80652	Immunogen
27	16.4	91.1	20	4	AAC80614	Immunogen
28	16.4	91.1	20	4	AAC80612	Immunogen
29	16.4	91.1	20	4	AAC80617	Immunogen
30	16.4	91.1	20	4	AAC80618	Immunogen
31	16.4	91.1	20	4	AAC80623	Immunogen
32	16.4	91.1	20	4	AAS09622	Immunorea
33	16.4	91.1	20	4	AAS09591	Immunorea
34	16.4	91.1	20	4	AAS09582	Immunorea
35	16.4	91.1	20	4	AAS09587	Immunorea
36	16.4	91.1	20	4	AAS09589	Immunorea
37	16.4	91.1	20	4	AAS09593	Immunorea
38	16.4	91.1	20	4	AAS09584	Immunorea
39	16.4	91.1	20	4	AAS09652	Immunorea
40	16.4	91.1	20	4	AAS09588	Immunorea
41	16.4	91.1	20	6	ABL35576	Immunosti
42	16.4	91.1	20	6	ABL35582	Immunosti
43	16.4	91.1	20	6	ABL35586	Immunosti
44	16.4	91.1	20	6	ABL35568	Immunosti
45	16.4	91.1	20	6	ABL35624	Immunosti

CC (AAC80581-C80723). The oligonucleotide are at least 10 bases long and
 CC comprise one of the generic sequences 5'-NNNT-CpG-WNNN-3' or 5'-RY-CpG-RY
 CC -3'. The central CpG motif is unmethylated, and the oligonucleotides
 CC optionally have phosphorothioate linkages which make them more resistant
 CC to degradation. The invention also relates to an oligonucleotide delivery
 CC complex comprising an oligonucleotide of the invention and a targeting
 CC agent, and a pharmaceutical composition comprising the oligonucleotide
 CC delivery complex. The oligonucleotides are able to induce either a cell-
 CC mediated (T-cell) response or a humoral (B-cell, antibody) response, with
 CC oligonucleotides of the sequence 5'-RY-CpG-RY-3', being able to induce a
 CC cell-mediated response, and those of the sequence 5'-NNNT-CpG-WNNN-3',
 CC being able to induce a humoral response. It is thought that after
 CC administration, the oligonucleotide acts on antigen-presenting cells
 CC (e.g., macrophages and dendritic cells), which then release cytokines,
 CC leading to activation of natural killer (NK) cells. A cell-mediated or
 CC humoral response can then occur by activation of T- or B-cells. The
 CC induction of an immune response is useful for treating, preventing or
 CC ameliorating an allergic reaction (preferably asthma), or an infection,
 CC where an immunogenic CpG oligonucleotide is administered either alone or
 CC in combination with an anti-allergenic agent or anti-infectious agent.
 CC The allergic conditions which may be treated include eczema, allergic
 CC rhinitis, hayfever, urticaria, food allergies and other atopic
 CC conditions, and the infections which may be treated include viral,
 CC bacterial, fungal and protozoal infections such as tuberculosis, AIDS,
 CC leishmania and schistosomiasis. Immune response induction may also be
 CC used in the treatment of an autoimmune disorder (e.g., lupus
 CC erythematosus, rheumatoid arthritis and multiple sclerosis), a disease
 CC associated with immune system deficiency, and symptoms resulting from
 CC exposure to an agent of biological warfare. An immunogenic CpG
 CC oligonucleotide, either alone or in combination with an anti-cancer
 CC agent, is useful for treating solid tumour cancer. The induction of an
 CC immune response is used in antisense therapy and to improve the efficacy
 CC of a vaccine. The oligonucleotide is preferably administered to
 CC lymphocytes ex vivo, producing activated lymphocytes which are then
 CC administered to the host. The present sequence represents an immunogenic
 CC CpG oligodeoxynucleotide of the invention

XX SQ Sequence 20 BP; 2 A; 3 C; 12 G; 3 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 4; Length 20;
 Best Local Similarity 100.0%; Pred. No. 17;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGGCTCGATGCGAGGGG 18
 Db 3 TGGCTCGATGCGAGGGG 20

RESULT 2
 AAC80561
 ID AAC80661 standard; DNA; 20 BP.
 AC AAC80661;
 XX
 XX 14-FEB-2001 (first entry)
 XX
 XX Immunogenic CpG oligodeoxynucleotide, SEQ ID NO:81.
 DE
 XX CpG oligodeoxynucleotide; unmethylated, antigen-presenting cell;
 KW immunogenic; cytokine release; natural killer cell; NK cell activation;
 KW cell-mediated immune response; T-cell response; humoral response;
 KW B-cell response; antibody production; immune response induction; vaccine;
 KW allergy; asthma; infection; bacterial; viral; fungal; protozoal;
 KW parasitic; tuberculosis; AIDS; autoimmune disease; lupus erythematosus;
 KW rheumatoid arthritis; multiple sclerosis; solid tumour; cancer;
 KW immune deficiency; biological warfare agent; cytostatic; antiarthritic;
 KW antimicrobial; antiallergic; protozoal; tuberculothioate; ss.
 KW antiasthmatic; dermatological; phosphorothioate; ss.
 OS Synthetic.
 XX
 XX WO200061151-A2.
 PN
 XX

PD 19-OCT-2000.
 XX 12-APR-2000; 2000WO-US009839.
 PF
 XX 12-APR-1999; 99US-0128898P.
 PR
 XX (KLIN/) KLINMAN D.
 PA (ISHI/) ISHII K.
 PA (VERT/) VERTHELYI D.
 XX
 XX Klinman D, Ishii K, Verthelyi D;
 FI WPI; 2001-005880/01.
 XX
 XX Novel oligonucleotides useful for the prevention and treatment of
 DR allergies, cancer, and autoimmune disorders and for ameliorating symptoms
 PT resulting from exposure to a bio-warfare agent.
 PT
 XX Claim 4; Page 36; 46pp; English.
 PS
 XX The invention relates to novel immunogenic CpG oligodeoxynucleotides
 CC (AAC80581-C80723). The oligonucleotide are at least 10 bases long and
 CC comprise one of the generic sequences 5'-NNNT-CpG-WNNN-3' or 5'-RY-CpG-RY
 CC -3'. The central CpG motif is unmethylated, and the oligonucleotides
 CC optionally have phosphorothioate linkages which make them more resistant
 CC to degradation. The invention also relates to an oligonucleotide delivery
 CC complex comprising an oligonucleotide of the invention and a targeting
 CC agent, and a pharmaceutical composition comprising the oligonucleotide
 CC delivery complex. The oligonucleotides are able to induce either a cell-
 CC mediated (T-cell) response or a humoral (B-cell, antibody) response, with
 CC oligonucleotides of the sequence 5'-RY-CpG-RY-3', being able to induce a
 CC cell-mediated response, and those of the sequence 5'-NNNT-CpG-WNNN-3',
 CC being able to induce a humoral response. It is thought that after
 CC administration, the oligonucleotide acts on antigen-presenting cells
 CC (e.g., macrophages and dendritic cells), which then release cytokines,
 CC leading to activation of natural killer (NK) cells. A cell-mediated or
 CC humoral response can then occur by activation of T- or B-cells. The
 CC induction of an immune response is useful for treating, preventing or
 CC ameliorating an allergic reaction (preferably asthma), or an infection,
 CC where an immunogenic CpG oligonucleotide is administered either alone or
 CC in combination with an anti-allergenic agent or anti-infectious agent.
 CC The allergic conditions which may be treated include eczema, allergic
 CC rhinitis, hayfever, urticaria, food allergies and other atopic
 CC conditions, and the infections which may be treated include viral,
 CC bacterial, fungal and protozoal infections such as tuberculosis, AIDS,
 CC leishmania and schistosomiasis. Immune response induction may also be
 CC used in the treatment of an autoimmune disorder (e.g., lupus
 CC erythematosus, rheumatoid arthritis and multiple sclerosis), a disease
 CC associated with immune system deficiency, and symptoms resulting from
 CC exposure to an agent of biological warfare. An immunogenic CpG
 CC oligonucleotide, either alone or in combination with an anti-cancer
 CC agent, is useful for treating solid tumour cancer. The induction of an
 CC immune response is used in antisense therapy and to improve the efficacy
 CC of a vaccine. The oligonucleotide is preferably administered to
 CC lymphocytes ex vivo, producing activated lymphocytes which are then
 CC administered to the host. The present sequence represents an immunogenic
 CC CpG oligodeoxynucleotide of the invention

XX SQ Sequence 20 BP; 2 A; 3 C; 12 G; 3 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 4; Length 20;
 Best Local Similarity 100.0%; Pred. No. 17;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGGCTCGATGCGAGGGG 18
 Db 3 TGGCTCGATGCGAGGGG 20

RESULT 3
 AAC80620
 ID AAC80620 standard; DNA; 20 BP.
 XX

AAC80620;
 14-FEB-2001 (first entry)
 Immunogenic CpG oligodeoxynucleotide, SEQ ID NO:40.
 CpG oligodeoxynucleotide; unmethylated; antigen-presenting cell;
 immunogenic; cytokine release; natural killer cell; NK cell activation;
 cell-mediated immune response; T-cell response; humoral response; vaccine;
 B-cell response; antibody production; immune response induction; allergic
 allergy; asthma; infection; bacterial; viral; fungal; protozoal;
 parasitic; tuberculosis; AIDS; autoimmune disease; lupus erythematosus;
 rheumatoid arthritis; multiple sclerosis; solid tumour; cancer;
 immune deficiency; biological warfare agent; cytostatic; antiarthritic;
 antimicrobial; antiallergic; protozoicide; tuberculostatic;
 antiasthmatic; dermatological; phosphorothioate; ss.
 Synthetic.
 WO200061151-A2.
 19-OCT-2000.
 12-APR-2000; 2000WO-US009839.
 12-APR-1999; 99US-0128898P.
 (KLIN/) KLINMAN D.
 (ISHI/) ISHII K.
 (VERT/) VERTHELYI D.
 Klinman D, Ishii K, Verthelyi D;
 WPI; 2001-006880/01.
 Novel oligonucleotides useful for the prevention and treatment of
 allergies, cancer, and autoimmune disorders and for ameliorating symptoms
 resulting from exposure to a bio-warfare agent.
 Claim 4; Page 30; 46pp; English.
 The invention relates to novel immunogenic CpG oligodeoxynucleotides
 (AAC80591-C80723). The oligonucleotide are at least 10 bases long and
 comprise one of the generic sequences 5'-NNNT-CpG-WNNN-3' or 5'-RY-CpG-RY
 -3'. The central CpG motif is unmethylated, and the oligonucleotides
 optionally have phosphorothioate linkages which make them more resistant
 to degradation. The invention also relates to an oligonucleotide delivery
 complex comprising an oligonucleotide of the invention and a targeting
 agent, and a pharmaceutical composition comprising the oligonucleotide
 delivery complex. The oligonucleotides are able to induce either a cell-
 mediated (T-cell) response or a humoral (B-cell, antibody) response, with
 oligonucleotides of the sequence 5'-RY-CpG-RY-3' being able to induce a
 cell-mediated response, and those of the sequence 5'-NNNT-CpG-WNNN-3'
 being able to induce a humoral response. It is thought that after
 administration, the oligonucleotide acts on antigen-presenting cells
 (e.g., macrophages and dendritic cells), which then release cytokines,
 leading to activation of natural killer (NK) cells. A cell-mediated or
 humoral response can then occur by activation of T- or B-cells. The
 induction of an immune response is useful for treating, preventing or
 ameliorating an allergic reaction (preferably asthma), or an infection,
 where an immunogenic CpG oligonucleotide is administered either alone or
 in combination with an anti-allergenic agent or anti-infectious agent.
 The allergic conditions which may be treated include eczema, allergic
 rhinitis, hayfever, urticaria, food allergies and other atopic
 conditions, and the infections which may be treated include viral,
 bacterial, fungal and protozoal infections such as tuberculosis, AIDS,
 leishmania and schistosomiasis. Immune response induction may also be
 used in the treatment of an autoimmune disorder (e.g., lupus
 erythematosus, rheumatoid arthritis and multiple sclerosis), a disease
 associated with immune system deficiency, and symptoms resulting from
 exposure to an agent of biological warfare. An immunogenic CpG
 oligonucleotide, either alone or in combination with an anti-cancer
 agent, is useful for treating solid tumour cancer. The induction of an

CC immune response is used in antisense therapy and to improve the efficacy
 CC of a vaccine. The oligonucleotide is preferably administered to
 CC lymphocytes ex vivo, producing activated lymphocytes which are then
 CC administered to the host. The present sequence represents an immunogenic
 CC CpG oligodeoxynucleotide of the invention
 XX
 SQ Sequence 20 BP; 2 A; 3 C; 12 G; 3 T; 0 U; 0 Other;
 Query Match 100.0%; Score 18; DB 4; Length 20;
 Best Local Similarity 100.0%; Pred. No. 17; Indels 0; Gaps 0;
 Matches 18; Conservative 0; Mismatches 0;
 QY 1 TGCCTCGATGCAGGGGGG 18
 |||||
 Db 3 TGCCTCGATGCAGGGGGG 20
 |||||
 RESULT 4
 AAS09631
 ID AAS09631 standard; DNA; 20 BP.
 XX
 AC AAS09631;
 XX
 DT 26-SEP-2001 (first entry)
 XX
 DE Immunoreactive CpG sequence-containing oligonucleotide #81.
 XX
 KW CpG sequence; immune response; non-B cell activation; interferon gamma;
 KW IFN-gamma; humoral; antibody production; interleukin-6 production;
 KW therapeutic; allergy; asthma; cancer; autoimmune disorder; infection;
 KW bio-warfare; vaccine; antisense therapy; eczema; allergic rhinitis;
 KW coryza; hay fever; urticaria; hives; food allergy; atopic condition;
 KW hepatitis; human immunodeficiency virus; HIV; malaria; francisella;
 KW lupus erythematosus; rheumatoid arthritis; multiple sclerosis;
 KW schistosomiasis; tuberculosis; acquired immunodeficiency syndrome; AIDS;
 KW leishmania; Ebola; Anthrax; Listeria; ss.
 XX
 OS Synthetic.
 XX
 PN WO200151500-A1.
 XX
 PD 19-JUL-2001.
 XX
 PF 12-JAN-2001; 2001WO-US001122.
 XX
 PR 14-JAN-2000; 2000US-0176115P.
 XX
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX
 PI Klinman D, Ishii K, Verthelyi D;
 XX
 DR WPI; 2001-442129/47.
 XX
 PT Oligodeoxynucleotides for inducing an immune response to treat and
 PT prevent an allergic reaction, cancer, an autoimmune disorder and symptoms
 PT resulting from exposure to bio-warfare agents, comprise multiple CpG
 PT sequences.
 XX
 PS Claim 5; Page 40; 46pp; English.
 XX
 CC AAS09551-AAS09662 represent oligodeoxynucleotides (ODN) of at least 10
 CC nucleotides comprising multiple CpG sequences, where one of the CpG
 CC sequences is different from another of the multiple CpG sequences. The
 CC ODN are useful for inducing an immune response, preferably a cell-
 CC mediated immune response, involving non-B cell activation, interferon
 CC gamma (IFN-gamma) production or a humoral immune response involving B
 CC cell activation, antibody and interleukin-6 production in a host, for
 CC treating, preventing or ameliorating an allergic reaction, e.g. asthma,
 CC cancer, e.g. solid tumour cancer, a disease associated with the immune
 CC system e.g. autoimmune disorder or an immune system deficiency, infection
 CC or a symptom resulting from exposure to bio-warfare agent in a human. The
 CC induction of immune response improves the efficacy of a vaccine and is
 CC used in antisense therapy. The ODN are useful for treating, preventing or

CC ameliorating allergic reactions, including eczema, allergic rhinitis or
 CC coryza, hay fever, bronchial asthma, urticaria (hives), food allergies
 CC and other atopic conditions, for improving the efficacy of vaccines
 CC against hepatitis A, B and C, human immunodeficiency virus (HIV) and
 CC malaria, for treating immune system deficiencies, e.g. lupus
 CC erythematous and autoimmune diseases such as rheumatoid arthritis and
 CC multiple sclerosis, infections including Francisella, schistosomiasis,
 CC tuberculosis, acquired immunodeficiency syndrome (AIDS), Leishmania and
 CC symptoms resulting from exposure of bio-warfare agent, including Ebola,
 CC Anthrax and Listeria
 CC
 SQ Sequence 20 BP; 2 A; 3 C; 12 G; 3 T; 0 U; 0 Other;
 Query Match 100.0%; Score 18; DB 4; Length 20;
 Best Local Similarity 100.0%; Pred. No. 17;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 TGGCTCGATCGAGGGGG 18
 Db 3 TGGCTCGATCGAGGGGG 20
 RESULT 5
 AAS09590
 ID AAS09590 standard; DNA; 20 BP.
 AC AAS09590;
 XX
 XX 26-SEP-2001 (first entry)
 DT
 DE Immunoreactive CpG sequence-containing oligonucleotide #40.
 KW CpG sequence; immune response; non-B cell activation; interferon gamma;
 KW IFN-gamma; humoral; antibody production; interleukin-6 production;
 KW therapeutic; allergy; asthma; cancer; autoimmune disorder; infection;
 KW bio-warfare; vaccine; antisense therapy; eczema; allergic rhinitis;
 KW coryza; hay fever; urticaria; hives; food allergy; atopic condition;
 KW hepatitis; human immunodeficiency virus; HIV; malaria; Francisella;
 KW lupus erythematosus; rheumatoid arthritis; multiple sclerosis;
 KW schistosomiasis; tuberculosis; acquired immunodeficiency syndrome; AIDS;
 KW Leishmania; Ebola; Anthrax; Listeria; ss.
 XX Synthetic.
 OS
 XX WO200151500-A1.
 PN
 XX 19-JUL-2001.
 PD
 XX 12-JAN-2001; 2001WO-US001122.
 PF
 XX 14-JAN-2000; 2000US-0176115P.
 PR
 XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
 PA
 XX Kliman D, Ishii K, Verthelyi D;
 PI
 XX WPI; 2001-442129/47.
 DR
 XX Oligodeoxynucleotides for inducing an immune response to treat and
 PT prevent an allergic reaction; cancer, an autoimmune disorder and symptoms
 PT resulting from exposure to bio-warfare agents, comprise multiple CpG
 FT sequences.
 XX
 FS Claim 5; Page 33; 48pp; English.
 PS
 XX AAS09551-AAS09662 represent oligodeoxynucleotides (ODN) of at least 10
 CC nucleotides comprising multiple CpG sequences, where one of the CpG
 CC sequences is different from another of the multiple CpG sequences. The
 CC ODN are useful for inducing an immune response, preferably a cell-
 CC mediated immune response, involving non-B cell activation, interferon
 CC gamma (IFN-gamma) production or a humoral immune response involving B
 CC cell activation, antibody and interleukin-6 production in a host, for
 CC treating, preventing or ameliorating an allergic reaction, e.g. asthma,

CC cancer, e.g. solid tumour cancer, a disease associated with the immune
 CC system e.g. autoimmune disorder or an immune system deficiency, infection
 CC or a symptom resulting from exposure to bio-warfare agent in a human. The
 CC induction of immune response improves the efficacy of a vaccine and is
 CC used in antisense therapy. The ODN are useful for treating, preventing or
 CC ameliorating allergic reactions, including eczema, allergic rhinitis or
 CC coryza, hay fever, bronchial asthma, urticaria (hives), food allergies
 CC and other atopic conditions, for improving the efficacy of vaccines
 CC against hepatitis A, B and C, human immunodeficiency virus (HIV) and
 CC malaria, for treating immune system deficiencies, e.g. lupus
 CC erythematous and autoimmune diseases such as rheumatoid arthritis and
 CC multiple sclerosis, infections including Francisella, schistosomiasis,
 CC tuberculosis, acquired immunodeficiency syndrome (AIDS), Leishmania and
 CC symptoms resulting from exposure of bio-warfare agent, including Ebola,
 CC Anthrax and Listeria
 CC
 SQ Sequence 20 BP; 2 A; 3 C; 12 G; 3 T; 0 U; 0 Other;
 Query Match 100.0%; Score 18; DB 4; Length 20;
 Best Local Similarity 100.0%; Pred. No. 17;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 TGGCTCGATCGAGGGGG 18
 Db 3 TGGCTCGATCGAGGGGG 20
 RESULT 6
 AAS09632
 ID AAS09632 standard; DNA; 20 BP.
 AC AAS09632;
 XX
 XX 26-SEP-2001 (first entry)
 DT
 DE Immunoreactive CpG sequence-containing oligonucleotide #82.
 KW CpG sequence; immune response; non-B cell activation; interferon gamma;
 KW IFN-gamma; humoral; antibody production; interleukin-6 production;
 KW therapeutic; allergy; asthma; cancer; autoimmune disorder; infection;
 KW bio-warfare; vaccine; antisense therapy; eczema; allergic rhinitis;
 KW coryza; hay fever; urticaria; hives; food allergy; atopic condition;
 KW hepatitis; human immunodeficiency virus; HIV; malaria; Francisella;
 KW lupus erythematosus; rheumatoid arthritis; multiple sclerosis;
 KW schistosomiasis; tuberculosis; acquired immunodeficiency syndrome; AIDS;
 KW Leishmania; Ebola; Anthrax; Listeria; ss.
 XX Synthetic.
 OS
 XX WO200151500-A1.
 PN
 XX 19-JUL-2001.
 PD
 XX 12-JAN-2001; 2001WO-US001122.
 PF
 XX 14-JAN-2000; 2000US-0176115P.
 PR
 XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
 PA
 XX Kliman D, Ishii K, Verthelyi D;
 PI
 XX WPI; 2001-442129/47.
 DR
 XX Oligodeoxynucleotides for inducing an immune response to treat and
 PT prevent an allergic reaction; cancer, an autoimmune disorder and symptoms
 PT resulting from exposure to bio-warfare agents, comprise multiple CpG
 FT sequences.
 XX
 FS Claim 5; Page 40; 48pp; English.
 PS
 XX AAS09551-AAS09662 represent oligodeoxynucleotides (ODN) of at least 10
 CC nucleotides comprising multiple CpG sequences, where one of the CpG
 CC sequences is different from another of the multiple CpG sequences. The

CC ODN are useful for inducing an immune response, preferably a cell-mediated immune response, involving non-B cell activation, interferon gamma (IFN-gamma) production or a humoral immune response involving B cell activation, antibody and interleukin-6 production in a host, for treating, preventing or ameliorating an allergic reaction, e.g. asthma, cancer, e.g. solid tumor cancer, a disease associated with the immune system e.g. autoimmune disorder or an immune system deficiency, infection or a symptom resulting from exposure to bio-warfare agent in a human. The induction of immune response improves the efficacy of a vaccine and is used in antitumor therapy. The ODN are useful for treating, preventing or ameliorating allergic reactions, including eczema, allergic rhinitis or coryza, hay fever, bronchial asthma, urticaria (hives), food allergies and other atopic conditions, for improving the efficacy of vaccines against hepatitis A, B and C, human immunodeficiency virus (HIV) and malaria, for treating immune system deficiencies, e.g. lupus erythematosus and autoimmune diseases such as rheumatoid arthritis and multiple sclerosis, infections including Francisella, schistosomiasis, tuberculosis, acquired immunodeficiency syndrome (AIDS), Leishmania and symptoms resulting from exposure of bio-warfare agent, including Ebola, Anthrax and Listeria

XX
SQ Sequence 20 BP; 2 A; 3 C; 12 G; 3 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCGGTCGATGCAGGGGG 18
|||||
Db 3 TCGGTCGATGCAGGGGG 20

RESULT 7
ABK46510
ID ABK46510 standard; DNA; 20 BP.
XX
AC ABK46510;
XX
DT 05-JUN-2002 (first entry)
XX
DE Immunostimulatory unmethylated CpG oligodeoxynucleotide #100.
XX
KW unmethylated CpG; oligodeoxynucleotide; ODN; virucide; vaccine;
XX Paromyxoviridae; F protein; respiratory syncytial virus; RSV;
KW viral bronchiolitis; pneumonia; infectious pulmonary disease;
KW bronchopulmonary dysplasia; congenital heart condition; ss.
XX
OS Synthetic.
XX
PN WO200211761-A2.
XX
PD 14-FEB-2002.

PF 09-AUG-2001; 2001WO-US041633.
XX
PR 10-AUG-2000; 2000US-0224011P.
PR 01-SEP-2000; 2000US-0229307P.
XX
PA (JACK-) JACKSON FOUND ADVANCEMENT MILITARY MED.
XX
PI Mond JJ, Prince G, Klinman DM;
XX WPI; 2002-227118/28.
XX
PT Vaccine for immunizing patient against respiratory syncytial virus, has epitopes of Paromyxoviridae F protein, and cytosine followed by guanine linked by phosphate bond-oligodeoxynucleotides.
XX
PS Claim 4; Page 9; 30pp; English.

XX The invention describes a vaccine comprising one or more epitopes of a Paromyxoviridae F protein, and one or more CpG (cytosine followed by guanine linked by phosphate bond)-oligodeoxynucleotides (ODNs). The

CC vaccine is useful for vaccinating a patient especially against viruses of the Paromyxoviridae family e.g. respiratory syncytial virus (RSV), the primary cause of viral bronchiolitis and pneumonia in infants and children, and infectious pulmonary disease in infants. RSV has been particularly implicated in death of infants that are premature, have bronchopulmonary dysplasia, or congenital heart conditions. This sequence represents an oligodeoxynucleotide that can be used in the creation of the vaccine

XX
SQ Sequence 20 BP; 2 A; 3 C; 12 G; 3 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 6; Length 20;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCGGTCGATGCAGGGGG 18
|||||
Db 3 TCGGTCGATGCAGGGGG 20

RESULT 8
ABK46468
ID ABK46468 standard; DNA; 20 BP.
XX
AC ABK46468;
XX
DT 05-JUN-2002 (first entry)
XX
DE Immunostimulatory unmethylated CpG oligodeoxynucleotide #58.
XX
KW unmethylated CpG; oligodeoxynucleotide; ODN; virucide; vaccine;
XX Paromyxoviridae; F protein; respiratory syncytial virus; RSV;
KW viral bronchiolitis; pneumonia; infectious pulmonary disease;
KW bronchopulmonary dysplasia; congenital heart condition; ss.
XX
OS Synthetic.
XX
PN WO200211761-A2.
XX
PD 14-FEB-2002.

PF 09-AUG-2001; 2001WO-US041633.
XX
PR 10-AUG-2000; 2000US-0224011P.
PR 01-SEP-2000; 2000US-0229307P.
XX
PA (JACK-) JACKSON FOUND ADVANCEMENT MILITARY MED.
XX
PI Mond JJ, Prince G, Klinman DM;
XX WPI; 2002-227118/28.

PT Vaccine for immunizing patient against respiratory syncytial virus, has epitopes of Paromyxoviridae F protein, and cytosine followed by guanine linked by phosphate bond-oligodeoxynucleotides.
XX
PS Claim 4; Page 8; 30pp; English.
XX
CC The invention describes a vaccine comprising one or more epitopes of a Paromyxoviridae F protein, and one or more CpG (cytosine followed by guanine linked by phosphate bond)-oligodeoxynucleotides (ODNs). The vaccine is useful for vaccinating a patient especially against viruses of the Paromyxoviridae family e.g. respiratory syncytial virus (RSV), the primary cause of viral bronchiolitis and pneumonia in infants and children, and infectious pulmonary disease in infants. RSV has been particularly implicated in death of infants that are premature, have bronchopulmonary dysplasia, or congenital heart conditions. This sequence represents an oligodeoxynucleotide that can be used in the creation of the vaccine

XX
SQ Sequence 20 BP; 2 A; 3 C; 12 G; 3 T; 0 U; 0 Other;
Query Match 100.0%; Score 18; DB 6; Length 20;

AC	ACC48298;	
XX		
XX	11-AUG-2003 (first entry)	
XX		
DE	CpG oligodeoxynucleotide DV35 used for dendritic cell maturation.	
XX		
KW	CpG oligodeoxynucleotide; dendritic cell; tumour; immunotherapy; vaccine	
KW	cytostatic; immunostimulant; gene therapy; ss.	
XX		
OS	Synthetic.	
XX		
XX	WO2003020884-A2.	
XX		
PD	13-MAR-2003.	
XX		
PF	13-AUG-2002; 2002WO-US025732.	
XX		
XX	14-AUG-2001; 2001US-0312190P.	
PR		
XX	(USSH) US DEPT HEALTH & HUMAN SERVICES.	
PA		
XX	Klinman DM, Gursel M, Verthelyi D;	
PI		
XX	WPI; 2003-300874/29.	
DR		
XX		
XX	Generating mature dendritic cells for tumor immunotherapy or as vaccines	
PT	for activating the immune system to treat diseases such as cancer,	
PT	comprise contacting a dendritic cell precursor with a D type	
PT	oligodeoxynucleotide.	
XX		
XX	Disclosure; Fig 8; 69pp; English.	
XX		
CC	The present sequence is that of D type CpG oligodeoxynucleotide DV28, an	
CC	example of claimed D type oligodeoxynucleotides (see ACC48298) of the	
CC	invention. Mature dendritic cells are obtained by contacting a dendritic	
CC	cell precursor, such as a monocyte, with such an oligodeoxynucleotide.	
CC	The method is useful for generating mature dendritic cells and enhancing	
CC	T cell responses, thus enhancing antigen presentation. Mature dendritic	
CC	cells are useful for tumour immunotherapy, for augmenting an immune	
CC	response to an infectious agent or to a vaccine, and as vaccines to	
CC	prevent future infection or to activate the immune system to treat	
CC	diseases such as cancer. Mature dendritic cells may also be used to	
CC	produce activated T lymphocytes	
XX		
SQ	Sequence 20 BP; 2 A; 3 C; 12 G; 3 T; 0 U; 0 Other;	
	Query Match 100.0%; Score 18; DB 7; Length 20;	
	Best Local Similarity 100.0%; Pred. No. 17;	
	Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
QY	1 TCGGTCGATGCGGGGG 18	
Db	3 TCGGTCGATGCGGGGG 20	
RESULT 11		
ACC48312		
ID	ACC48312 standard; DNA; 20 BP.	
XX		
AC	ACC48312;	
XX		
DE	11-AUG-2003 (first entry)	
XX		
XX	CpG oligodeoxynucleotide DV52.	
XX		
KW	CpG oligodeoxynucleotide; dendritic cell; tumour; immunotherapy; vaccine;	
KW	cytostatic; immunostimulant; gene therapy; ss.	
XX		
OS	Synthetic.	
XX		
XX	WO2003020884-A2.	
XX		
PD	13-MAR-2003.	

```

XX 13-AUG-2002; 2002WO-US025732.
XX PF
XX PR
XX PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX PI
XX PI Klinman DM, Gursel M, Verthelyi D;
XX XX
XX WPI; 2003-300874/29.
XX DR
XX PS Disclosure; Fig 8; 69pp; English.
XX CC The present sequence is that of CpG oligodeoxynucleotide DV52 of the
XX CC invention. A claimed method for generating dendritic cells involves
XX CC contacting a dendritic cell precursor, especially a monocyte, with a D
XX CC type oligodeoxynucleotide (see ACC48294) containing a central
XX CC unethyated CpG motif. The method is useful for generating mature
XX CC dendritic cells and enhancing T cell responses, thus enhancing antigen
XX CC presentation. Mature dendritic cells are useful for tumour immunotherapy,
XX CC for augmenting an immune response to an infectious agent or to a vaccine,
XX CC and as vaccines to prevent future infection or to activate the immune
XX CC system to treat diseases such as cancer. Mature dendritic cells may also
XX CC be used to produce activated T lymphocytes
XX SQ Sequence 20 BP; 2 A; 3 C; 12 G; 3 T; 0 U; 0 Other;
XX
Query Match 100.0%; Score 18; DB 7; Length 20;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 TGGTCGATGCAGGGGG 18
XX Db 3 TGGTCGATGCAGGGGG 20
XX
RESULT 12
ACC48306
XX ID ACC48306 standard; DNA; 20 BP.
XX AC
XX AC ACC48306;
XX DT
XX DT 11-AUG-2003 (first entry)
XX DE
XX DE CpG oligodeoxynucleotide used for dendritic cell maturation.
XX KW CpG oligodeoxynucleotide; dendritic cell; tumour; immunotherapy; vaccine;
XX KW cytostatic; immunostimulant; gene therapy; ss.
XX OS Synthetic.
XX XX
XX Key Location/Qualifiers
XX misc_difference 1 /*tag= a
XX FT /*note= "N is any base (especially G) or no base"
XX FT misc_difference 2 /*tag= b
XX FT /*note= "N is any base (especially G) or no base"
XX FT
XX PN WO2003020884-A2.
XX PD
XX PD 13-MAR-2003.
XX XX
XX PF 13-AUG-2002; 2002WO-US025732.
XX PR
XX PR 14-AUG-2001; 2001US-0312190P.
XX PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX XX

```

```

XX Klinman DM, Gursel M, Verthelyi D;
XX PI
XX DR WPI; 2003-300874/29.
XX XX
XX PF Generating mature dendritic cells for tumor immunotherapy or as vaccines
XX PF for activating the immune system to treat diseases such as cancer,
XX PF comprises contacting a dendritic cell precursor with a D type
XX PF oligodeoxynucleotide.
XX XX
XX PS Disclosure; Page 26; 69pp; English.
XX XX
XX CC The present sequence is that of a D type CpG oligodeoxynucleotide that is
XX CC an example of claimed D type oligodeoxynucleotides (see ACC48294) of the
XX CC invention. Mature dendritic cells are obtained by contacting a dendritic
XX CC cell precursor, such as a monocyte, with such an oligodeoxynucleotide.
XX CC The method is useful for generating mature dendritic cells and enhancing
XX CC T cell responses, thus enhancing antigen presentation. Mature dendritic
XX CC cells are useful for tumour immunotherapy, for augmenting an immune
XX CC response to an infectious agent or to a vaccine, and as vaccines to
XX CC prevent future infection or to activate the immune system to treat
XX CC diseases such as cancer. Mature dendritic cells may also be used to
XX CC produce activated T lymphocytes
XX SQ Sequence 20 BP; 2 A; 3 C; 10 G; 3 T; 0 U; 2 Other;
XX
Query Match 100.0%; Score 18; DB 7; Length 20;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 TGGTCGATGCAGGGGG 18
XX Db 3 TGGTCGATGCAGGGGG 20
XX
RESULT 13
ACC48319
XX ID ACC48319 standard; DNA; 20 BP.
XX XX
XX AC ACC48319;
XX DT
XX DT 11-AUG-2003 (first entry)
XX DE
XX DE CpG oligodeoxynucleotide DV28.
XX KW CpG oligodeoxynucleotide; dendritic cell; tumour; immunotherapy; vaccine;
XX KW cytostatic; immunostimulant; gene therapy; ss.
XX OS Synthetic.
XX XX
XX PN WO2003020884-A2.
XX PD
XX PD 13-MAR-2003.
XX XX
XX PF 13-AUG-2002; 2002WO-US025732.
XX PR
XX PR 14-AUG-2001; 2001US-0312190P.
XX PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX XX
XX PI Klinman DM, Gursel M, Verthelyi D;
XX XX
XX DR WPI; 2003-300874/29.
XX XX
XX PF Generating mature dendritic cells for tumor immunotherapy or as vaccines
XX PF for activating the immune system to treat diseases such as cancer,
XX PF comprises contacting a dendritic cell precursor with a D type
XX PF oligodeoxynucleotide.
XX XX
XX PS Disclosure; Fig 8; 69pp; English.
XX CC The present sequence is that of CpG oligodeoxynucleotide DV28 of the
XX CC invention. A claimed method for generating dendritic cells involves

```


CC contacting a dendritic cell precursor, especially a monocyte, with a D
CC type oligodeoxynucleotide (see ACC48294) containing a central
CC unmethylated CpG motif. The method is useful for generating mature
CC dendritic cells and enhancing T cell responses, thus enhancing antigen
CC presentation. Mature dendritic cells are useful for tumour immunotherapy.
CC for augmenting an immune response to an infectious agent or to a vaccine,
CC and as vaccines to prevent future infection or to activate the immune
CC system to treat diseases such as cancer. Mature dendritic cells may also
CC be used to produce activated T lymphocytes

XX
SQ Sequence 20 BP; 2 A; 3 C; 12 G; 3 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 7; Length 20;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGGTCGATGCAGGGGGG 18
|||
DB 3 TGGTCGATGCAGGGGGG 20

RESULT 14
ACC83117
ID ACC83117 standard; DNA; 20 BP.
XX
AC ACC83117;
XX
DT 27-AUG-2003 (first entry)
XX
DE D class CpG ODN sequence useful for encapsulating in SSCL, DV28.
XX
KW Sterically stabilised cationic liposome; SSCL; ODN; oligodeoxynucleotide;
KW tuberculosis; cytokine; leishmaniasis; AIDS-associated Kaposi's tumour;
KW thyroid; cancer; allergy; eczema; allergic rhinitis; coryza; hay fever;
KW schistosomiasis; interferon gamma; lupus erythematosus; antimicrobial;
KW asthma; urticaria; autoimmune disease; diabetes; rheumatoid arthritis;
KW CpG motif; interleukin-13; cytostatic; tularemia; malaria; psoriasis;
KW multiple sclerosis; infection; tumour; ss.

XX Unidentified.
XX
XX WO2003040308-A2.
XX
XX 15-MAY-2003.
XX
XX 29-JUL-2002; 2002WO-US024235.
XX
XX 27-JUL-2001; 2001US-0308283P.
XX
XX 25-JUL-2002; 2002US-00206407.
XX
XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
XX Klinman DM, Gursel I, Ishii KJ, Kawakami K, Joshi BH, Puri RK;
XX WPI; 2003-482260/45.

XX Cationic liposome composition for delivering oligodeoxynucleotides
XX including a CpG motif in clinical applications, comprises a cationic
XX lipid, a co-lipid, stabilizing agent and an encapsulated oligonucleotide.
XX
XX Disclosure; Fig 10C; 110pp; English.

XX The invention relates to sterically stabilised cationic liposomes (SSCL)
XX which comprises a cationic lipid, a co-lipid, stabilising agent and
XX encapsulating a K type oligodeoxynucleotide (ODN) including a CpG motif.
XX The invention is useful in pharmaceutical composition for impairing
XX growth of a solid tumour cell (e.g. human tumour cell) bearing an
XX interleukin-13 receptor in a subject; for stimulating an immune response,
XX which is expression of a cytokine (e.g. interferon gamma), particularly
XX immunotherapeutic response against tumours or stimulating an in vivo or
XX an in vitro immune cell, and for inducing an immune response against an
XX infectious agent e.g. virus, bacteria and fungus. It is also useful for
XX delivering oligodeoxynucleotides including a CpG motif in clinical

CC applications; for treating infectious diseases (e.g. tularemia, malaria,
CC francisella, schistosomiasis, tuberculosis and leishmaniasis), cancer
CC (e.g. solid tumours, AIDS-associated Kaposi's tumour, thyroid cancer
CC etc), allergy (e.g. eczema, allergic rhinitis or coryza, hay fever,
CC bronchial or allergic asthma, urticaria, food allergies), autoimmune
CC diseases (e.g. diabetes, rheumatoid arthritis, lupus erythematosus and
CC multiple sclerosis) and psoriasis. The present sequence is a D class CpG
CC ODN potentially useful for encapsulating in SSCL

XX
SQ Sequence 20 BP; 2 A; 3 C; 12 G; 3 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 8; Length 20;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGGTCGATGCAGGGGGG 18
|||
DB 3 TGGTCGATGCAGGGGGG 20

RESULT 15
ACC83124
ID ACC83124 standard; DNA; 20 BP.
XX
AC ACC83124;
XX
DT 27-AUG-2003 (first entry)
XX
DE D class CpG ODN sequence useful for encapsulating in SSCL, DV52.
XX
KW Sterically stabilised cationic liposome; SSCL; ODN; oligodeoxynucleotide;
KW tuberculosis; cytokine; leishmaniasis; AIDS-associated Kaposi's tumour;
KW thyroid; cancer; allergy; eczema; allergic rhinitis; coryza; hay fever;
KW schistosomiasis; interferon gamma; lupus erythematosus; antimicrobial;
KW asthma; urticaria; autoimmune disease; diabetes; rheumatoid arthritis;
KW CpG motif; interleukin-13; cytostatic; tularemia; malaria; psoriasis;
KW multiple sclerosis; infection; tumour; ss.

XX Unidentified.
XX
XX WO2003040308-A2.
XX
XX 15-MAY-2003.
XX
XX 29-JUL-2002; 2002WO-US024235.
XX
XX 27-JUL-2001; 2001US-0308283P.
XX
XX 25-JUL-2002; 2002US-00206407.
XX
XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
XX Klinman DM, Gursel I, Ishii KJ, Kawakami K, Joshi BH, Puri RK;
XX WPI; 2003-482260/45.

XX Cationic liposome composition for delivering oligodeoxynucleotides
XX including a CpG motif in clinical applications, comprises a cationic
XX lipid, a co-lipid, stabilizing agent and an encapsulated oligonucleotide.
XX
XX Disclosure; Fig 10C; 110pp; English.

XX The invention relates to sterically stabilised cationic liposomes (SSCL)
XX which comprises a cationic lipid, a co-lipid, stabilising agent and
XX encapsulating a K type oligodeoxynucleotide (ODN) including a CpG motif.
XX The invention is useful in pharmaceutical composition for impairing
XX growth of a solid tumour cell (e.g. human tumour cell) bearing an
XX interleukin-13 receptor in a subject; for stimulating an immune response,
XX which is expression of a cytokine (e.g. interferon gamma), particularly
XX immunotherapeutic response against tumours or stimulating an in vivo or
XX an in vitro immune cell, and for inducing an immune response against an
XX infectious agent e.g. virus, bacteria and fungus. It is also useful for
XX delivering oligodeoxynucleotides including a CpG motif in clinical
XX applications; for treating infectious diseases (e.g. tularemia, malaria,

CC francisella, schistosomiasis, tuberculosis and leishmaniasis), cancer
 CC (e.g. solid tumours, AIDS-associated Kaposi's tumour, thyroid cancer
 CC etc), allergy (e.g. eczema, allergic rhinitis or coryza, hay fever,
 CC bronchial or allergic asthma, urticaria, food allergies), autoimmune
 CC diseases (e.g. diabetes, rheumatoid arthritis, lupus erythematosus and
 CC multiple sclerosis) and psoriasis. The present sequence is a D class Cpg
 CC ODN potentially useful for encapsulating in SSCL

XX Sequence 20 BP; 2 A; 3 C; 12 G; 3 T; 0 U; 0 Other;

Query Match 100.0%; Score 18; DB 8; Length 20;
 Best Local Similarity 100.0%; Pred. No. 17;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGGCTCATGCAGGGGG 18
 |||||
 Db 3 TGGCTCATGCAGGGGG 20

Search completed: July 2, 2004, 08:31:35
 Job time : 134.89 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 2, 2004, 08:09:30 ; Search time 28.2073 Seconds
(without alignments)
354.132 Million cell updates/sec

Title: US-10-068-160-16

Perfect score: 18
Sequence: 1 tgcgtcgatgcagggggg 18

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents NA:**
1: /cgn2_6/ptodata/2/ina/5A COMB.seq.*
2: /cgn2_6/ptodata/2/ina/5B COMB.seq.*
3: /cgn2_6/ptodata/2/ina/6A COMB.seq.*
4: /cgn2_6/ptodata/2/ina/6B COMB.seq.*
5: /cgn2_6/ptodata/2/ina/PTUS COMB.seq.*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	14.4	80.0	2870	4	US-09-799-875-16
2	14.4	80.0	2891	4	US-09-578-441-1
3	14.4	80.0	4403765	3	US-09-103-840A-2
4	14.4	80.0	4411529	3	US-09-103-840A-1
5	14	77.8	759	4	US-09-252-991A-1486
6	14	77.8	1308	4	US-09-252-991A-1592
7	14	77.8	1356	4	US-09-252-991A-1425
8	14	77.8	3591	4	US-09-252-991A-1690
9	13.8	76.7	20	4	US-09-659-845A-106
10	13.8	76.7	552	4	US-09-252-991A-6091
11	13.8	76.7	585	4	US-09-252-991A-6007
12	13.8	76.7	594	4	US-09-489-039A-7023
13	13.8	76.7	609	4	US-09-252-991A-6173
14	13.8	76.7	642	4	US-09-252-991A-6014
15	13.8	76.7	655	3	US-08-851-774B-55
16	13.8	76.7	822	4	US-09-252-991A-6377
17	13.8	76.7	885	4	US-09-252-991A-7552
18	13.8	76.7	906	4	US-09-489-039A-3080
19	13.8	76.7	912	4	US-09-252-991A-7811
20	13.8	76.7	978	4	US-09-252-991A-6384
21	13.8	76.7	1242	4	US-09-252-991A-7949
22	13.8	76.7	1255	4	US-09-659-845A-104
23	13.8	76.7	1365	4	US-09-659-845A-10
24	13.8	76.7	1392	4	US-09-489-039A-4664
25	13.8	76.7	1571	1	US-08-726-525-1
26	13.8	76.7	1571	1	US-08-487-942-1
27	13.8	76.7	1571	2	US-08-726-036A-1

ALIGNMENTS

RESULT 1

US-09-799-875-16

; Sequence 16, Application US/09799875

; Patent No. 6638721

; GENERAL INFORMATION:

; APPLICANT: Meyers, Rachel

; APPLICANT: Kapeller-Libermann, Rosana

; APPLICANT: Williamson, Mark

; TITLE OF INVENTION: NO. 6638721 Human Protein Kinases and Uses

; FILE OF INVENTION: Therefor

; FILE REFERENCE: 35800/209596

; CURRENT APPLICATION NUMBER: US/09/799,875

; CURRENT FILING DATE: 2001-03-06

; PRIOR APPLICATION NUMBER: 60/182,059

; PRIOR FILING DATE: 2000-02-11

; PRIOR APPLICATION NUMBER: 09/659,287

; PRIOR FILING DATE: 2000-09-12

; NUMBER OF SEQ ID NOS: 32

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 16

; LENGTH: 2870

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (114)...(2000)

; US-09-799-875-16

Query Match 80.0%; Score 14.4; DB 4; Length 2870;

Best Local Similarity 93.8%; Pred. No. 2.1e+02;

Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 CGTCGATGCAGGGGG 18

DB 109 CGCGATGCAGGGGG 124

RESULT 2

US-09-578-441-1

; Sequence 1, Application US/09578441

; Patent No. 6562571

; GENERAL INFORMATION:

; APPLICANT: Wu, J.H. David

; APPLICANT: Omata, Takeshi

; APPLICANT: Mantalaris, Athanasios

; APPLICANT: Chen, Yi-Guang

; APPLICANT: Tsai, Ying-Chueh

; TITLE OF INVENTION: HUMAN HEME-REGULATED INITIATION FACTOR 2.ALPHA KINASE

; FILE REFERENCE: 176/60571

; CURRENT APPLICATION NUMBER: US/09/578,441

Sequence 1, Appli
Sequence 7681, Ap
Sequence 1, Appli
Sequence 1, Appli
Sequence 66, Appli
Sequence 66, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 2, Appli
Sequence 1, Appli
Sequence 105, Appli
Sequence 3, Appli
Patent No. 546585
Patent No. 546585
Sequence 2941, Ap
Sequence 8040, Ap

28 13.8 76.7 1571 4 US-09-083-516-1
c 29 13.8 76.7 1794 4 US-09-252-991A-7681
c 30 13.8 76.7 5561 2 US-08-400-159-1
c 31 13.8 76.7 5561 3 US-08-611-729A-1
c 32 13.8 76.7 6814 4 US-09-484-970B-66
c 33 13.8 76.7 6814 4 US-09-484-970B-66
c 34 13.8 76.7 8378 5 PCT-US91-09055-1
c 35 13.8 76.7 32155 4 US-08-311-731A-1
c 36 13.8 76.7 536165 4 US-09-214-808-1
c 37 13.8 76.7 4403765 3 US-09-103-840A-2
c 38 13.8 76.7 4411529 3 US-09-103-840A-1
c 39 13.4 74.4 20 4 US-09-659-845A-105
c 40 13.4 74.4 171 4 US-09-187-108-3
c 41 13.4 74.4 171 6 546585-4
c 42 13.4 74.4 253 4 US-09-187-108-5
c 43 13.4 74.4 253 6 546585-5
c 44 13.4 74.4 333 4 US-09-489-039A-2941
c 45 13.4 74.4 471 4 US-09-252-991A-8040

Db 369 TGCCTGATGCAGG 382

RESULT 7

US-09-252-991A-1425/c
; Sequence 1425, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 1425
; LENGTH: 1356
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-1425

Query Match 77.8%; Score 14; DB 4; Length 1356;

Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGCCTGATGCAGG 14

Db 979 TGCCTGATGCAGG 966

RESULT 8

US-09-252-991A-1690
; Sequence 1690, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 1690
; LENGTH: 3591
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-1690

Query Match 77.8%; Score 14; DB 4; Length 3591;

Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGCCTGATGCAGG 14

Db 295 TGCCTGATGCAGG 308

RESULT 9

US-09-659-845A-106/c
; Sequence 106, Application US/09659845A
; Patent No. 6492170
; GENERAL INFORMATION:
; APPLICANT: Hong Zhang
; APPLICANT: Andrew T. Watt
; TITLE OF INVENTION: ANTISENSE MODULATION OF CASPASE 9 EXPRESSION

; FILE REFERENCE: RTS-0183
; CURRENT APPLICATION NUMBER: US/09/659,845A
; CURRENT FILING DATE: 2001-07-23
; NUMBER OF SEQ ID NOS: 174
; SEQ ID NO 106
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Antisense Oligonucleotide
US-09-659-845A-106

Query Match 76.7%; Score 13.8; DB 4; Length 20;

Best Local Similarity 88.2%; Pred. No. 3.8e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TCGCTGATGCAGGGG 17

Db 18 TCGCTGATGCAGGGG 2

RESULT 10

US-09-252-991A-6091/c
; Sequence 6091, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 6091
; LENGTH: 552
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-6091

Query Match 76.7%; Score 13.8; DB 4; Length 552;

Best Local Similarity 88.2%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GCGTTCATGCAGGGG 18

Db 123 GCGTTCATGCAGGGG 107

RESULT 11

US-09-252-991A-6007/c
; Sequence 6007, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 6007
; LENGTH: 585
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-6007

```
Query Match      76.7%; Score 13.8; DB 4; Length 585;
Best Local Similarity 88.2%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2 GCGTCGATCGAGGGGG 18
      |||||
Db      354 GCGTCGATCGAGGGGG 338

RESULT 12
US-09-489-039A-7023/c
; Sequence 7023, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 7023
; LENGTH: 594
; TYPE: DNA
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-7023

Query Match      76.7%; Score 13.8; DB 4; Length 594;
Best Local Similarity 88.2%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 TCGGTCGATCGAGGGGG 17
      |||||
Db      262 TCGGTCGATCGAGGGGG 246

RESULT 13
US-09-252-991A-6173/c
; Sequence 6173, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 6173
; LENGTH: 609
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-6173

Query Match      76.7%; Score 13.8; DB 4; Length 609;
Best Local Similarity 88.2%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2 GCGTCGATCGAGGGGG 18
      |||||
Db      83 GCGTTGCTGCAGGGGG 67

RESULT 14
US-09-252-991A-6014/c
; Sequence 6014, Application US/09252991A
```

```
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 6014
; LENGTH: 642
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-6014

Query Match      76.7%; Score 13.8; DB 4; Length 642;
Best Local Similarity 88.2%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2 GCGTCGATCGAGGGGG 18
      |||||
Db      229 GCGTTGCTGCAGGGGG 213

RESULT 15
US-08-861-774E-55
; Sequence 55, Application US/08861774E
; Patent No. 6297007
; GENERAL INFORMATION:
; APPLICANT: Waters, Barbara
; APPLICANT: Miao, Vivian
; APPLICANT: Ho, Yap
; APPLICANT: Tong, Seow
; TITLE OF INVENTION: METHOD FOR ISOLATION OF BIOSYNTHESIS GENES FOR
; TITLE OF INVENTION: BIOACTIVE MOLECULES
; FILE REFERENCE: 9993-006
; CURRENT APPLICATION NUMBER: US/08/861,774E
; CURRENT FILING DATE: 1997-05-22
; NUMBER OF SEQ ID NOS: 94
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 55
; LENGTH: 655
; TYPE: DNA
; ORGANISM: Peltigera neopolydactyla
US-08-861-774E-55

Query Match      76.7%; Score 13.8; DB 3; Length 655;
Best Local Similarity 88.2%; Pred. No. 4.1e+02;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      2 GCGTCGATCGAGGGGG 18
      |||||
Db      75 GCGTTATCGAGGGGG 91

Search completed: July 2, 2004, 13:37:40
Job time : 44.2073 secs
```

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 2, 2004, 08:11:05 ; Search time 138.732 Seconds
(without alignments)
625.926 Million cell updates/sec

Title: US-10-068-160-16

Perfect score: 18
Sequence: 1 tgcgtcgatgcagg9999 18

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 3163042 seqs, 2412103800 residues

Total number of hits satisfying chosen parameters: 6326084

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications NA:*

- 1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
- 6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
- 7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
- 8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
- 10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
- 12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
- 13: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
- 14: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
- 15: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
- 16: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
- 17: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
- 18: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
- 19: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	18	100.0	18	15	US-10-068-160-16
2	18	100.0	20	15	US-10-068-160-7
3	18	100.0	20	15	US-10-194-035-40
4	18	100.0	20	15	US-10-194-035-81
5	18	100.0	20	15	US-10-194-035-82
6	18	100.0	20	17	US-10-666-022-4
7	18	100.0	20	17	US-10-666-022-16
8	17	94.4	19	15	US-10-194-035-83
9	16.4	91.1	18	13	US-09-874-991C-503
10	16.4	91.1	18	13	US-09-874-991C-513
11	16.4	91.1	18	13	US-09-874-991C-551
12	16.4	91.1	18	15	US-10-068-160-12
13	16.4	91.1	18	15	US-10-068-160-14
14	16.4	91.1	18	15	US-10-068-160-18

15	16.4	91.1	18	15	US-10-068-160-20
16	16.4	91.1	20	13	US-09-874-991C-494
17	16.4	91.1	20	13	US-09-874-991C-497
18	16.4	91.1	20	13	US-09-874-991C-502
19	16.4	91.1	20	13	US-09-874-991C-505
20	16.4	91.1	20	13	US-09-874-991C-508
21	16.4	91.1	20	13	US-09-874-991C-512
22	16.4	91.1	20	13	US-09-874-991C-538
23	16.4	91.1	20	13	US-09-874-991C-541
24	16.4	91.1	20	13	US-09-874-991C-546
25	16.4	91.1	20	13	US-09-874-991C-550
26	16.4	91.1	20	15	US-10-068-160-1
27	16.4	91.1	20	15	US-10-068-160-26
28	16.4	91.1	20	15	US-10-068-160-31
29	16.4	91.1	20	15	US-10-068-160-38
30	16.4	91.1	20	15	US-10-068-160-54
31	16.4	91.1	20	15	US-10-194-035-32
32	16.4	91.1	20	15	US-10-194-035-34
33	16.4	91.1	20	15	US-10-194-035-37
34	16.4	91.1	20	15	US-10-194-035-38
35	16.4	91.1	20	15	US-10-194-035-39
36	16.4	91.1	20	15	US-10-194-035-41
37	16.4	91.1	20	15	US-10-194-035-43
38	16.4	91.1	20	15	US-10-194-035-72
39	16.4	91.1	20	15	US-10-194-035-102
40	16.4	91.1	20	17	US-10-666-022-1
41	16.4	91.1	20	17	US-10-666-022-3
42	16.4	91.1	20	17	US-10-666-022-6
43	16.4	91.1	20	17	US-10-666-022-8
44	16.4	91.1	20	17	US-10-666-022-176
45	16.4	91.1	20	17	US-10-666-022-177

ALIGNMENTS

RESULT 1

US-10-068-160-16

; Sequence 16, Application US/10068160

; Publication No. US20030060440A1

; GENERAL INFORMATION:

; APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA, REPRESENTED BY THE APPLICANT: SECRETARY, DEPARTMENT OF HEALTH AND HUMAN SERVICES

; APPLICANT: KLINMAN, Dennis

; APPLICANT: ISHII, Ken

; APPLICANT: VERTHELYI, Daniela

; TITLE OF INVENTION: OLIGODENOXNUCLEOTIDE AND ITS USE TO INDUCE AN IMMUNE RESPONSE

; FILE REFERENCE: 4239-61999

; CURRENT APPLICATION NUMBER: US/10/068,160

; PRIOR FILING DATE: 2002-02-06

; PRIOR APPLICATION NUMBER: 60/128,898

; PRIOR FILING DATE: 1999-04-12

; NUMBER OF SEQ ID NOS: 120

; SOFTWARE: Patent in version 3.1

; SEQ ID NO 16

; LENGTH: 18

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURES:

; OTHER INFORMATION: Oligonucleotide

US-10-068-160-16

Query Match 100.0%; Score 18; DB 15; Length 18;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 TCGTCGATGCAGGGGG 18

DB 1 TCGTCGATGCAGGGGG 18

RESULT 2

US-10-068-160-7

```
; Sequence 7, Application US/10068160
; Publication No. US2003006040A1
; GENERAL INFORMATION:
; APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA, AS REPRESENTED BY THE
; APPLICANT: SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES
; APPLICANT: KLINMAN, Dennis
; APPLICANT: ISHII, Ken
; APPLICANT: VERTHELYI, Daniela
; TITLE OF INVENTION: OLIGODEOXYNUCLEOTIDE AND ITS USE TO INDUCE AN IMMUNE RESPONSE
; FILE REFERENCE: 4239-61999
; CURRENT APPLICATION NUMBER: US/10/068,160
; CURRENT FILING DATE: 2002-02-06
; PRIOR APPLICATION NUMBER: 60/128,898
; PRIOR FILING DATE: 1998-04-12
; NUMBER OF SEQ ID NOS: 120
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide
US-10-068-160-7

Query Match      100.0%; Score 18; DB 15; Length 20;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGGGTGCGATGCAGGGGGG 18
Db 3 TGGGTGCGATGCAGGGGGG 20

RESULT 3
US-10-194-035-40
; Sequence 40, Application US/10194035
; Publication No. US20030144229A1
; GENERAL INFORMATION:
; APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS REPRESENTED BY THE
; APPLICANT: SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES
; APPLICANT: KLINMAN, Dennis
; APPLICANT: ISHII, Ken
; APPLICANT: VERTHELYI, Daniela
; TITLE OF INVENTION: OLIGODEOXYNUCLEOTIDE AND ITS USE TO INDUCE AN IMMUNE RESPONSE
; FILE REFERENCE: 4239-63317
; CURRENT APPLICATION NUMBER: US/10/194,035
; CURRENT FILING DATE: 2002-07-12
; PRIOR APPLICATION NUMBER: PCT/US01/01122
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: US 60/176,115
; PRIOR FILING DATE: 2000-01-14
; NUMBER OF SEQ ID NOS: 119
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 40
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
US-10-194-035-40

Query Match      100.0%; Score 18; DB 15; Length 20;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGGGTGCGATGCAGGGGGG 18
Db 3 TGGGTGCGATGCAGGGGGG 20

RESULT 4
US-10-194-035-81
; Sequence 81, Application US/10194035
; Publication No. US20030144229A1
; GENERAL INFORMATION:
; APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS REPRESENTED BY THE
; APPLICANT: SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES
; APPLICANT: KLINMAN, Dennis
; APPLICANT: ISHII, Ken
; APPLICANT: VERTHELYI, Daniela
; TITLE OF INVENTION: OLIGODEOXYNUCLEOTIDE AND ITS USE TO INDUCE AN IMMUNE RESPONSE
; FILE REFERENCE: 4239-63317
; CURRENT APPLICATION NUMBER: US/10/194,035
; CURRENT FILING DATE: 2002-07-12
; PRIOR APPLICATION NUMBER: PCT/US01/01122
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: US 60/176,115
; PRIOR FILING DATE: 2000-01-14
; NUMBER OF SEQ ID NOS: 119
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 81
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
US-10-194-035-81

Query Match      100.0%; Score 18; DB 15; Length 20;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGGGTGCGATGCAGGGGGG 18
Db 3 TGGGTGCGATGCAGGGGGG 20

RESULT 5
US-10-194-035-82
; Sequence 82, Application US/10194035
; Publication No. US20030144229A1
; GENERAL INFORMATION:
; APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS REPRESENTED BY THE
; APPLICANT: SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES
; APPLICANT: KLINMAN, Dennis
; APPLICANT: ISHII, Ken
; APPLICANT: VERTHELYI, Daniela
; TITLE OF INVENTION: OLIGODEOXYNUCLEOTIDE AND ITS USE TO INDUCE AN IMMUNE RESPONSE
; FILE REFERENCE: 4239-63317
; CURRENT APPLICATION NUMBER: US/10/194,035
; CURRENT FILING DATE: 2002-07-12
; PRIOR APPLICATION NUMBER: PCT/US01/01122
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: US 60/176,115
; PRIOR FILING DATE: 2000-01-14
; NUMBER OF SEQ ID NOS: 119
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 82
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
US-10-194-035-82

Query Match      100.0%; Score 18; DB 15; Length 20;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGGGTGCGATGCAGGGGGG 18
Db 3 TGGGTGCGATGCAGGGGGG 20

RESULT 6
US-10-666-022-4
; Sequence 81, Application US/10194035
; Publication No. US20030144229A1
; GENERAL INFORMATION:
; APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS REPRESENTED BY THE
; APPLICANT: SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES
; APPLICANT: KLINMAN, Dennis
; APPLICANT: ISHII, Ken
; APPLICANT: VERTHELYI, Daniela
; TITLE OF INVENTION: OLIGODEOXYNUCLEOTIDE AND ITS USE TO INDUCE AN IMMUNE RESPONSE
; FILE REFERENCE: 4239-63317
; CURRENT APPLICATION NUMBER: US/10/194,035
; CURRENT FILING DATE: 2002-07-12
; PRIOR APPLICATION NUMBER: PCT/US01/01122
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: US 60/176,115
; PRIOR FILING DATE: 2000-01-14
; NUMBER OF SEQ ID NOS: 119
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 81
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
US-10-666-022-4

Query Match      100.0%; Score 18; DB 15; Length 20;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGGGTGCGATGCAGGGGGG 18
Db 3 TGGGTGCGATGCAGGGGGG 20
```


Sequence 4, Application US/10666022
 ; Publication No. US20040105872A1
 ; GENERAL INFORMATION:
 ; APPLICANT: The Government of the United States of America, as represented by the
 ; APPLICANT: Secretary of the Department of Health and Human Services
 ; APPLICANT: Klinman, Dennis M.
 ; APPLICANT: Verthelyi, Daniela
 ; TITLE OF INVENTION: METHOD OF TREATING AND PREVENTING INFECTIONS IN IMMUNOCOMPROMISED
 ; FILE REFERENCE: 4239-66899
 ; CURRENT APPLICATION NUMBER: US/10/666,022
 ; CURRENT FILING DATE: 2003-09-17
 ; PRIOR APPLICATION NUMBER: US 60/411,944
 ; PRIOR FILING DATE: 2002-09-18
 ; NUMBER OF SEQ ID NOS: 181
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 4
 ; LENGTH: 20
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: synthetic
 ; NAME/KEY: misc feature
 ; LOCATION: (1)..(20)
 ; OTHER INFORMATION: n is a, c, g, or t, or no nucleotide
 US-10-666-022-4

Query Match 100.0%; Score 18; DB 17; Length 20;
 Best Local Similarity 100.0%; Pred. No. 18;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGGTCGATCGAGGGGG 18
 |||||
 DB 3 TGGTCGATCGAGGGGG 20

RESULT 7

US-10-666-022-16
 ; Sequence 16, Application US/10666022
 ; Publication No. US20040105872A1
 ; GENERAL INFORMATION:
 ; APPLICANT: The Government of the United States of America, as represented by the
 ; APPLICANT: Secretary of the Department of Health and Human Services
 ; APPLICANT: Klinman, Dennis M.
 ; APPLICANT: Verthelyi, Daniela
 ; TITLE OF INVENTION: METHOD OF TREATING AND PREVENTING INFECTIONS IN IMMUNOCOMPROMISED
 ; FILE REFERENCE: 4239-66899
 ; CURRENT APPLICATION NUMBER: US/10/666,022
 ; CURRENT FILING DATE: 2003-09-17
 ; PRIOR APPLICATION NUMBER: US 60/411,944
 ; PRIOR FILING DATE: 2002-09-18
 ; NUMBER OF SEQ ID NOS: 181
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 16
 ; LENGTH: 20
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: synthetic
 US-10-666-022-16

Query Match 100.0%; Score 18; DB 17; Length 20;
 Best Local Similarity 100.0%; Pred. No. 18;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGGTCGATCGAGGGGG 18
 |||||
 DB 3 TGGTCGATCGAGGGGG 20

RESULT 8

US-10-194-035-83
 ; Sequence 83, Application US/10194035
 ; Publication No. US20030144229A1
 ; GENERAL INFORMATION:
 ; APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS REPRESENTED BY THE
 ; APPLICANT: SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES
 ; APPLICANT: KLINMAN, Dennis
 ; APPLICANT: ISHII, Ken
 ; APPLICANT: VERTHELYI, Daniela
 ; TITLE OF INVENTION: OLIGODENOXNUCLEOTIDE AND ITS USE TO INDUCE AN IMMUNE RESPONSE
 ; FILE REFERENCE: 4239-63317
 ; CURRENT APPLICATION NUMBER: US/10/194,035
 ; CURRENT FILING DATE: 2002-07-12
 ; PRIOR APPLICATION NUMBER: PCT/US01/01122
 ; PRIOR FILING DATE: 2001-07-19
 ; PRIOR APPLICATION NUMBER: US 60/176,115
 ; PRIOR FILING DATE: 2000-01-14
 ; NUMBER OF SEQ ID NOS: 119
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 83
 ; LENGTH: 19
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic DNA
 US-10-194-035-83

Query Match 94.4%; Score 17; DB 15; Length 19;
 Best Local Similarity 100.0%; Pred. No. 60;
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGGTCGATCGAGGGGG 17
 |||||
 DB 3 TGGTCGATCGAGGGGG 19

RESULT 9

US-09-874-991C-503
 ; Sequence 503, Application US/09874991C
 ; Publication No. US20040052763A1
 ; GENERAL INFORMATION:
 ; APPLICANT: MOND, JAMES J.
 ; APPLICANT: FLORA, MICHAEL
 ; APPLICANT: KLINMAN, DENNIS M.
 ; TITLE OF INVENTION: IMMUNOSTIMULATORY RNA/DNA HYBRID MOLECULES
 ; FILE REFERENCE: 07787.0042-0
 ; CURRENT APPLICATION NUMBER: US/09/874,991C
 ; CURRENT FILING DATE: 2001-06-07
 ; PRIOR APPLICATION NUMBER: 60/209,797
 ; PRIOR FILING DATE: 2000-06-07
 ; NUMBER OF SEQ ID NOS: 620
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 503
 ; LENGTH: 18
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic HDR
 US-09-874-991C-503

Query Match 91.1%; Score 16.4; DB 13; Length 18;
 Best Local Similarity 94.4%; Pred. No. 1.2e+02;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TGGTCGATCGAGGGGG 18
 |||||
 DB 1 TGCATCGATCGAGGGGG 18

RESULT 10

US-09-874-991C-513
 ; Sequence 513, Application US/09874991C
 ; Publication No. US20040052763A1

```
; GENERAL INFORMATION:
; APPLICANT: WOND, JAMES J.
; APPLICANT: FLORA, MICHAEL
; APPLICANT: KLINMAN, DENNIS M.
; TITLE OF INVENTION: IMMUNOSTIMULATORY RNA/DNA HYBRID MOLECULES
; FILE REFERENCE: 07787.0042-0
; CURRENT APPLICATION NUMBER: US/09/874.991C
; PRIOR FILING DATE: 2001-06-07
; CURRENT FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: 60/209,797
; PRIOR FILING DATE: 2000-06-07
; NUMBER OF SEQ ID NOS: 620
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 513
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic HDR
US-09-874-991C-513

Query Match          91.1%; Score 16.4; DB 13; Length 18;
Best Local Similarity 94.4%; Pred. No. 1.2e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TCGTCGATGCAGGGGGG 18
   ||| ||||| ||||| |||||
Db 1 TGCATCGATGCAGGGGGG 18

RESULT 11
US-09-874-991C-551
; Sequence 551, Application US/09874991C
; Publication No. US20040052763A1
; GENERAL INFORMATION:
; APPLICANT: WOND, JAMES J.
; APPLICANT: FLORA, MICHAEL
; APPLICANT: KLINMAN, DENNIS M.
; TITLE OF INVENTION: IMMUNOSTIMULATORY RNA/DNA HYBRID MOLECULES
; FILE REFERENCE: 07787.0042-0
; CURRENT APPLICATION NUMBER: US/09/874.991C
; PRIOR FILING DATE: 2001-06-07
; CURRENT FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: 60/209,797
; PRIOR FILING DATE: 2000-06-07
; NUMBER OF SEQ ID NOS: 620
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 551
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic HDR
US-09-874-991C-551

Query Match          91.1%; Score 16.4; DB 13; Length 18;
Best Local Similarity 94.4%; Pred. No. 1.2e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TCGTCGATGCAGGGGGG 18
   ||| ||||| ||||| |||||
Db 1 TGCATCGATGCAGGGGGG 18

RESULT 12
US-10-068-160-12
; Sequence 12, Application US/10068160
; Publication No. US20030060440A1
; GENERAL INFORMATION:
; APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA, REPRESENTED BY THE
; APPLICANT: SECRETARY, DEPARTMENT OF HEALTH AND HUMAN SERVICES
; APPLICANT: KLINMAN, Dennis
; APPLICANT: ISHII, Ken
; APPLICANT: VERTHELYI, Daniela
; TITLE OF INVENTION: OLIGODEOXYNUCLEOTIDE AND ITS USE TO INDUCE AN IMMUNE RESPONSE
; FILE REFERENCE: 4239-61999
; CURRENT APPLICATION NUMBER: US/10/068.160
; CURRENT FILING DATE: 2002-02-06
```

```
; FILE REFERENCE: 4239-61999
; CURRENT APPLICATION NUMBER: US/10/068.160
; CURRENT FILING DATE: 2002-02-06
; PRIOR APPLICATION NUMBER: 60/128.898
; PRIOR FILING DATE: 1999-04-12
; NUMBER OF SEQ ID NOS: 120
; SOFTWARE: Patent In version 3.1
; SEQ ID NO 12
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide
US-10-068-160-12

Query Match          91.1%; Score 16.4; DB 15; Length 18;
Best Local Similarity 94.4%; Pred. No. 1.2e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TCGTCGATGCAGGGGGG 18
   ||| ||||| ||||| |||||
Db 1 TGCATCGATGCAGGGGGG 18

RESULT 13
US-10-068-160-14
; Sequence 14, Application US/10068160
; Publication No. US20030060440A1
; GENERAL INFORMATION:
; APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA, REPRESENTED BY THE
; APPLICANT: SECRETARY, DEPARTMENT OF HEALTH AND HUMAN SERVICES
; APPLICANT: KLINMAN, Dennis
; APPLICANT: ISHII, Ken
; APPLICANT: VERTHELYI, Daniela
; TITLE OF INVENTION: OLIGODEOXYNUCLEOTIDE AND ITS USE TO INDUCE AN IMMUNE RESPONSE
; FILE REFERENCE: 4239-61999
; CURRENT APPLICATION NUMBER: US/10/068.160
; CURRENT FILING DATE: 2002-02-06
; PRIOR APPLICATION NUMBER: 60/128.898
; PRIOR FILING DATE: 1999-04-12
; NUMBER OF SEQ ID NOS: 120
; SOFTWARE: Patent In version 3.1
; SEQ ID NO 14
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide
US-10-068-160-14

Query Match          91.1%; Score 16.4; DB 15; Length 18;
Best Local Similarity 94.4%; Pred. No. 1.2e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TCGTCGATGCAGGGGGG 18
   ||||| ||||| ||||| |||||
Db 1 TCGTCGATGCAGGGGGG 18

RESULT 14
US-10-068-160-18
; Sequence 18, Application US/10068160
; Publication No. US20030060440A1
; GENERAL INFORMATION:
; APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA, REPRESENTED BY THE
; APPLICANT: SECRETARY, DEPARTMENT OF HEALTH AND HUMAN SERVICES
; APPLICANT: KLINMAN, Dennis
; APPLICANT: ISHII, Ken
; APPLICANT: VERTHELYI, Daniela
; TITLE OF INVENTION: OLIGODEOXYNUCLEOTIDE AND ITS USE TO INDUCE AN IMMUNE RESPONSE
; FILE REFERENCE: 4239-61999
; CURRENT APPLICATION NUMBER: US/10/068.160
; CURRENT FILING DATE: 2002-02-06
```

; PRIOR APPLICATION NUMBER: 60/128,898
; PRIOR FILING DATE: 1999-04-12
; NUMBER OF SEQ ID NOS: 120
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide
US-10-068-160-18

Query Match 91.1%; Score 16.4; DB 15; Length 18;
Best Local Similarity 94.4%; Pred. No. 1.2e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TGCCTCGATGCAGGGGG 18
||| ||||| |||||
Db 1 TGCCTCGATGCAGGGGG 18

RESULT 15

US-10-068-160-20
; Sequence 20, Application US/10068160
; Publication No. US2003006040A1
; GENERAL INFORMATION:
; APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA, REPRESENTED BY THE
; APPLICANT: SECRETARY, DEPARTMENT OF HEALTH AND HUMAN SERVICES
; APPLICANT: KLINMAN, Dennis
; APPLICANT: ISHII, Ken
; APPLICANT: VERTHELYI, Daniela
; TITLE OF INVENTION: OLIGODEOXYNUCLEOTIDE AND ITS USE TO INDUCE AN IMMUNE RESPONSE
; FILE REFERENCE: 4239-61999
; CURRENT APPLICATION NUMBER: US/10/068,160
; PENDING FILING DATE: 2002-02-06
; PRIOR APPLICATION NUMBER: 60/128,898
; PRIOR FILING DATE: 1999-04-12
; NUMBER OF SEQ ID NOS: 120
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide
US-10-068-160-20

Query Match 91.1%; Score 16.4; DB 15; Length 18;
Best Local Similarity 94.4%; Pred. No. 1.2e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TGCCTCGATGCAGGGGG 18
||| ||||| |||||
Db 1 TGCCTCGATGCAGGGGG 18

Search completed: July 2, 2004, 13:58:25
Job time : 139.732 secs

Qy	2	GC	CGCGGCGCAGGGGG	18
Dd	943	GC	CGCGGCGCAGGGGG	959
RESULT 4				
BUS40484/c				
LOCUS	BUS40484 linear EST 13-SEP-2002			
DEFINITION	AGENCOURT_10325169 NIH_MGC_18 Homo sapiens CDNA clone IMAGE:6571942 5', mRNA sequence.			
ACCESSION	BUS40484			
VERSION	BUS40484.1 GI:22850925			
KEYWORDS	EST.			
SOURCE	Homo sapiens (human)			
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
REFERENCE	NIH-MGC http://mgc.nci.nih.gov/.			
AUTHORS	National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)			
TITLE	Contact: Robert Strausberg, Ph.D.			
JOURNAL	Email: cgapbs-r@mail.nih.gov			
COMMENT	Tissue Procurement: DCTD/BTP/Gazdar CDNA Library Preparation: Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: ILCM2763 row: d column: 22 High quality sequence start: 57 High quality sequence stop: 392. Location/Qualifiers 1..1417 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /clone="IMAGE:6571942" /tissue type="large cell carcinoma" /lab host="DH10B (phage-resistant)" /clone lib="NIH_MGC_18" /note="Organ: lung; Vector: pOTB7; Site: 1: XhoI; Site 2: EcoRI; CDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: This is a NIH_MGC Library."			
ORIGIN				
Query Match	94.4%; Score 17; DB 13; Length 1417;			
Best Local Similarity	100.0%; Pred. No. 2.6e+04;			
Matches	17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
Qy	2	GC	CGCGGCGCAGGGGG	18
Dd	852	GC	CGCGGCGCAGGGGG	836
RESULT 5				
CNS01T3H/c				
LOCUS	CNS01T3H linear GSS 01-SEP-2000			
DEFINITION	Tetraodon nigroviridis genome survey sequence T7 end of clone 194E11 of library G from Tetraodon nigroviridis, genomic survey sequence.			
ACCESSION	AL166022			
VERSION	AL166022.1 GI:7803760			
KEYWORDS	GSS: genome survey sequence.			
SOURCE	Tetraodon nigroviridis			
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetraodontidae; Tetraodontidae; Tetraodon.			
REFERENCE	Roest Crollius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C., Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F., Saurin,W. and Weissenbach,J. Estimate of human gene number provided by genome-wide analysis using Tetraodon nigroviridis DNA sequence Nat. Genet. 25 (2), 235-238 (2000)			
TITLE				
JOURNAL	freshwater pufferfish Tetraodon nigroviridis			
MEDLINE	Genome Res. 10 (7), 939-949 (2000)			
PUBMED	20359837			
FEATURES	Source			
1..630	Location/Qualifiers			
/organism="Tetraodon nigroviridis"				
/mol_type="genomic DNA"				
/db_xref="taxon:99883"				
/clone="194E11"				
/clone lib="G"				
/note="Genoscope sequence ID : COAG194AC06LP1-end : T7"				
ORIGIN				
Query Match	92.2%; Score 16.6; DB 29; Length 630;			
Best Local Similarity	94.1%; Pred. NO. 3.4e+04;			
Matches	16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;			
Qy	2	GC	CGCGGCGCAGGGGG	18
Dd	152	GC	CGCGGCGCAGGGGG	136
RESULT 6				
CNS026IH				
LOCUS	CNS026IH linear GSS 01-SEP-2000			
DEFINITION	Tetraodon nigroviridis genome survey sequence PUC-Ori end of clone 24IC17 of library G from Tetraodon nigroviridis, genomic survey sequence.			
ACCESSION	AL183410			
VERSION	AL183410.1 GI:7821514			
KEYWORDS	GSS: genome survey sequence.			
SOURCE	Tetraodon nigroviridis			
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetraodontidae; Tetraodontidae; Tetraodon.			
REFERENCE	Roest Crollius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C., Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F., Saurin,W. and Weissenbach,J. Estimate of human gene number provided by genome-wide analysis using Tetraodon nigroviridis DNA sequence Nat. Genet. 25 (2), 235-238 (2000)			
TITLE				
JOURNAL	freshwater pufferfish Tetraodon nigroviridis			
MEDLINE	Genome Res. 10 (7), 939-949 (2000)			
PUBMED	20359837			
FEATURES	Source			
1..630	Location/Qualifiers			
/organism="Tetraodon nigroviridis"				
/mol_type="genomic DNA"				
/db_xref="taxon:99883"				
/clone="194E11"				
/clone lib="G"				
/note="Genoscope sequence ID : COAG194AC06LP1-end : T7"				
ORIGIN				
Query Match	92.2%; Score 16.6; DB 29; Length 630;			
Best Local Similarity	94.1%; Pred. NO. 3.4e+04;			
Matches	16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;			
Qy	2	GC	CGCGGCGCAGGGGG	18
Dd	152	GC	CGCGGCGCAGGGGG	136
RESULT 6				
CNS026IH				
LOCUS	CNS026IH linear GSS 01-SEP-2000			
DEFINITION	Tetraodon nigroviridis genome survey sequence PUC-Ori end of clone 24IC17 of library G from Tetraodon nigroviridis, genomic survey sequence.			
ACCESSION	AL183410			
VERSION	AL183410.1 GI:7821514			
KEYWORDS	GSS: genome survey sequence.			
SOURCE	Tetraodon nigroviridis			
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetraodontidae; Tetraodontidae; Tetraodon.			
REFERENCE	Roest Crollius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C., Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F., Saurin,W. and Weissenbach,J. Estimate of human gene number provided by genome-wide analysis using Tetraodon nigroviridis DNA sequence Nat. Genet. 25 (2), 235-238 (2000)			
TITLE				
JOURNAL	freshwater pufferfish Tetraodon nigroviridis			
MEDLINE	Genome Res. 10 (7), 939-949 (2000)			
PUBMED	20359837			
FEATURES	Source			
1..630	Location/Qualifiers			
/organism="Tetraodon nigroviridis"				
/mol_type="genomic DNA"				
/db_xref="taxon:99883"				
/clone="194E11"				
/clone lib="G"				
/note="Genoscope sequence ID : COAG194AC06LP1-end : T7"				
ORIGIN				
Query Match	92.2%; Score 16.6; DB 29; Length 630;			
Best Local Similarity	94.1%; Pred. NO. 3.4e+04;			
Matches	16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;			
Qy				

CA757679
 CA757679.1 G1:25801718
 EST.
 SOURCE
 ORGANISM
 Oryza sativa
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Ehrhartoideae; Oryzoideae; Oryza.
 1 (bases 1 to 577)
 Bohnert,H.J., Borchert,C., Brazille,S., Brooks,J., Eaton,M.,
 Ferreira,H., Kawasaki,S., McCollough,A., Michalowski,C.B.,
 Palacio,C., Scarpa,G., Wheeler,M. and Zepeda,G.R.
 Functional Genomics of Plant Stress Tolerance
 Unpublished (2000)
 CONTACT: Mark Fredrickson
 Department of Plant Biology
 University of Illinois
 1201 W. Gregory Dr., Urbana, IL 61801, USA
 Tel: 2172655473
 Email: bohnertlab@life.uiuc.edu.
 Location/Qualifiers
 1..577
 /organism="Oryza sativa"
 /mol_type="mRNA"
 /strain="Pokkali"
 /db_xref="taxon:4530"
 /clone="O306P11-T3.ab1"
 /tissue_type="roots"
 /dev_stage="1 week"
 /clone_lib="OS"
 /note="2-3 d 150mM NaCl"
 ORIGIN
 Query Match 91.1%; Score 16.4; DB 14; Length 577;
 Best Local Similarity 94.4%; Pred. No. 4e+04; 1; Indels 0; Gaps 0;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 TGCGCCGCGCGAGGGGG 18
 |||||
 DB 119 TGCGCCGCGCGAGGGGG 102
 |||||
 RESULT 12
 CG852075 583 bp DNA linear GSS 18-NOV-2003
 LOCUS ZMWBB0343121.f ZMWBB Zea mays subsp. mays genomic clone
 DEFINITION ZMWBB0343121 5', genomic survey sequence.
 ACCESSION CG852075
 VERSION CG852075.1 G1:38378936
 KEYWORDS GSS.
 SOURCE Zea mays subsp. mays (maize)
 ORGANISM Zea mays subsp. mays
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoidae; Andropogoneae; Zea.
 1 (bases 1 to 583)
 Yu,Y., Kim,H.R., Hatfield,J., Soderlund,C., Bharti,A.K., Messing,J.
 and Wing,R.
 Sequencing of the maize genome
 Unpublished (2003)
 CONTACT: Rod Wing
 Arizona Genomics Institute
 University of Arizona
 Biological Sciences West, 448A, P.O. Box 210088, Tucson, AZ
 85721-0088, USA
 Tel: 520 626 3967
 Fax: 520 621 9288
 Email: http://genome.arizona.edu
 PCR Primers
 FORWARD: T7
 BACKWARD: M13r
 Plate: 0343 Row: I column: 21
 Seq primer: T7

Class: BAC ends.
 Location/Qualifiers
 1..583
 /organism="Zea mays subsp. mays"
 /mol_type="genomic DNA"
 /cultivar="B73"
 /sub_species="mays"
 /db_xref="taxon:4578"
 /clone="ZMWBB0343121"
 /lab_host="DH10B"
 /clone_lib="ZMWBB"
 /note="Vector: pBelosAC11; Site 1: HindIII; Site 2:
 HindIII; Zea mays L. ssp. mays"
 ORIGIN
 Query Match 91.1%; Score 16.4; DB 29; Length 583;
 Best Local Similarity 94.4%; Pred. No. 4e+04; 1; Indels 0; Gaps 0;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 TGCGCCGCGCGAGGGGG 18
 |||||
 DB 284 TGCGCCGCGCGAGGGGG 301
 |||||
 RESULT 13
 BQ465952/c
 LOCUS HT01C12T HT Hordeum vulgare subsp. vulgare cDNA clone HT01C12
 DEFINITION 5-PRIME, mRNA sequence.
 ACCESSION BQ465952
 VERSION BQ465952.1 G1:21273734
 KEYWORDS EST.
 SOURCE Hordeum vulgare subsp. vulgare
 ORGANISM Hordeum vulgare subsp. vulgare
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 Pooidae; Triticeae; Hordeum.
 1 (bases 1 to 660)
 Zhang,H., Potokina,E., Michalek,W., Weschke,W., Stein,N. and
 Graner,A.
 Barley ESTs from germinating seeds
 Unpublished (2002)
 CONTACT: Stein Nils
 Molecular Markers Group, Department Genbank
 Institute of Plant Genetics and Crop Plant Research (IPK)
 Corrensstr. 3, 06466, Gatersleben, Germany
 Tel: 039482-5522
 Fax: 039482-5595
 Email: stein@ipk-gatersleben.de
 Insert length: 660 Std Error: 0.00
 Plate: 1 row: C column: 12
 Seq primer: T3
 Location/Qualifiers
 1..660
 /organism="Hordeum vulgare subsp. vulgare"
 /mol_type="mRNA"
 /cultivar="barke"
 /sub_species="vulgare"
 /db_xref="taxon:112509"
 /clone="HT01C12"
 /tissue_type="endosperm early"
 /dev_stage="0-16 hours after imbibition"
 /lab_host="XL10-Gold"
 /clone_lib="HT"
 /note="Vector: pBluescript SK+; Site 1: EcoRI (5'-end of
 cDNA); Site 2: XhoI (3'-end of cDNA); Due to a cloning
 artefact caused by the kit, in most cases the EcoRI site
 is NOT present, as well as the EcoRI adapter used for
 cloning. To excise the insert, restriction sites upstream
 EcoRI should be used (e.g. BamHI, SalI, PstI). NOTE: Also
 due to the cloning system used Blue/white selection for
 recombinants is not 100% reliable."

ORIGIN

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 2, 2004, 07:36:05 ; Search time 633.732 Seconds
(without alignments)
1231.080 Million cell updates/sec

Title: US-10-068-160-17

Perfect score: 18

Sequence: 1 tgcgcggcgccagggggg 18

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl:

1: gb_ba:
2: gb_hgt:
3: gb_in:
4: gb_om:
5: gb_ov:
6: gb_pat:
7: gb_ph:
8: gb_pl:
9: gb_pr:
10: gb_ro:
11: gb_sts:
12: gb_sy:
13: gb_un:
14: gb_vi:
15: em_ba:
16: em_fun:
17: em_hum:
18: em_in:
19: em_mu:
20: em_or:
21: em_ov:
22: em_pat:
23: em_ph:
24: em_pl:
25: em_ro:
26: em_sts:
27: em_un:
28: em_vi:
29: em_vt:
30: em_htg_hum:
31: em_htg_inv:
32: em_htg_other:
33: em_htg_mus:
34: em_htg_pln:
35: em_htg_rod:
36: em_htg_mam:
37: em_htg_vrt:
38: em_sy:
39: em_htgo_hum:
40: em_htgo_mus:
41: em_htgo_other:

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
C 1	17	94.4	1405	14	SHE581560	AJ581560 suid herp
C 2	17	94.4	23276	2	AC144804	AC144804 Gallus ga
C 3	16.4	91.1	816	8	AK122136	AK122136 Oryza sat
C 4	16.4	91.1	1655	8	AK060251	AK060251 Oryza sat
C 5	16.4	91.1	4225	10	AB017578S1	AB017578 Rattus no
C 6	16.4	91.1	4898	1	AY422718	AY422718 Pseudomon
C 7	16.4	91.1	5278	1	AB004065	AB004065 Pseudomon
C 8	16.4	91.1	96256	9	HS117715	AL0223315 Human DNA
C 9	16.4	91.1	106117	9	AC103564	AC103564 Homo sapi
C 10	16.4	91.1	118436	8	AP005064	AP005064 Oryza sat
C 11	16.4	91.1	161617	9	AC093724	AC093724 Homo sapi
C 12	16.4	91.1	182944	2	AC133783	AC133783 Homo sapi
C 13	16.4	91.1	235115	2	AC133256	AC133256 Rattus no
C 14	16.4	91.1	235785	2	AC121480	AC121480 Rattus no
C 15	16	88.9	10029	1	AE008002	AE008002 Agrobacte
C 16	16	88.9	10029	1	AE009036	AE009036 Agrobacte
C 17	16	88.9	14952	1	SMAJ4445	AJ224445 Sinorhizo
C 18	16	88.9	134940	2	AC018939	AC018939 Homo sapi
C 19	16	88.9	147984	2	AC141987	AC141987 Rattus no
C 20	16	88.9	176967	2	AC135864	AC135864 Oryza sat
C 21	16	88.9	300000	1	SME591784	AL591784 Sinorhizo
C 22	15.4	85.6	852	11	PM3H12G	AL685751 Penicilli
C 23	15.4	85.6	885	8	BT005764	BT005764 Arabidops
C 24	15.4	85.6	887	8	AK107743	AK107743 Oryza sat
C 25	15.4	85.6	900	6	BD267140	BD267140 Compositi
C 26	15.4	85.6	969	6	AX654633	AX654633 Sequence
C 27	15.4	85.6	976	11	PM12D6G	AL684370 Penicilli
C 28	15.4	85.6	988	8	AK061421	AK061421 Oryza sat
C 29	15.4	85.6	1028	8	AK104181	AK104181 Oryza sat
C 30	15.4	85.6	1032	8	AK061195	AK061195 Oryza sat
C 31	15.4	85.6	1039	8	AK104630	AK104630 Oryza sat
C 32	15.4	85.6	1043	8	AK104655	AK104655 Oryza sat
C 33	15.4	85.6	1061	6	AX305960	AX305960 Sequence
C 34	15.4	85.6	1072	8	AF049888	AF049888 Oryza sat
C 35	15.4	85.6	1204	8	AK120540	AK120540 Oryza sat
C 36	15.4	85.6	1246	8	AK105338	AK105338 Oryza sat
C 37	15.4	85.6	1300	8	BT008959	BT008959 Triticum
C 38	15.4	85.6	1426	8	AK058296	AK058296 Oryza sat
C 39	15.4	85.6	1577	8	AK111436	AK111436 Oryza sat
C 40	15.4	85.6	1595	8	OSIA1COX	X85747 O.sativa mr
C 41	15.4	85.6	1605	8	AK109694	AK109694 Oryza sat
C 42	15.4	85.6	1637	8	D83391	D83391 Zea mays mr
C 43	15.4	85.6	1808	10	MMMB6	X99143 M.musculus
C 44	15.4	85.6	1820	10	RNU55179	U55179 Rattus norv
C 45	15.4	85.6	1841	9	HSAL132887	AJ132887 Homo sapi

ALIGNMENTS

RESULT 1
SHE581560/c
LOCUS SHE581560
DEFINITION suid herpesvirus 1 partial ORF1.2 and left end of unique long region.
ACCESSION AJ581560
VERSION AJ581560.1 GI:34368527
KEYWORDS ORF1.2; unique long region.
SOURCE Suid herpesvirus 1
ORGANISM Suid herpesvirus 1
Viruses; dsDNA viruses, no RNA stage; Herpesviridae; Alphaherpesvirinae; Varicellovirus.
REFERENCE 1
AUTHORS Klupp, B.G., Hengartner, C.J., Mettenleiter, T.C. and Enquist, L.W.
TITLE The complete annotated sequence of the pseudorabies virus genome

Pred. No. is the number of results predicted by chance to have a

```

JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1405)
AUTHORS Klupp B.G.
TITLE Direct Submission
JOURNAL Submitted (27-AUG-2003) Klupp B.G., Institute of Molecular Biology,
Greifswald - Insel Rügen, GERMANY
FEATURES
source
    /organism="Suid herpesvirus 1"
    /virus
    /mol_type="genomic DNA"
    /strain="Kaplan"
    /db_xref="taxon:10345"
    3..84
    /note="inverted repeat of nt 442-523"
    /rpt_type=INVERTED
    156..251
    /note="spaced direct imperfect repeats"
    /rpt_type=DIRECT
    /rpt_unit="156..183"
    complement(443..523)
    /note="inverted repeat of nt 3-84"
    /rpt_type=INVERTED
    529..655
    /note="3 spaced imperfect repeats"
    /rpt_type=DIRECT
    /rpt_unit="529..566"
    751..958
    /rpt_type=DIRECT
    /rpt_unit="751..776"
    1252..1405
    /note="ORF1.2"
    /codon_start=1
    /product="ORF1.2 protein"
    /protein_id="CA846334.1"
    /db_xref="GI:34368528"
    /translation="MGGTRGSDAPTWCHTRPTPRPSFSRAARPDPAEPDVGRTGMDV
    ERGTAAQ"
    1375..1405
    /note="ORF1.2
    alternative"
    /codon_start=1
    /product="ORF1.2 protein"
    /protein_id="CA846335.1"
    /db_xref="GI:34368529"
    /translation="MDVERGTAAQ"

ORIGIN
Query Match 94.4%; Score 17; DB 14; Length 1405;
Best Local Similarity 100.0%; Pred. No. 3.9e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGCGCGCGCGCAGGGG 17
Db 1168 TGCGCGCGCGCAGGGG 1152

RESULT 2
AC144804/c
LOCUS AC144804
DEFINITION Gallus gallus clone CH261-22A23, WORKING DRAFT SEQUENCE, 14 ordered
pieces.
ACCESSION AC144804
VERSION AC144804.1 GI:30962733
KEYWORDS HTG; HTGS PHASE2; HTGS DRAFT.
SOURCE Gallus gallus (Chicken)
ORGANISM Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
REFERENCE 1 (bases 1 to 232176)
AUTHORS Cheng, J.-F., Hamilton, M., Peng, Y., Mukherjee, S., Hosseini, R.,

```

```

TITLE
JOURNAL
REFERENCE
AUTHORS
PENG, Z., Malinov, I. and Rubin, E.M.
Direct Submission
2 (bases 1 to 232176)
Cheng, J.-F., Hamilton, M., Peng, Y., Mukherjee, S., Hosseini, R.,
PENG, Z., Malinov, I. and Rubin, E.M.
Direct Submission
Submitted (21-MAY-2003) Genome Sciences, Lawrence Berkeley National
Laboratory, 1 Cyclotron Rd., Berkeley, CA 94720, USA
3 (bases 1 to 232176)
Cheng, J.-F., Hamilton, M., Peng, Y., Mukherjee, S., Hosseini, R.,
PENG, Z., Malinov, I. and Rubin, E.M.
Direct Submission
Submitted (24-JUN-2003) Genome Sciences, Lawrence Berkeley National
Laboratory, 1 Cyclotron Rd., Berkeley, CA 94720, USA

```

```

Sequence Produced by Berkeley FGA
Web site: http://pga.lbl.gov
Center Code: PGABERK
Center Project Name: G104
Bac Clone Name: CH261-22A23

```

This sequence has been compared to sequences of other species using Vista (<http://www-gsd.lbl.gov/visiA>). The results can be viewed at: http://pga.lbl.gov/cgi-bin/search_cvcgd?type=ntvalue=SREBFI

The order-orientation of the draft sequence was accomplished by using: <http://baboon.math.berkeley.edu/mavid>, Lagan (<http://lagan.stanford.edu/>) and paired end information.

Funding agent: Programs for Genomic Applications (NHLBI)

Summary Statistics:
Sequencing vector: Plasmid: pUC18
Chemistry: Dye-terminator Big Dye
Assembly program: Phrap version 0.990329.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 14 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* been provided by the submitter.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.

```

1 1187: contig of 1187 bp in length
1188 1287: gap of unknown length
1288 12634: contig of 11347 bp in length
12635 12734: gap of unknown length
12735 16356: contig of 3722 bp in length
16357 16556: gap of unknown length
16557 26480: contig of 9924 bp in length
26481 26580: gap of unknown length
26581 29898: contig of 3318 bp in length
29899 29998: gap of unknown length
29999 36395: contig of 6597 bp in length
36396 36895: gap of unknown length
36896 39486: contig of 2791 bp in length
39487 42321: contig of 2735 bp in length
42322 42421: gap of unknown length
42422 116738: contig of 74317 bp in length
116739 116838: gap of unknown length
116839 159322: contig of 42484 bp in length
159323 159422: gap of unknown length
159423 177789: contig of 18367 bp in length
177790 177889: gap of unknown length
177890 181431: contig of 3542 bp in length
181432 181531: gap of unknown length
181532 229280: contig of 47749 bp in length
229281 229380: gap of unknown length

```



```

* 229381 232176: contig of 2796 bp in length.
FEATURES             Location/Qualifiers
     source           1..232176
                     /organism="Gallus gallus"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9031"
                     /clone="CH261-22A23"

ORIGIN
Query Match          94.4%; Score 17; DB 2; Length 232176;
Best Local Similarity 100.0%; Pred. No. 1.4e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCGCGCGCGCGCGCGGG 17
    |||||
Db 177704 TCGCGCGCGCGCGGG 177688

RESULT 3
AK1221136/c
LOCUS              616 bp mRNA linear PLN 29-OCT-2003
DEFINITION         Oryza sativa (japonica cultivar-group) cDNA clone:J033135J16, full
                     insert sequence.
ACCESSION          AK1221136
VERSION            GI:37991782
KEYWORDS           FUJ_CDNA; CAP trapper.
SOURCE             Oryza sativa (japonica cultivar-group)
ORGANISM           Oryza sativa (japonica cultivar-group)
                   Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
                   Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
                   Ehrhartoideae; Oryzeae; Oryza.

REFERENCE
AUTHORS            Tanaka,T., Tomaru,A., Toya,T., Tsunoda,Y., Ueda,M., Waki,K.,
                   Xie,Q., Yahagi,W., Yamada,H., Yamamoto,M., Yasunishi,A., Yazaki,J.,
                   Yokomizo,S. and Yoshimura,A.
                   Collection, mapping, and annotation of 28K full-length cDNA clones
                   from japonica rice
                   Unpublished
                   3 (bases 1 to 616)
                   Kikuchi,S.
                   Direct Submission
                   Submitted (31-JAN-2003) Shoshi Kikuchi, National Institute of
                   Agrobiological Sciences, Department of Molecular Genetics, Head of
                   Laboratory of Gene Expression; 2-1-2 Kannondai, Tsukuba, Ibaraki
                   305-8602, Japan (E-mail:skikuchi@nias.affrc.go.jp,
                   Tel:81-29-838-7007, Fax:81-29-838-7007)
                   This clone is one of the 32K full-length cDNA clones from japonica
                   rice.
                   URL : http://cdna01.dna.affrc.go.jp/cDNA/
                   NIAS Rice Full-length cDNA Project Team: Kikuchi,S., Satoh,K.,
                   Nagata,T., Kawagashira,N., Doi,K., Kishimoto,N., Yazaki,J.,
                   Ishikawa,M., Yamada,H., Ooka,H., Hotta,I., Kojima,K., Namiki,T.,
                   Ohneda,E., Yahagi,W., Suzuki,K., Li,C., Ohtsuki,K., Shishiki,T.,
                   Yamamoto,M. and Nakahama,Y.
                   FAIS Genome Sequencing & Analysis Group: Otono,Y., Iida,Y.,
                   Fujimura,T., Ikeda,R., Ishibiki,J., Kawamata,M.,
                   Kobayashi,M., Kodama,T., Kurosaki,T., Kusumegi,T., Lu,M.,
                   Masuda,H., Miura,J., Mizuno,K., Narikawa,R., Niikura,J., Oka,M.,
                   Ryu,R., Sugano,S., Sugiyama,A., Suzuki,Y., Tsunoda,Y., Ueda,M.,
                   Xie,Q., Yokomizo,S., Yoshimura,A., Matsubara,K. and Murakami,K.
                   Genome Exploration Research Group in Riken Genomic Sciences Center
                   and Genome Science Laboratory in Riken: Adachi,J., Aizawa,K.,
                   Akimura,T., Arakawa,T., Carninci,P., Fukuda,S., Hanagaki,T.,
                   Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K.,
                   Hiraoaka,T., Hori,P., Iida,J., Imamura,K., Imotani,K., Ishii,Y.,
                   Itoh,M., Kagawa,I., Kanagawa,S., Katoh,H., Kawai,J.,
                   Kishikawa-Hirozane,T., Kojima,Y., Kondo,S., Konno,H., Kouda,M.,
                   Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M.,
                   Nakamura,M., Nishii,K., Nomura,K., Numasaki,R., Ohno,M., Osato,N.,
                   Ota,Y., Saitoh,H., Sakai,C., Sakai,K.,
                   Sakazume,N., Sano,H., Sasaki,D., Sato,K., Shibata,K.,
                   Sakazume,N., Sano,H., Sasaki,D., Sato,K., Shibata,K.,
                   Shinagawa,A., Shiraki,T., Sogabe,Y., Tagami,M.,
                   Tagami-Takeda,Y., Tagawa,A., Takahashi,P.,
                   Takaku-Akahira,S., Tanaka,T., Tomaru,A., Toya,T., Waki,K.,
                   Yasunishi,A. and Hayashizaki,Y.
                   Location/Qualifiers
                   1..616
                   /organism="Oryza sativa (japonica cultivar-group)"
                   /mol_type="mRNA"
                   /cultiVar="Nippombare"
                   /db_xref="taxon:39947"
                   /clone="J033135J16"

ORIGIN
Query Match          91.1%; Score 16.4; DB 8; Length 616;
Best Local Similarity 94.4%; Pred. No. 8.2e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TCGCGCGCGCGCGCGGG 18
    |||||
Db 224 TCGCGCGCGCGCGGGAG 207

RESULT 4
AK060251/c
LOCUS              1665 bp mRNA linear PLN 24-JUL-2003
DEFINITION         Oryza sativa (japonica cultivar-group) cDNA clone:001-004-C03, full
                     insert sequence.
ACCESSION          AK060251
VERSION            GI:32970269
KEYWORDS           FLI_CDNA; oligo-capping.
SOURCE             Oryza sativa (japonica cultivar-group)
ORGANISM           Oryza sativa (japonica cultivar-group)
                   Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
                   Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
                   Takaku-Akahira,S.

```

REFERENCE
AUTHORS

Ehrhartoidae; Oryzae; Oryza.

1 The Rice Full-length cDNA Consortium, National Institute of Agrobiological Sciences Rice Full-length cDNA Project Team: Kikuchi, S., Satoh, K., Nagata, T., Kawagashira, N., Doi, K., Kishimoto, N., Yazaki, J., Ishikawa, M., Yamada, H., Ooka, H., Hotta, I., Kojima, K., Namiki, T., Ohneda, E., Yahagi, W., Suzuki, K., Li, C., Ohsuka, K., Shishiki, T., Foundation of Advancement of International Science Genome Sequencing & Analysis Group, Tsunoda, Y., Iida, Y., Sugano, S., Fujimura, T., Suzuki, Y., Tsunoda, Y., Kurosaki, T., Kodama, T., Masuda, H., Kobayashi, M., Xie, Q., Lu, M., Narikawa, R., Sugiyama, A., Mizuno, K., Yokomizo, S., Niikura, J., Ikeda, R., Ishibiki, J., Kawamata, M., Yoshimura, A., Miura, J., Kusumegi, T., Oka, M., Ryu, R., Ueda, M., Matsubara, K., RIKEN, Kawai, J., Carninci, P., Adachi, J., Aizawa, K., Arakawa, T., Fukuda, S., Hara, A., Hashidume, W., Hayatsu, N., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kondo, S., Konno, H., Miyazaki, A., Osato, N., Oka, Y., Saito, R., Sasaki, D., Sato, K., Shibata, K., Shinagawa, A., Shiraki, T., Yoshino, M., and Hayashizaki, Y.

TITLE Collection, mapping, and annotation of over 28,000 cDNA clones from japonica rice

JOURNAL Science 301 (5631), 376-379 (2003)

MEDLINE 22752273

PUBMED 12869764

2 (bases 1 to 1665)

Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Doi, K., Fujimura, T., Fukuda, S., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayashizaki, Y., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hori, F., Hotta, I., Iida, Y., Ikeda, R., Inamura, K., Imoto, K., Imotani, K., Ishibiki, J., Ishii, Y., Ishikawa, M., Itoh, M., Kagawa, I., Kanagawa, S., Katoh, H., Kawagashira, N., Kawai, J., Kawamata, M., Kikuchi, S., Kishikawa-Hirozane, T., Kishimoto, N., Kobayashi, M., Kodama, T., Kojima, K., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Kurosaki, T., Kusumegi, T., Li, C., Lu, M., Masuda, H., Matsubara, K., Matsuyama, T., Miura, J., Miyazaki, A., Mizuno, K., Murakami, K., Murakami, M., Nagata, T., Nakamura, M., Namiki, T., Narikawa, R., Niikura, J., Nishi, K., Nomura, K., Numasaki, R., Ohneda, E., Ohno, M., Ohtsuki, K., Oka, M., Ooka, H., Osato, N., Ota, Y., Otomo, Y., Ryu, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Sato, K., Satoh, K., Shibata, K., Shinagawa, A., Shiraki, T., Shishiki, T., Sogabe, Y., Sugano, S., Sugiyama, A., Suzuki, K., Suzuki, Y., Tagami, M., Tagami-Takeda, Y., Tagawa, A., Takahashi, P., Takaku-Akahira, S., Tanaka, T., Tomaru, A., Toya, T., Tsunoda, Y., Ueda, M., Waki, K., Xie, Q., Yahagi, W., Yamada, H., Yamamoto, M., Yasunishi, A., Yazaki, J., Yokomizo, S. and Yoshimura, A.

Direct Submission

Submitted (05-DEC-2001) Shoshi Kikuchi, National Institute of Agrobiological Sciences, Department of Molecular Genetics, Head of Laboratory of Gene Expression; 2-1-2 Kannondai, Tsukuba, Ibaraki 305-8602 Japan (E-mail: shikuchi@nias.affrc.go.jp, Tel: 81-29-839-7007, Fax: 81-29-839-7007)

This clone is one of the 28K full-length cDNA clones from japonica rice.

URL : <http://cdna01.dna.affrc.go.jp/cdna/>

NIAS Rice Full-length cDNA Project Team: Kikuchi, S., Satoh, K., Nagata, T., Kawagashira, N., Doi, K., Kishimoto, N., Yazaki, J., Ishikawa, M., Yamada, H., Ooka, H., Hotta, I., Kojima, K., Namiki, T., Ohneda, E., Yahagi, W., Suzuki, K., Li, C., Ohsuka, K., Shishiki, T., and Yamamoto, M.

FAIS Genome Sequencing & Analysis Group: Ootomo, Y., Iida, Y., Fujimura, T., Ikeda, R., Ishibiki, J., Kawamata, M., Kobayashi, M., Kodama, T., Kurosaki, T., Kusumegi, T., Lu, M., Masuda, H., Miura, J., Mizuno, K., Narikawa, R., Niikura, J., Oka, M., Ryu, R., Sugano, S., Sugiyama, A., Suzuki, Y., Tsunoda, Y., Ueda, M., Xie, Q., Yokomizo, S., Yoshimura, A., Matsubara, K., and Murakami, K.

Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken: Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hori, F., Iida, J., Imamura, K., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kanagawa, S., Katoh, H., Kawai, J., Kishikawa-Hirozane, T., Kojima, Y., Kondo, S., Konno, H., Kouda, M.,

TITLE
JOURNAL

AB017578S1 4225 bp DNA linear ROD 20-NOV-1999

Rattus norvegicus gene for cGMP-binding cGMP-specific phosphodiesterase, exon1a, exon1b and 5'-flanking region.

AB017578 1 GI:5926761

cGMP-binding cGMP-specific phosphodiesterase; alternative splicing.

1 of 3

Rattus norvegicus (Norway rat)

Rattus norvegicus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

1

Kotera, J., Fujishige, K., Imai, Y., Kawai, E., Michibata, H., Akatsuka, H., Yanaka, N. and Omori, K.

Genomic origin and transcriptional regulation of two variants of cGMP-binding cGMP-specific phosphodiesterases

Eur. J. Biochem. 262 (3), 866-873 (1999)

99339957

10411650

2 (bases 1 to 4225)

Omori, K.

Direct Submission

Submitted (10-SEP-1998) Kenji Omori, Tanabe Seiyaku Co. Ltd., Discovery Research Laboratory, Basic Technology Department; 2-50 Kawagishi-2-chome, Toda, Saitama 335-8505, Japan (E-mail: k-omori@tanabe.co.jp, Tel: +81-48-433-8069, Fax: +81-48-433-8159)

COMMENT

FEATURES
source

1. 4225

/organism="Rattus norvegicus"

/mol_type="genomic DNA"

/db_xref="taxon:10116"

/clone_lib="EMBL3 SP6/T7 library (Clontech, USA)"

/clone="prpDEVglab"

/product="cGMP-binding cGMP-specific phosphodiesterase"

/note="alternative splicing exon1a"

3444..4166

/product="cGMP-binding cGMP-specific phosphodiesterase"

/note="alternative splicing exon1b"

ORIGIN

Query Match 91.1%; Score 16.4; DB 10; Length 4225;

FEATURES
source

1. 1665

/organism="Oryza sativa (japonica cultivar-group)"

/mol_type="mRNA"

/cultivar="Nipponbare"

/db_xref="taxon:39947"

/clone="001-004-C03"

ORIGIN

Query Match 91.1%; Score 16.4; DB 8; Length 1665;

Best Local Similarity 94.4%; Pred. No. 6.7e+03;

Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TGGCGCGCGCGCGCGGGG 18

Db 1338 TGCCTCGCGCGCGCGGGGAG 1321

RESULT 5
AB017578S1

LOCUS

DEFINITION

AB017578S1 4225 bp DNA linear ROD 20-NOV-1999

Rattus norvegicus gene for cGMP-binding cGMP-specific phosphodiesterase, exon1a, exon1b and 5'-flanking region.

ACCESSION

AB017578 1 GI:5926761

VERSION

AB017578.1

KEYWORDS

cGMP-binding cGMP-specific phosphodiesterase; alternative splicing.

SEGMENT

1 of 3

SOURCE

Rattus norvegicus (Norway rat)

ORGANISM

Rattus norvegicus

REFERENCE

1

Kotera, J., Fujishige, K., Imai, Y., Kawai, E., Michibata, H., Akatsuka, H., Yanaka, N. and Omori, K.

AUTHORS

Genomic origin and transcriptional regulation of two variants of cGMP-binding cGMP-specific phosphodiesterases

JOURNAL

Eur. J. Biochem. 262 (3), 866-873 (1999)

MEDLINE

99339957

PUBMED

10411650

REFERENCE

2 (bases 1 to 4225)

AUTHORS

Omori, K.

TITLE

Direct Submission

JOURNAL

Submitted (10-SEP-1998) Kenji Omori, Tanabe Seiyaku Co. Ltd., Discovery Research Laboratory, Basic Technology Department; 2-50 Kawagishi-2-chome, Toda, Saitama 335-8505, Japan (E-mail: k-omori@tanabe.co.jp, Tel: +81-48-433-8069, Fax: +81-48-433-8159)

FEATURES
source

1. 4225

/organism="Rattus norvegicus"

/mol_type="genomic DNA"

/db_xref="taxon:10116"

/clone_lib="EMBL3 SP6/T7 library (Clontech, USA)"

/clone="prpDEVglab"

/product="cGMP-binding cGMP-specific phosphodiesterase"

/note="alternative splicing exon1a"

3444..4166

/product="cGMP-binding cGMP-specific phosphodiesterase"

/note="alternative splicing exon1b"

exon

3444..4166

exon

3444..4166

ORIGIN

Query Match 91.1%; Score 16.4; DB 10; Length 4225;

Best Local Similarity 94.4%; Pred. No. 5.5e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TCGCGCGCGCGAGGGGG 18
||||| |||||||
Db 3447 TCGCGCGCGCGAGGGGG 3464

RESULT 6
AY422718/c
LOCUS
DEFINITION Pseudomonas sp. K82 catechol 2,3 gene cluster, partial sequence.
ACCESSION AY422718
VERSION AY422718.1 GI:37790591
KEYWORDS
SOURCE
ORGANISM Pseudomonas sp. K82
Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
Pseudomonadaceae; Pseudomonas.
REFERENCE
1 (bases 1 to 4898)
Kim,S.-I., Kim,J.-Y. and Kim,E.-A.
TITLE
Proteome analysis of aromatic compounds degrading bacterium,
Pseudomonas sp. K82
JOURNAL
REFERENCE
2 (bases 1 to 4898)
Kim,S.-I.
Direct Submission
TITLE
Submitted (25-SEP-2003) Proteome Analysis, Korea Basic Science
Institute, 52, Yeosu-Dong, Yusong-Ku, Daejeon 305-806, Korea
JOURNAL
FEATURES
source
1..4898
/organism="Pseudomonas sp. K82"
/mol_type="genomic DNA"
/strain="K82"
/db_xref="taxon:251433"
<1..318
/codon_start=1
/transl_table=11
/product="aniline dioxygenase beta subunit"
/protein_id="AA03447.1"
/db_xref="GI:37790592"
/translation="EFHRRRLDRVSRIGTGLAFSOPPTSRTHWGLGVWPSDDR
GNEWRARYSTLAESREGRVLAGNGFVLRQSAQGLVILKQVNLIDSDCLQGNNS
FTL"
335..1342
/codon_start=1
/transl_table=11
/product="aniline dioxygenase reductase"
/protein_id="AA03448.1"
/db_xref="GI:37790593"
/translation="MKLASHLTAVSPQSDAILSLGVGGORHFSQSGVITL
RFTLARGQPLVLYAGSGGIATPFALEALILQAPQVRLFYACDRATAMLLAHLQ
LQAGSQRLIRHYDAEQGLPTQALLAQTOGLEAADAYLCQPEAFHSHVLAALAA
GIEPSRVYEDFCAALGAVETGAEGPDABLTVQLKGQTHVTVRQGLLGMILDAAR
AGRPHACRVGECASCMLRVGDEVLRDSDVLEDDAAGWELLACHTRAASQVLR
S"
1390..2292
/codon_start=1
/transl_table=11
/product="putative Lys-R type regulator"
/protein_id="AA03449.1"
/db_xref="GI:37790594"
/translation="WTRDGTTPMDLIRAPLALRHGSGVEVAADMEGIDSTLRRI
RVLEQRFGTTLVRSEAGWKASADLHALVSAQHMEARASFSQHQEGAGVYRSLM
DYPNRPAPVYALGKPRLLNITTEHFNLEQDQVDIAVRLARFVNSLRVR
KIGAVAGYAGRAIDHTSASPAFVDDHLLAMNQQFHQDHNFYALNDWKF
GUTGKRVQSDSFVPMHICALGHWGVALLPKFAADYPELVYPEKLPFETELVLSR
FOLLAQWQRELAHQEAWTPQ"
2403..2678
/codon_start=1
/transl_table=11
/product="ferredoxin"

/protein_id="AA03450.1"
/db_xref="GI:37790595"
/translation="WVRLGRKGI PVGVNGCGVCKVRI VEGQIKALGPISR AHVTL D
EENQGYTLACRAVAPQTPVNLVAGLKKPFSKRAESATASPSIQQ"
2700..3644
/codon_start=1
/transl_table=11
/product="catechol 2,3-dioxygenase"
/protein_id="AA03451.1"
/db_xref="GI:37790596"
/translation="MGVMRIGHASLKVMDAAVRHYENVYVGLMKTMMKAGNVYLK
RWMDKYSVILTPSDQAGMHLAYKVEADLEALQCKT EANGVKTITMLDGLPSTG
MLQFKLPSCHEMRLYASKEFGVTDVGNINPDWPDGLAGAGHLDHCLLMCEMPE
AGINTVADNTRFMTEALDFLTEQVLVGEQNMQAATWARTTTPHDIAFPVGGPSGL
HHLAFELDSHWDVLSADVNAKTRIDVAPTRHGTRGETIYFFDPSGRNRETFAGL
GYLAQRDRPVTTWTEDQLGSGIPYHTGYLVPSTFEVYT"
3790..4221
/codon_start=1
/transl_table=11
/product="unknown"
/protein_id="AA03452.1"
/db_xref="GI:37790597"
/translation="MTSALVSPSSVITASAAACQAAVAHAESAASIRINNAVTDASG
TUTAFMRPHAFILHSIDIAIDKAYTAASFGFTSQMGVIGDDELLRIGLNRQRLVL
FGGLPIVAGGQRIIGIGVSGSAEQDEACARAGLKALGLD"
4247..54898
/codon_start=1
/transl_table=11
/product="2-hydroxymuconic 6-semialdehyde dehydrogenase"
/protein_id="AA03453.1"
/db_xref="GI:37790598"
/translation="MKQFLNFINFGDFVATAKTFENRNPNATNEVVGIVHEAGAEVDA
VAAGRAALKGEMTMSVVKRAELHVADEINRRPDDFLAASLADTGKPSLASHDI
PRGAANFKIFADIVKQVPTSPQMTTPDQGTATSYGLRPLGVGVICPMNPLILLMT
WKVGPALACRQHQS SVKPSSETPATALLGEVNAVGVPKSGVPGNARLRPLGRRI"
Query Match 91.1%; Score 16.4; DB 1; Length 4898;
Best Local Similarity 94.4%; Pred. No. 5.4e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TCGCGCGCGCGAGGGGG 18
||||| |||||||
Db 1519 TCGCGCGCGCGAGGGGG 1502

ORIGIN

RESULT 7
AB004065/c
LOCUS
DEFINITION Pseudomonas sp. genes for ORF1, ORF2, ORF3, chloroplast-type
ferredoxin, catechol 2,3-dioxygenase, 2-hydroxymuconic
6-semialdehyde dehydrogenase, partial and complete cds.
ACCESSION AB004065 D86528
VERSION AB004065.1 GI:11610562
KEYWORDS 2-hydroxymuconic 6-semialdehyde dehydrogenase; catechol
2,3-dioxygenase; chloroplast-type ferredoxin; ORF3; ORF2; ORF1.
SOURCE Pseudomonas sp.
ORGANISM Bacteria; Proteobacteria.
REFERENCE
1
Murakami,S., Nakanishi,Y., Kodama,N., Takenaka,S., Shinke,R. and
Aoki,K.
TITLE
Purification, characterization, and gene analysis of catechol
2,3-dioxygenase from the aniline-assimilating bacterium Pseudomonas
species AN-2
JOURNAL Biosci. Biotechnol. Biochem. 62 (4), 747-752 (1998)
MEDLINE 98276889
PUBMED 9614705
REFERENCE
2 (bases 1 to 5278)
Murakami,S.
AUTHORS
Direct Submission
TITLE
Submitted (16-MAY-1997) Shuichi Murakami, Kobe University,
Department of Biofunctional Chemistry; 1-1 Rokkodai-cho, Nada-ku,

Kobe 657, Japan (E-mail:hakko2@kobe-u.ac.jp, Tel.81-78-803-0681,
 Fax:81-78-803-0680)
 D86528:Submitted (08-Jul-1996).
 Location/Qualifiers
 source 1. .5278
 /organism="Pseudomonas sp."
 /mol_type="genomic DNA"
 /strain="Y-2"
 /db_xref="taxon:306"
 /clone="pks11"
 <1. .318
 /codon_start=1
 /evidence=not experimental
 /transl_table=11
 /product="ORF1"
 /protein_id="BAB18929.1"
 /db_xref="GI:11610563"
 /translations="EFDRRLDRVSRLTGLAFSPFTRTARHWGLEVWPSFDR
 GNEWRARYSFTLAESRECHNRVLGNGFVLRQSAQGLVIVLKQVNLIDSDCLQGNNS
 FEL"
 335..1342
 /codon_start=1
 /evidence=not experimental
 /transl_table=11
 /product="ORF2"
 /protein_id="BAB18930.1"
 /db_xref="GI:11610564"
 /translations="MKLAHSLTVAVSQSDAILLTGLVDGQGORPSPQSQYITL
 AVFQDEHWRCSYISAPDQGAISLLVRVAGRVSNWLCDDHARGGQRLQVLPAG
 RFLARHGQVLLVWYDAGSLTAPFALAREALLOQAPVRLFYACRDRATMLLAHQ
 LQAGSGQRLRWYDAGSLTAPFALAREALLOQAPVRLFYACRDRATMLLAHQ
 GIEPSRYRDPGAALGAVETGAEGPDALTVQLKGQHTVSVRGQFLLAGMLDAG
 LAVPHACRVGECASCMLRVLDSSVLDDDAAGWLLACRTRAASAQVRLRF
 S"
 1390..2292
 /codon_start=1
 /evidence=not experimental
 /transl_table=11
 /product="ORF3"
 /protein_id="BAB18931.1"
 /db_xref="GI:11610565"
 /translations="MTRDGTTPDWDLIRAFILALRHGVSVEVADMEGIDSLRERI
 RVLEQRPGRFLVRSNGWASADLHALVSAQMEEARSPSQNCHGAGVVRISLM
 DVPAKPAFVPLVSENGWASADLHALVSAQMEEARSPSQNCHGAGVVRISLM
 KIGAVAVGASAYLARHDSNPAFVDDHLLANLQFQHDNFTYVAILDWAIF
 GLTKVRQSDSPVPAHLGALGHVALLPKFVAADYPELVPEKLFETELWLVS
 FDLAAWQREBLDRLOEAMTPQ"
 2403..2678
 /gene="alnD"
 2403..2678
 /gene="alnD"
 /function="electron transfer protein"
 /codon_start=1
 /evidence=not experimental
 /transl_table=11
 /product="chloroplast-type ferredoxin"
 /protein_id="BAB18932.1"
 /db_xref="GI:11610566"
 /translations="VRLGRKGIPVCGVNGCGVKRIVBGGIKALGPIRAHVTL
 ENQGYTLACRVAPQPVNLVAGKLSKPFSGRAESATASPSIQQQ"
 2700..3644
 /gene="alnE"
 2700..3644
 /gene="alnE"
 /EC_number="1.13.11.2"
 /function="meta-cleavage of catechol"
 /codon_start=1
 /evidence=experimental
 /transl_table=11
 /product="catechol 2,3-dioxygenase"
 /protein_id="BAB18933.1"
 /db_xref="GI:11610567"
 /translations="MGVMRIGHASLKMMDMDAARHYENVLGKTTMKDKAGNVYIKC

MDWKYSVILTPSPDQAGNHLAYKVEKADLEALQOKIEAMGVKTTMLDEGLPSTG
 RMLQKLPSEHMRILYASKEFYGTQVGNINPDWPDGLKGAHMLDHLCLLACENWPE
 AGINTVADNTRFMTALDFFLEQVLVGPEGNMQAATWMAITTHDIAFVGGPSGL
 HIAFELDSHVDVLKSAVMAKTRIDVAPTRHGI TRGETIYFPDPSNRNETAGL
 GYLAQRDRPVTWTWEDQLGSGIFYHTGLVLPSTEVYI"
 4245..4808
 /gene="alnG"
 4245..4808
 /gene="alnG"
 /note="7 amino acids coded by Tns attached at C terminal."
 /codon_start=1
 /evidence=experimental
 /transl_table=11
 /product="2-hydroxymuconic 6-semialdehyde dehydrogenase"
 /protein_id="BAB18934.1"
 /db_xref="GI:11610568"
 /translation="NKQFLNFINGDFVATKTFENRNPATNEWVGLVHENGQAEVDAA
 VVAGRAALKGWGTMSVVKRAELHVADEINRRPDDFLAELADTKPRSLASHDI
 PRGANFKIFADIVKNVPTESFQMTTDSGTATSYGLRTPGLGVGVICPMNPLLLMT
 WVGPAALGCTIVIVKPSSEITLLHK"
 4788..5278
 /note="transposon Tns-Mob"
 /organism="Escherichia coli"

gene

CDS

misc_recomb

ORIGIN

Query Match 91.1%; Score 16.4; DB 1; Length 5278;
 Best Local Similarity 94.4%; Pred No. 5.3e+03;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 TCGCGCGCGCGAGGGGG 18
 |||||
 DB 1519 TCGCGCGCGCGAGGGTGG 1502

RESULT 8

HS117715

LOCUS

DEFINITION

Human DNA sequence from clone RPS-117715 on chromosome 22q13.1
 Contains a novel gene, the MS55 gene for serum constituent protein
 MSE55, the LGALS2 gene for soluble Galactose-binding Lectin 2
 (Lectin 2, S-Lac Lectin 2, HL14), ESTs, an STS, GSSs and two
 putative CpG islands, complete sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

AL022315
 AL022315.1 GI:3820991
 HTG; CpG island; galactin; lectin; LGALS2; MSE55.
 Homo sapiens (human)
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 96256)
 Coville,G.
 Direct Submission
 Submitted (05-JUN-2003) Wellcome Trust Sanger Institute, Hinxton,
 Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
 humquerry@sanger.ac.uk Clone requests: clonesrequest@sanger.ac.uk
 On Nov 2, 1998 this sequence version replaced gi:3550020.
 During sequence assembly data is compared from overlapping clones.
 Where differences are found these are annotated as variations
 together with a note of the overlapping clone name. Note that the
 variation annotation may not be found in the sequence submission
 corresponding to the overlapping clone, as we submit sequences with
 only a small overlap as described above.
 The following abbreviations are used to associate primary accession
 numbers given in the feature table with their source databases:
 Em., ENBL; Swi, SWISSPROT; Tr, TREMBL; Wp, WORMPEP; Information
 on the WORMPEP database can be found at
 http://www.sanger.ac.uk/Projects/C_elegans/wormpep -----
 Genome Center
 Center: Wellcome Trust Sanger Institute
 Center code: SC
 Web site: http://www.sanger.ac.uk
 Contact: humquerry@sanger.ac.uk

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.

This sequence was generated from part of bacterial clone contigs of human chromosome 22, constructed by the Sanger Centre Chromosome 22 Mapping Group. Further information can be found at <http://www.sanger.ac.uk/HGP/Chr22>

RP5-117715 is from the library RPI-5 constructed by the group of Pieter de Jong. For further details see <http://www.chori.org/bacpac/home.htm>

VACATOR: pCYPAC2

This sequence is the entire insert of clone RP5-117715.

FEATURES

```

    source
        1..96256
            /organism="Homo sapiens"
            /mol_type="genomic DNA"
            /db_xref="taxon:9606"
            /chromosome="22"
            /map="q13.1"
            /clones="RP5-117715"
            /clone_lib="RPI-5"
    1..231
        repeat_region
            /note="AluSq repeat: matches 59. .299 of consensus"
            complement(480. .554)
        repeat_region
            /note="MIR repeat: matches 186. .262 of consensus"
            1092. .1102
        repeat_region
            /note="2.2 copies 5 mer CCTGG 22% conserved"
            1260. .1278
        repeat_region
            /note="19.0 copies 1 mer G 29% conserved"
            1866. .1775
        repeat_region
            /note="MIR repeat: matches 29. .137 of consensus"
            1851. .1877
        repeat_region
            /note="3.0 copies 9 mer CCACCCACC 36% conserved"
            1863. .1874
        repeat_region
            /note="2.4 copies 5 mer CCCAC 24% conserved"
            1967. .2076
        repeat_region
            /note="L2 repeat: matches 2986. .3098 of consensus"
            2294. .2310
        repeat_region
            /note="2.4 copies 7 mer AGCTACC 25% conserved"
            2321. .2334
        repeat_region
            /note="2.8 copies 5 mer GTCCAG 28% conserved"
            2358. .2379
        repeat_region
            /note="2.4 copies 9 mer TCTGCCAGC 44% conserved"
            complement(2493. .2617)
        repeat_region
            /note="MIR repeat: matches 60. .212 of consensus"
            2735. .2755
        repeat_region
            /note="2.1 copies 10 mer CTCCAGTGCT 35% conserved"
            2853. .2868
        repeat_region
            /note="2.3 copies 7 mer CCACCAT 23% conserved"
            2900. .2911
        repeat_region
            /note="2.4 copies 5 mer AGGC 24% conserved"
            3071. .3174
        repeat_region
            /note="MIR repeat: matches 84. .191 of consensus"
            complement(3188. .3399)
        repeat_region
            /note="MIR repeat: matches 36. .262 of consensus"
            3462. .3483
        repeat_region
            /note="3.7 copies 6 mer TCTCCC 37% conserved"
            3466. .3483
        repeat_region
            /note="3.6 copies 5 mer CTCT 27% conserved"
            3494. .3523
        repeat_region
            /note="15.0 copies 2 mer CT 51% conserved"
            3719. .3736
        repeat_region
            /note="2.2 copies 8 mer GGAGGAG 36% conserved"
            4020. .4132
        repeat_region
            /note="MIR repeat: matches 60. .169 of consensus"
            4270. .4284
        repeat_region
            /note="5.0 copies 3 mer CCT 21% conserved"
            complement(4630. .4853)

```

```

repeat_region
    /note="MIR repeat: matches 16. .253 of consensus"
    5577. .5604
    /note="2.5 copies 11 mer GGGCAGAGA 38% conserved"
    5817. .5876
    /note="L2 repeat: matches 3003. .3060 of consensus"
    5878. .5895
    /note="3.0 copies 6 mer CCTCA 29% conserved"
    5879. .5895
    /note="3.4 copies 5 mer CTCA 25% conserved"
    6852. .6914
    /note="MIR repeat: matches 81. .143 of consensus"
    7058. .7069
    /note="2.4 copies 5 mer GAGG 24% conserved"
    7140. .7157
    /note="3.6 copies 5 mer GGAGA 29% conserved"
    complement(7185. .7506)
    /note="L2 repeat: matches 2917. .3259 of consensus"
    7637. .7650
    /note="14.0 copies 1 mer A 28% conserved"
    7755. .8018
    /note="AluSx repeat: matches 1. .302 of consensus"
    8067. .8176
    /note="MIR3 repeat: matches 49. .171 of consensus"
    8242. .8260
    /note="2.4 copies 8 mer GCACACAG 29% conserved"
    8365. .8386
    /note="4.4 copies 5 mer CCAGC 26% conserved"
    8754. .8765
    /note="2.4 copies 5 mer GGGGA 24% conserved"
    complement(8836. .9040)
    /note="MIR repeat: matches 13. .262 of consensus"
    9235. .9333
    /note="MIRSA repeat: matches 63. .163 of consensus"
    9358. .9652
    /note="AluSx repeat: matches 1. .303 of consensus"
    complement(join(10190. .10315,10888. .10998))
    /gene="dJ117715.1"
    /gene="dJ117715.1"
    /gene="dJ117715.1"
    /note="supported by predicted exons
    match: ESTs: Sm:AA316883"
    /codon_start=1
    /evidence=not_experimental
    /product="dJ117715.1 (PUTATIVE novel protein)"
    /protein_id="CAB42832.1"
    /db_xref="GI:4808220"
    /translation="DILEHMRQADSRQELCOKLHVGQSLQNAEILRDQVLQEMED
    LRKARTLKQCDLKYHRMATVLAQLESIEKRDQ"
    10413. .10522
    /note="MIR repeat: matches 43. .153 of consensus"
    10579. .10750
    /note="L2 repeat: matches 3103. .3269 of consensus"
    10863. .10882
    /note="4.0 copies 5 mer GGGCA 31% conserved"
    11054. .11064
    /note="2.2 copies 5 mer CAGGG 22% conserved"
    11102. .11111
    /note="2.5 copies 4 mer GGA 20% conserved"
    11139. .11275
    /note="MIR repeat: matches 70. .198 of consensus"
    11485. .11499
    /note="2.5 copies 6 mer CCCACA 21% conserved"
    11591. .11611
    /note="1.9 copies 11 mer CTGACCTGCCA 42% conserved"
    11934. .11947
    /note="2.3 copies 6 mer ACCCCC 28% conserved"
    11967. .12590
    /note="15.6 copies 40 mer
    CCTGTACTCTGTGAGGCCCTCTTACACACCCCCAG 526% conserved"
    12128. .12139
    /note="2.0 copies 6 mer CCCATG 24% conserved"
    12441. .12452
    /note="2.0 copies 6 mer GCCCTG 24% conserved"

```

```

repeat_region 12557..12569
/note="2.2 copies 6 mer GCGCTG 26% conserved"
repeat_region 12663..12697
/note="5.8 copies 6 mer CTTCTT 70% conserved"
repeat_region 12763..12775
/note="2.2 copies 6 mer TTGAGC 26% conserved"
repeat_region 13154..13168
/note="AluX repeat: matches 1..308 of consensus"
repeat_region 13480..13747
/note="AluYB repeat: matches 30..311 of consensus"
repeat_region 13760..13846
/note="29.0 copies 3 mer GAG 77% conserved"
repeat_region 13762..13784
/note="2.1 copies 11 mer GGAGGAGGAGG 46% conserved"
repeat_region 13779..13788
/note="2.5 copies 4 mer GGAG 20% conserved"
repeat_region 13860..13880
Query Match 91.1%; Score 16.4; DB 9; Length 96256;
Best Local Similarity 94.4%; Pred. No. 2.9e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TCGCGCGCGCGAGGGGG 18
Db 21755 TCGCGCGCGCGAGGGGG 21772

RESULT 9
AC103564 106117 bp DNA linear PRI 23-MAR-2002
LOCUS Homo sapiens BAC clone RP11-788A1 from 2, complete sequence.
DEFINITION AC103564
VERSION AC103564.5 GI:19482407
KEYWORDS HTG.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 106117)
AUTHORS Sulston,J.E. and Waterston,R.
TITLE Toward a complete human genome sequence
JOURNAL Genome Res. 8 (11), 1097-1108 (1998)
MEDLINE 99063792
PUBMED 9847074
REFERENCE 2 (bases 1 to 106117)
AUTHORS VanBrunt,A., Kozlowski,A. and Spalding,L.
TITLE The sequence of Homo sapiens BAC clone RP11-788A1
JOURNAL Unpublished (2001)
REFERENCE 3 (bases 1 to 106117)
AUTHORS Waterston,R.H.
TITLE Direct Submission
JOURNAL Submitted (28-NOV-2001) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
REFERENCE 4 (bases 1 to 106117)
AUTHORS Waterston,R.H.
TITLE Direct Submission
JOURNAL Submitted (15-FEB-2002) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
REFERENCE 5 (bases 1 to 106117)
AUTHORS Waterston,R.H.
TITLE Direct Submission
JOURNAL Submitted (15-MAR-2002) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
REFERENCE 6 (bases 1 to 106117)
AUTHORS Waterston,R.
TITLE Direct Submission
JOURNAL Submitted (23-MAR-2002) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
COMMENT On Mar 15, 2002 this sequence version replaced gi:18677687.
----- Genome Center

```

Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: <http://genome.wustl.edu/gsc>
Contact: sapiens@wustl.edu
----- Summary Statistics
Center project name: H_NH0788A01

NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:
Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see <http://genome.wustl.edu/gsc>

SOURCE INFORMATION:
The RP11-11 human BAC library was made from the blood of one male donor, as described by Osoegawa,K., Woon,P.Y., Zhao,B., Frengen,E., Tatenio,M., Catanese,J.J. and de Jong,P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (<http://www.resgen.com>) or Pieter de Jong and coworkers at <http://www.chori.org>
VECTOR: pBAC3.6

NEIGHBORING SEQUENCE INFORMATION:
The clone sequenced to the right is AJ239322, 2000 bp overlap.
Actual start of this clone is at base position 1 of RP11-788A1.
Polymorphisms exist between AC103564, AC093724 and AJ239322. Data from AC093724 was used to finish AC103564.

FEATURES	source
location/Qualifiers	1..106117
/organism="Homo sapiens"	
/mol_type="genomic DNA"	
/db_xref="taxon:9606"	
/chromosome="2"	
/map="2"	
/clone="RP11-788A1"	
/clone_lib="RPC1-11"	
548..568	
repeat_region	/rpt_family="AT_rich"
659..1023	
misc_feature	/note="similar to Homo sapiens EST A1651841 (NID:G4735820)"
707..791	
repeat_region	/rpt_family="MIR"
954..960	
misc_feature	/note="similar to Homo sapiens EST A1824189 (NID:G5444860)"
wj07h03.x1"	
1331..1605	
repeat_region	/rpt_family="Alu"
1743..2012	
repeat_region	/rpt_family="Alu"
2213..2320	
repeat_region	/rpt_family="ERV1"
2451..2767	
repeat_region	/rpt_family="ERV1"
2772..2914	
repeat_region	/rpt_family="L1"
2915..3208	

```
repeat_region /rpt_family="Alu"
3209. .3921
/rpt_family="L1"
repeat_region 4396. .5149
/rpt_family="L1"
repeat_region 5153. .5365
/rpt_family="ERV1"
repeat_region 5421. .5535
/rpt_family="ERV1"
repeat_region 5536. .5999
/rpt_family="ERV1"
misc_feature 5977. .6763
/notes="match to EST BG221914 (NID:gl3747935)"
misc_feature 6031. .6813
/notes="match to EST BG221911 (NID:gl3747932)"
repeat_region 6245. .6650
/rpt_family="MaLR"
repeat_region 6661. .7534
/rpt_family="MaLR"
repeat_region 7537. .8028
/rpt_family="ERV1"
repeat_region 8037. .8331
/rpt_family="Alu"
repeat_region 8359. .8990
/rpt_family="MaLR"
repeat_region 8993. .9386
/rpt_family="MaLR"
misc_feature 10006. .10226
/notes="match to EST BF879314 (NID:gl2269444)"
misc_feature 10259. .10262
/notes="match to EST BG221911 (NID:gl3747932)"
misc_feature 10284. .10707
/notes="match to EST BG221795 (NID:gl3747816)"
repeat_region 10285. .10570
/rpt_family="Alu"
misc_feature 10701. .10707
/notes="match to EST BG221794 (NID:gl3747815)"
repeat_region 10966. .10993
/rpt_family="AT-rich"
repeat_region 11141. .11169
/rpt_family="AT-rich"
misc_feature 11202. .11364
/notes="match to EST BG221794 (NID:gl3747815)"
misc_feature 11202. .11364
/notes="match to EST BG221795 (NID:gl3747816)"
misc_feature 11237. .11247
/notes="similar to Homo sapiens EST AA453375 (NID:gl2167044)
zx47e02.r1"
repeat_region 11409. .11767
/rpt_family="ERV1"
repeat_region 11766. .11949
/rpt_family="ERV1"
repeat_region 12574. .12641
/rpt_family="MaLR"
repeat_region 12642. .12753
/rpt_family="Alu"
repeat_region 12762. .13191
/rpt_family="(TA)n"
repeat_region 13193. .13473
/rpt_family="Alu"
repeat_region 13528. .13596
/rpt_family="L2"
repeat_region 14116. .14329
/rpt_family="ERV1"
repeat_region 14474. .14586
/rpt_family="ERV1"
repeat_region 15168. .15423
/rpt_family="Alu"
misc_feature 15168. .15188
/notes="similar to Homo sapiens EST BF062548
(NID:gl0821458)"
misc_feature 15168. .15180
/notes="similar to Homo sapiens EST AA211483 (NID:gl1810137)

zn55c01.sl"
15599. .15932
/rpt_family="ERV1"
15933. .16267
/rpt_family="MaLR"
16269. .16592
/rpt_family="ERV1"
16598. .17385
/notes="similar to EST BMS55762 (NID:gl8796462)"
16598. .17168

Query Match 91.1%; Score 16.4; DB 9; Length 106117;
Best Local Similarity 94.4%; Pred. No. 2.9e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TCGCGCGCGCGCGGGG 18
|||||
Db 24281 TCGCGCGCGCGCGGGG 24298

RESULT 10
AP005064/c
LOCUS
DEFINITION
Oryza sativa (japonica cultivar-group) genomic DNA, chromosome 8,
BAC clone:OSUNBa0049G15, complete sequence.
ACCESSION
AP005064
VERSION
AP005064.2 GI:30984143
KEYWORDS
HTG.
SOURCE
Oryza sativa (japonica cultivar-group)
ORGANISM
Oryza sativa (japonica cultivar-group)
Sukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
REFERENCE
1
AUTHORS
Sasaki,T., Matsumoto,T. and Katayose,Y.
TITLES
Oryza sativa nipponbare(GAL) genomic DNA, chromosome 8, BAC
clone:OSUNBa0049G15
JOURNAL
Published Only in Database (2002)
REFERENCE
2 (bases 1 to 118436)
AUTHORS
Sasaki,T., Matsumoto,T. and Katayose,Y.
TITLES
Direct Submission
JOURNAL
Submitted (11-APR-2002) Takuji Sasaki, National Institute of
Agrobiological Sciences, Rice Genome Research Program, Kamondai
2-1-2, Tsukuba, Ibaraki 305-8602, Japan
(E-mail:tsasakienias.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/,
Tel:81-298-38-7441, Fax:81-298-38-7468)
COMMENT
On May 21, 2003 this sequence version replaced gi:20142142.
The orientation of the sequence is from -21M13 to M13rev of the BAC
clone.
FEATURES
Location/Qualifiers
source
1. .118436
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="genomic DNA"
/cultivar="Nipponbare"
/db_xref="taxon:39947"
/chromosome="8"
/clone="OSUNBa0049G15"

Query Match 91.1%; Score 16.4; DB 8; Length 118436;
Best Local Similarity 94.4%; Pred. No. 2.8e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TCGCGCGCGCGCGGGG 18
|||||
Db 28966 TCGCGCGCGCGCGGGG 28949

RESULT 11
AC093724
LOCUS
DEFINITION
Homo sapiens BAC clone RP11-1L5 from 2, complete sequence.
ACCESSION
AC093724
```



```

VERSION AC093724.3 GI:31194053
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS 1 (bases 1 to 161617)
TITLES Sultston,J.E. and Wilson,R.
JOURNAL Toward a complete human genome sequence
MEDLINE Genome Res. 8 (11), 1097-1108 (1998)
PUBMED 99063792
9847074
REFERENCE
AUTHORS 2 (bases 1 to 161617)
TITLES Nguyen,C. and Kozlowski,A.
JOURNAL The sequence of Homo sapiens BAC clone RP11-11L5
Unpublished (2001)
REFERENCE
AUTHORS 3 (bases 1 to 161617)
TITLES Waterston,R.H.
JOURNAL Direct Submission
Submitted (10-SEP-2001) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
REFERENCE
AUTHORS 4 (bases 1 to 161617)
TITLES Waterston,R.
JOURNAL Direct Submission
Submitted (01-MAR-2002) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
REFERENCE
AUTHORS 5 (bases 1 to 161617)
TITLES Wilson,R.
JOURNAL Direct Submission
Submitted (30-MAY-2003) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
On May 30, 2003 this sequence version replaced gi:1903950.
----- Genome Center
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu/gsc
Contact: sapiens@wustl.edu
----- Summary Statistics
Center project name: H_NH0001L05
Drafting Center: WIBR
-----
NOTICE: This sequence may not represent the entire insert of this
clone. It may be shorter because we only sequence overlapping
clone sections once, or longer because we provide a small overlap
between neighboring data submissions.
This sequence was finished as follows unless otherwise noted:
all regions were double stranded, sequenced with an alternate
chemistry, or covered by high quality data (i.e., phred quality >=
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by sequence
from more than one subclone; and the assembly was confirmed by
restriction digest.
MAPPING INFORMATION:
Mapping information for this clone was provided by Dr. John D.
McPherson, Department of Genetics, Washington University, St. Louis
MO. For additional information about the map position of this
sequence, see http://genome.wustl.edu/gsc
SOURCE INFORMATION:
The RPC1-11 human BAC library was made from the blood of one male
donor, as described by Osogawa,K., Woon,P.Y., Zhao,B., Frengen,E.,
Tateno,M., Catanesi,J.J. and de Jong,P.J. (1998) An improved
approach for construction of bacterial artificial chromosome
libraries. Genomics 51:1-8. The clone may be obtained either from
Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong
and coworkers at http://www.choiri.org
VECTOR: pBACE3.6
NEIGHBORING SEQUENCE INFORMATION:

```

This sequence is the entire insert of the clone. This clone is overlapped by AC093838 and AC103564.

Bacterial transposon in unfinished region of the clone.

The sequence of AC012122 has been incorporated into AC093724.

FEATURES

source

1..161617

Location/Qualifiers

/organism="Homo sapiens"

/mol_type="genomic DNA"

/db_xref="taxon:9606"

/chromosome="2"

/map="2"

/clone="RP11-11L5"

/clone_lib="RPC1-11"

1894..1918

/rpt_family="AT_rich"

2193..2386

/rpt_family="L1"

2828..3125

/rpt_family="Alu"

3261..3382

/rpt_family="L1"

3383..3783

/rpt_family="L1"

3784..4077

/rpt_family="Alu"

4078..5130

/rpt_family="L1"

5131..5186

/rpt_family="ERV1"

5187..6400

/rpt_family="L1"

6401..6421

/rpt_family="(TA)n"

6422..6447

/rpt_family="ERV1"

6450..6901

/rpt_family="L1"

7020..7129

/rpt_family="MER2_type"

7937..8029

/rpt_family="L2"

8394..8622

/rpt_family="MER2_type"

9122..9278

/rpt_family="MaIR"

10031..10316

/rpt_family="Alu"

11309..11415

/rpt_family="(TAGA)n"

11891..12048

/rpt_family="MIR"

12119..12402

/rpt_family="Alu"

12403..12561

/rpt_family="L2"

12587..12833

/rpt_family="MIR"

12930..12950

/rpt_family="AT_rich"

15239..15296

/rpt_family="AT_rich"

16597..16883

/rpt_family="Alu"

17622..17803

/rpt_family="L2"

17830..17975

/rpt_family="Alu"

18541..18561

/rpt_family="AT_rich"

19578..19598

/rpt_family="AT_rich"


```

repeat_region 23547..23688
                /rpt_family="CR1"
repeat_region 24164..25186
                /rpt_family="ERVX"
repeat_region 25242..25264
                /rpt_family="AT_rich"
repeat_region 27124..27228
                /rpt_family="(CG)n"
repeat_region 27314..27342
                /rpt_family="(CCG)n"
repeat_region 27804..27826
                /rpt_family="AT_rich"
repeat_region 28216..28243
                /rpt_family="AT_rich"
repeat_region 28857..28898
                /rpt_family="(TG)n"
repeat_region 30012..30110
                /rpt_family="MIR"
repeat_region 30098..30294
                /rpt_family="MIR"
repeat_region 30335..30618
                /rpt_family="Mariner"
repeat_region 31418..31478
                /rpt_family="L2"
repeat_region 34032..34060
                /rpt_family="(T)n"
repeat_region 34406..34452
                /rpt_family="L2"
repeat_region 34554..34724
                /rpt_family="MIR"
repeat_region 35381..35728
                /rpt_family="Alu"
repeat_region 36183..36210
                /rpt_family="AT_rich"
repeat_region 36773..36795
                /rpt_family="AT_rich"
repeat_region 37271..37800
                /rpt_family="L2"
repeat_region 38115..38338
                /rpt_family="MER1_type"
repeat_region 39197..39231
                /rpt_family="AT_rich"
repeat_region 39360..39380
                /rpt_family="AT_rich"
repeat_region 39402..39429
                /rpt_family="AT_rich"
repeat_region 39944..39978
                /rpt_family="AT_rich"
repeat_region 40077..40106
                /rpt_family="AT_rich"
repeat_region 40549..40588
                /rpt_family="AT_rich"

Query Match      91.1%; Score 16.4; DB 9; Length 161617;
Best Local Similarity 94.4%; Pred.No. 2.6e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TGCCTGGCGGCGGCGGCGG 18
Db 105507 TGCCTGGCGGCGGCGGCGG 105524

RESULT 12
AC133783/C
LOCUS      AC133783      182944 bp      DNA      linear      HTG 18-SEP-2002
DEFINITION Homo sapiens chromosome 2 clone RP11-191D7, *** SEQUENCING IN
PROGRESS ***, 14 unordered pieces.
ACCESSION  AC133783
VERSION     AC133783.1  GI:23132694
KEYWORDS   HTG; HTGS_PHASE1.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

```

REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL

1 (bases 1 to 182944)
Waterston,R.H.
The sequence of Homo sapiens clone
Unpublished
2 (bases 1 to 182944)
Waterston,R.H.
Direct Submission
Submitted (18-SEP-2002) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA

COMMENT

----- Genome Center -----
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu/gsc/index.shtml
----- Project Information -----
Center project name: H.NH0191D07
----- Summary Statistics -----
Sequencing vector: M13; 0%
Sequencing vector: plasmid; 100%
Chemistry: Dye-terminator ET; 0% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 178033 bases at least Q40
Consensus quality: 179089 bases at least Q30
Consensus quality: 179748 bases at least Q20

* NOTE: This is a 'working draft' sequence. It currently
* consists of 14 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence.
* As soon as it is available and the accession number will
* be preserved.

1 1114: contig of 1114 bp in length
* 1115 1214: gap of unknown length
* 1215 2766: contig of 1552 bp in length
* 2767 2866: gap of unknown length
* 2867 4107: contig of 1241 bp in length
* 4108 4207: gap of unknown length
* 4208 5400: contig of 1193 bp in length
* 5401 5500: gap of unknown length
* 5501 6648: contig of 1148 bp in length
* 6649 6749: gap of unknown length
* 6749 8035: contig of 1286 bp in length
* 8035 8135: gap of unknown length
* 8135 9887: contig of 1752 bp in length
* 9887 13127: gap of unknown length
* 13127 13227: contig of 3141 bp in length
* 13228 20610: contig of 7383 bp in length
* 20611 20710: gap of unknown length
* 20711 31095: contig of 10385 bp in length
* 31096 31195: gap of unknown length
* 31196 40313: contig of 9118 bp in length
* 40314 40413: gap of unknown length
* 40414 68780: contig of 28367 bp in length
* 68781 68880: gap of unknown length
* 68881 108997: contig of 40117 bp in length
* 108998 109097: gap of unknown length
* 109098 182944: contig of 73847 bp in length.

FEATURES

Location/Qualifiers
1..182944
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="2"
/clone="RP11-191D7"
1..1114
/note="assembly_name:Contig16"
1215..2766
/note="assembly_name:Contig2"

misc_feature
misc_feature

```

misc_feature 2867. 4107 /note="assembly_name:Contig22"
misc_feature 4208. 5400 /note="assembly_name:Contig24"
misc_feature 5501. 6648 /note="assembly_name:Contig26"
misc_feature 5749. 8034 /note="assembly_name:Contig28"
misc_feature 8135. 9886 /note="assembly_name:Contig32"
misc_feature 9987. 13127 /note="assembly_name:Contig33"
misc_feature 13228. 20610 /note="assembly_name:Contig34"
misc_feature 20711. 31095 /note="assembly_name:Contig35"
misc_feature 31196. 40313 /note="assembly_name:Contig36"
misc_feature 40414. 68780 /note="assembly_name:Contig37"
misc_feature 68881. 108997 /note="assembly_name:Contig38"
misc_feature 109098. 182944 /note="assembly_name:Contig39
clone_end:SP6
vector_side:right"

ORIGIN
Query Match 91.1%; Score 16.4; DB 2; Length 182944;
Best Local Similarity 94.4%; Pred.No. 2.5e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TGC CGCGCGCGCGCGCGGG 18
Db 8872 TGC CGCGCGCGCGCGGG 8855

RESULT 13
AC133256/c
LOCUS AC133256 235115 bp DNA linear HTG 20-NOV-2002
DEFINITION Rattus norvegicus clone CH230-198G22, WORKING DRAFT SEQUENCE, 3
unordered pieces.
AC133256 AC133256.2 GI:25139160
VERSION HTG; HTGS PHASE1; HTGS DRAFT; HTGS_FULOTOP.
KEYWORDS Rattus norvegicus (Norway rat)
SOURCE Rattus norvegicus
ORGANISM Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1 (bases 1 to 235115)
Muzny,D.,Maric,A., Metzker,M.,Lee,A., Abramson,S., Adams,C., Alder,J.,
Allen,C., Allen,H., Alsbrooks,S., Amin,A., Anguiano,D.,
Anyalebechi,V., Aoyagi,A., Ayodeji,M., Baca,E., Baden,H.,
Baldwin,D., Bandaranaike,D., Barber,M., Barnstead,M., Benahmed,F.,
Biswal,K., Blair,J., Blankenburg,K., Blyth,P., Brown,M.,
Bryant,N., Buhay,C., Burch,P., Burrell,K., Calderon,E.,
Cardenas,J., Carter,K., Cavazos,I., Cesar,H., Chen,R.,
Chacko,V., Chavez,D., Chen,G., Chen,R., Chen,Y., Chen,Z., Chu,J.,
Cleveland,C., Cockrell,R., Cox,C., Coyle,M., Cree,A., D'Souza,L.,
Davila,M.L., Davis,C., Davy-Carroll,L., De Anda,C., Dederich,D.,
Delgado,O., Denson,S., Deramo,C., Ding,Y., Dinh,H., Divya,K.,
Draper,H., Dugan-Rocha,S., Dunn,A., Durbin,K., Duval,B., Eaves,K.,
Egan,A., Escotto,M., Eugene,C., Evans,C.A., Falls,T., Fan,G.,
Fernandez,S., Finley,M., Flegg,N., Forbes,L., Foster,M., Foster,P.,
Fraser,C.M., Gabisi,A., Ganta,A., Garcia,A., Garner,T., Garza,M.,
Gebrgeorgis,E., Geer,K., Gill,R., Grady,M., Guerra,W., Guevara,W.,
Guraratne,P., Haaland,W., Hamill,C., Hamilton,C., Hamilton,K.,
Harvey,Y., Havlak,P., Haves,A., Henderson,N., Hernandez,J.,
Hernandez,R., Hines,S., Hladun,S.L., Hodgson,A., Hogues,M.,
Hollins,B., Howells,S., Hulvyk,S., Hume,J., Idlebird,D., Jackson,A.,
Jackson,L., Jacob,L., Jiang,H., Johnson,B., Johnson,R., Jolivet,A.,
Karpathy,S., Kelly,S., Kelly,S., Khan,Z., King,L., Kovar,C.,

```

```

Kowis,C., Kraft,C.L., Lebow,H., Levan,J., Lewis,L., Li,Z., Liu,J.,
Liu,J., Liu,W., Liu,Y., London,P., Longacre,S., Lopez,J.,
Lorensukewa,L., Loulsegad,H., Lozado,R.J., Lu,X., Ma,J.,
Maheshwari,M., Mahindartine,M., Mahmoud,M., Malloy,K., Mangum,A.,
Mangum,B., Mapua,P., Martin,K., Martin,R., Martinez,E.,
Mawhney,S., McLeod,M.P., McNeill,T.Z., Meenen,E.,
Miosavljivic,A., Miner,G., Mirja,E., Montemayor,J., Moore,S.,
Morgan,M., Morris,K., Morris,S., Munidasa,M., Murphy,M., Nair,L.,
Nankervis,C., Neal,D., Newton,N., Nguyen,N., Norris,S.,
Nwaokemele,O., Okwuonu,G., Olarnpunsagoon,A., Pal,S., Parks,K.,
Pasternak,S., Paul,H., Perez,A., Perez,L., Pfannkuch,C.,
Plopper,F., Poindexter,A., Popovic,D., Primus,E., Pu,L.,
Puzo,M., Quiroz,J., Rachlin,E., Reeves,K., Regier,M.A., Reigh,R.,
Reilly,B., Reilly,M., Ren,Y., Reuter,M., Richards,S., Riggs,F.,
Rives,C., Rodkey,T., Rojas,A., Rose,M., Rose,R., Ruiz,S.J.,
Sanders,W., Savary,G., Scherer,S., Scott,G., Shatsman,S., Shen,H.,
Shetty,J., Shvartbeyn,A., Sisson,I., Sitter,C.D., Smajs,D.,
Sneed,A., Sodergren,E., Song,X.-Z., Sorelle,R., Sosa,J.,
Stelmle,M., Strong,R., Sutton,A., Svatek,A., Tabor,P., Taylor,C.,
Taylor,T., Thomas,N., Thomas,S., Tingey,A., Trejos,Z., Usmani,K.,
Valas,R., Vera,V., Villaseana,D., Waldron,L., Walker,B., Wang,J.,
Wang,Q., Wang,S., Warren,J., Warren,R., Waldron,L., Walker,B., Wang,J.,
Williams,G., Willson,R., Wiecezyk,R., Wooden,H., Worley,K.,
Wright,D., Wright,R., Wu,J., Yakub,S., Yen,J., Yoon,L., Yoon,V.,
Yu,F., Zhang,J., Zhou,J., Zhou,X., Zhao,S., Dunn,D., von
Niederhausern,A., Weiss,R., Smith,D.R., Holt,R.A., Smith,H.O.,
Weinstock,G. and Gibbs,R.A.
Direct Submission
Unpublished
2 (bases 1 to 235115)
Rat Genome Sequencing Consortium.
Direct Submission
Submitted (09-SEP-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 235115)
Rat Genome Sequencing Consortium.
Direct Submission
Submitted (20-NOV-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Nov 20, 2002 this sequence version replaced gi:22759154.
The sequence in this assembly is a combination of BAC based reads
and whole genome shotgun sequencing reads assembled using Atlas
(http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described
in the feature table below represents a scaffold in the Atlas
assembly (a 'contig-scaffold'). Within each contig-scaffold,
individual sequence contigs are ordered and oriented, and separated
by sized gaps filled with Ns to the estimated size. The sequence
may extend beyond the ends of the clone and there may be sequence
contigs within a contig-scaffold that consist entirely of whole
genome shotgun sequence reads. Both end sequences and whole genome
shotgun sequence only contigs will be indicated in the feature
table.
----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: KBQQ
Center clone name: CH230-198G22
----- Summary Statistics
Assembly program: Phrap; version 0.990329
Consensus quality: 213061 bases at least Q40
Consensus quality: 215965 bases at least Q30
Consensus quality: 217641 bases at least Q20
Estimated insert size: 214397; sum-of-contigs estimation
Quality coverage: 7x in Q20 bases; sum-of-contigs estimation
-----
* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently

```

* consists of 3 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 232089: contig of 232089 bp in length
* 232090 232189: gap of unknown length
* 232190 233481: contig of 1292 bp in length
* 233482 233581: gap of unknown length
* 233582 235115: contig of 1534 bp in length.
* Location/Qualifiers
* 1..235115
* /mol_type="Rattus norvegicus"
* /db_xref="taxon:10116"
* /clones="CH230-198G22"
* 1..1418
* /note="wgs end extension
* clone_end:Sp6"
* 3795..5846
* /note="wgs end extension
* clone_end:Sp6"
* 6088..8183
* /note="wgs end extension
* clone_end:Sp6"
* complement(8293..8848)
* /note="clone boundary
* site:
* end_sequence:BH348925"
ORIGIN
Query Match 91.13; Score 16.4; DB 2; Length 235115;
Best Local Similarity 94.43; Pred. No. 2.4e+03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 TGCGCCCGCGCAGGGGG 18
|||||
Db 126991 TGCGCCCGCGCAGGGGG 126974
|||||
RESULT 14
AC121480/c
LOCUS
DEFINITION Rattus norvegicus clone CH230-517B22, *** SEQUENCING IN PROGRESS
*** 3 unordered pieces.
AC121480
AC121480.4 GI:25138141
HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ENRICHED.
KEYWORDS Rattus norvegicus (Norway rat)
SOURCE Rattus norvegicus
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 235785)
Muzny,D,Marie., Metzker,M, Lee., Abramson,S., Adams,C., Alder,J.,
Allen,C., Allen,H., Alsbrooks,S., Amin,A., Anguiano,D.,
Anyalebechi,V., Aoyagi,A., Ayodeji,M., Baca,E., Baden,H.,
Baldwin,D., Bandaranaike,D., Barber,M., Barnstead,M., Benahmed,F.,
Biswal,K., Blair,J., Blankenburg,K., Blyth,P., Brown,M.,
Bryant,N., Buay,C., Burch,P., Burrell,K., Calderon,S.,
Cardenas,V., Carter,K., Cavazos,I., Ceasar,H., Chen,R.,
Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,Y., Chen,Z., Chu,J.,
Cleveland,C., Cockrell,R., Cox,C., Coyle,M., Cree,A., D'Souza,L.,
Devilla,M.L., Davis,C., Davy-Carroll,L., De Anda,C., Dederich,D.,
Delgado,O., Denson,S., Deramo,C., Ding,Y., Dinh,H., Diya,K.,
Draper,H., Dugan-Rocha,S., Dunn,A., Durbin,K., Duval,B., Eaves,K.,
Egan,A., Escotto,M., Eugene,C., Evans,C.A., Falls,I., Fan,G.,
Fernandez,S., Finley,M., Flagg,N., Forbes,L., Foster,M., Foster,P.,
Fraser,C.M., Gabisi,A., Ganta,R., Garcia,A., Garner,T., Garza,M.,
Gebregeorgis,E., Geer,K., Gill,R., Grady,M., Guerra,W., Guevara,W.,

Gunaratne,P., Haaland,W., Hamil,C., Hamilton,C., Hamilton,K.,
Harvey,Y., Havlak,P., Hawes,A., Henderson,N., Hernandez,J.,
Hernandez,R., Hines,S., Hladun,S.L., Hodgson,A., Hoque,M.,
Hollins,B., Howells,S., Hulik,S., Hume,J., Idlebird,D., Jackson,A.,
Jackson,L., Jacob,L., Jiang,H., Johnson,B., Johnson,R., Jolivet,A.,
Karpathy,S., Kelly,S., Kelly,S., Khan,Z., King,L., Kovar,C.,
Kowis,C., Kraft,C.L., Lebow,H., Levan,J., Lewis,L., Li,Z., Liu,J.,
Liu,J., Liu,W., Liu,Y., London,P., Longacre,S., Lopez,J.,
Lorensuhewa,L., Loulseged,H., Lozado,R.J., Lu,X., Ma,J.,
Maheshwari,M., Mahindartne,M., Mahmoud,M., Malloy,K., Mangum,A.,
Mangum,B., Mapua,P., Martin,K., Martin,R., Martinez,B.,
Mawhney,S., McLeod,M.P., McNeill,T.Z., Meenen,E.,
Milosavljevic,A., Miner,G., Minja,B., Montemayor,J., Moore,S.,
Morgan,M., Morris,K., Morris,S., Munidasa,M., Murphy,M., Mair,L.,
Nankervis,C., Neal,D., Newton,N., Nguyen,N., Norris,S.,
Nwaokemele,O., Okwuonu,G., Olarnpunsagoon,A., Pal,S., Parks,K.,
Pasternak,S., Paul,H., Perez,A., Perez,L., Pfannkuch,C.,
Plopper,P., Poindexter,A., Popovic,D., Primus,E., Pu,L.,
Puazo,M., Quiroz,J., Rachlin,E., Reeves,K., Regier,M.A., Reigh,R.,
Reilly,B., Reilly,M., Ren,Y., Reuter,M., Richards,S., Riggs,F.,
Rives,C., Rodkey,T., Rojas,A., Rose,M., Rose,R., Ruiz,S.J.,
Sanders,W., Savary,G., Scherer,S., Scott,G., Shatsman,S., Shen,H.,
Shetty,J., Shvartbeyn,A., Sisson,I., Sitter,C.D., Smajls,D.,
Sneed,A., Sodergren,E., Song,X.-Z., Sorelle,R., Soosa,J.,
Steimle,M., Strong,R., Sutton,A., Svatek,A., Tabor,P., Taylor,C.,
Taylor,T., Thomas,N., Thomas,S., Tingey,A., Trejos,Z., Usmani,K.,
Valas,R., Vera,V., Villaseca,D., Waldron,L., Walker,B., Wang,J.,
Wang,Q., Wang,S., Warren,J., Warren,R., Wei,X., White,F.,
Williams,G., Willson,R., Wleczky,R., Wooden,H., Worley,K.,
Wright,D., Wright,R., Wu,J., Yakub,S., Yen,J., Yoon,L., Yoon,V.,
Yu,F., Zhang,J., Zhou,X., Zhao,S., Dunn,D., von
Niederhausern,A., Weiss,R., Smith,D.R., Holt,R.A., Smith,H.O.,
Weinstock,G. and Gibbs,R.A.
Direct Submission
Unpublished
2 (bases 1 to 235785)
Worley,K.C.
Direct Submission
Submitted (18-MAY-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 235785)
Rat Genome Sequencing Consortium.
Direct Submission
Submitted (20-NOV-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Nov 20, 2002 this sequence version replaced gi:23907725.
The sequence in this assembly is a combination of BAC based reads
and whole genome shotgun sequencing reads assembled using Atlas
(http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described
in the feature table below represents a scaffold in the Atlas
assembly (a 'contig-scaffold'). Within each contig-scaffold,
individual sequence contigs are ordered and oriented, and separated
by sized gaps filled with Ns to the estimated size. The sequence
may extend beyond the ends of the clone and there may be sequence
contigs within a contig-scaffold that consist entirely of whole
genome shotgun sequence reads. Both end sequences and whole genome
shotgun sequence only contigs will be indicated in the feature
table.
----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: GYD
Center clone name: CH230-517B22
----- Summary Statistics
Assembly program: Phrap; version 0.990329
Consensus quality: 204933 bases at least Q40
Consensus quality: 208631 bases at least Q30
Consensus quality: 210832 bases at least Q20


```

/translation="MTITLPSKGRMKEDASAVLERAGLKVASVGNDRSYRGRIEGRD
DEIVYLSAREIEGAGTVDFVGTGEDLVREGLTNADAOQFPGHGFADVVA
VPEIWLVDVSMADICDVASBPRAHRGRRLATKYRLTQOFFSRONGIQIYRIVESL
GATECAPAAGQADIIIVDITSTGTLKANHLKILSDGILVRSEACFVRARKEHEGDA
IQETASRIKAAV"
complement(3903..4394)
/gene="AGR_C_1217"
/notes="AGR_C_1217"
complement(3903..4394)
/gene="AGR_C_1217"
/notes="AGR_C_1217"
/notes="HYPOTHETICAL 14.1 KDA PROTEIN IN EXUR-TDCC
INTERGENIC REGION"
/codon_start=1
/transl_table=11
/product="AGR_C_1217p"
/protein_id="AAK86493.1"
/db_xref="GI:15155643"
/translation="MQLTGDTPIYRRYSMSSSNALVLIARILLSPFIYSGRGKIT
DPACTAGMIAGAMPATATAYLAGLAFELVAGLAILAGFOTKIAMALAVFCVPTGLV
FHSCTVAVPGWPEPALGINTLNGIMMMKNITLAGAYILLATFCAGAYSVDKKGFWA
ARA"
complement(4505..4945)
/gene="AGR_C_1218"
/notes="AGR_C_1218"
complement(4505..4945)
/gene="AGR_C_1218"
/notes="hypoetical protein"
/codon_start=1
/transl_table=11
/product="AGR_C_1218p"
/protein_id="AAK86490.1"
/db_xref="GI:15155640"
/translation="MFVRGRDLFISRRNDALPAAVTTDPRTLSHFFISEWSSSL
SSGVIPLRGHTSFHGLPPGEGILLVRCVDRGDHARVLELFEQVSTEPSFCFSTS
VSILPAMROPVICGESSGEGDGGQGRISGLFLFPRFDIRFAA"
complement(5543..7177)
/gene="AGR_C_1220"
/notes="AGR_C_1220"
complement(5543..7177)
/gene="AGR_C_1220"
/notes="60 KDA CHAPERONIN (PROTEIN CPN60) (GROEL PROTEIN)"
/codon_start=1
/transl_table=11
/product="AGR_C_1220p"
/protein_id="AAK86491.1"
/db_xref="GI:15155641"
/translation="MAAKVKFGRSAREKKLKGVDILADAVKVTGLPKGRNVVDKSP
GAPRITKDGVSFAKEIELEDKFMGAQLVREASKTNIDLAGDGTTFATVLAQIVRE
DAXAAAGAMPMDLKRIGDILAVAEVQLQAKAKINTSEVAQVGTISANGEROIGL
DIAEMORVNGEVIIVSEAKTATELEVVEGQFDEGYLSPVFTNPKRWADLEDA
YILLHEKLSNLQAMLPVLEANNVQTKPLVIAEDVEGEALATLVNKLGGKLIAY
KAPGFRRRKAMLEDIALLGCTVISDGLIKLESVTLDMGKSKVYSIKENTITVD
GAGKSDIEGRVAGIKAKIIEETSDYDREKLQERLAKGAVAVIRVGSSTEVEVREK
KDIRIDNALTRAQVGI VPGGVALLRSSTRIYKGVNDQEGINTVYKALQSLV
ROIENAGDEASIVVGKILDKNEDNYGNAQTGYGLIAGLIVDPVKVVRTALQNA
SVASLLITTEANTAEPLKSSAMPQMPGGGGGMDP"
complement(7253..7549)
/gene="AGR_C_1221"
/notes="AGR_C_1221"
complement(7253..7549)
/gene="AGR_C_1221"
/notes="10 KD CHAPERONIN (PROTEIN CPN10) (PROTEIN GROSS)"
/codon_start=1
/transl_table=11
/product="AGR_C_1221p"
/protein_id="AAK86492.1"
/db_xref="GI:15155642"
/translation="MTSTNFRPLHDRVVRVVRSEAKTKGGIIPDTAKEKPOEGRIV
AVSGGARDEAGKVALDVGVDRVLFCKNSGSTEKLDGEDLLIMKEADINGIIG"
7919..8767
/gene="AGR_C_1226"
7919..8767
/gene="AGR_C_1226"
/notes="hypoetical protein PA3886 {imported} -
Pseudomonas aeruginosa (strain PAO1)"
/codon_start=1
/transl_table=11

```

```

/product="AGR_C_1226p"
/protein_id="AAK86493.1"
/db_xref="GI:15155643"
/translation="MAHRILTLGEITDGFVDVLIQVWGLVHNGVSAPPDAAVALHEAR
KAKTIVLLTNSPRPARGVIAQLRVILGVDPDEAYDRILITSGDVTREGLIAEGPKVFLIG
PERDMLLEGLDVERVGEARQSVVCTGFPDDTETETPEDYTEMLKGTIAKVKPMICAN
PDIVVERGERIIFIICAGAMRAYEQLGGEVRIAGKPHAPIYEACLAANDVYRGAPAKDR
VLAIGDGMPTDVKGAIASGLNLLIYISGGIHAAEYTLNGQTDEALLNAYLKGGGAAPGW
WMPRLA"
8825..9805
/gene="AGR_C_1228"
8825..9805
/notes="AGR_C_1228"
/notes="conserved hypothetical protein - Rhodobacter
capsulatus"
/codon_start=1
/transl_table=11
/product="AGR_C_1228p"
/protein_id="AAK86494.1"
/db_xref="GI:15155644"
/translation="MTVFRHNEKKBPALRGVIAIGNFDGVHGRHRAVLDALEL
AEARGVPALVLTPEPFRSVFDPDTFVRLTPAPLKARILEAIGFRSVIEVFPDFRFS
QRSADRFVQSILVDMLGASAVVTGDFHFCKREGGPAFLMAAGKHGHDVTLVDAPR
DEGSDVSSSRIRSLICEGDVACAGLLGVYFTVESEVIGGQKLGRTLGYPPTANMALA
PETELKAGIVAVRFRRLDGSIHGCVASFGVYPTVTENGAALETLFLDFSGDLYGEVC
SVSFFGHLRDELKFDGLDPLVAQIRDESEARMLSGVRPLSQLDAKIAF"
ORIGIN
Query Match 38.9%; Score 16; DB 1; Length 10029;
Best Local Similarity 100.0%; Pred. No. 6.8e+03;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TGGCGCGCGCGCGCGG 16
Db 8449 TGGCGCGCGCGCGCGG 8434
Search completed: July 2, 2004, 10:08:07
Job time : 637.732 secs

```

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 2, 2004, 06:05:50 ; Search time 134.89 Seconds
(without alignments)
566.887 Million cell updates/sec

Title: US-10-068-160-17

Perfect score: 18

Sequence: 1 tgcgcggcgaggggggg 18

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 212409041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_29Jan04:*

1: Geneseq1980s:*

2: Geneseq1990s:*

3: Geneseq2000s:*

4: Geneseq2001as:*

5: Geneseq2001bs:*

6: Geneseq2002s:*

7: Geneseq2003as:*

8: Geneseq2003bs:*

9: Geneseq2003cs:*

10: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	18	100.0	20	7	ACC48302
C 2	15.4	85.6	374	4	AAL10608 Human bre
C 3	15.4	85.6	450	4	AAL17683 Human bre
C 4	15.4	85.6	499	3	AAC41286 Zea mays
C 5	15.4	85.6	900	3	AAAT9481 Eucalyptu
C 6	15.4	85.6	969	3	ADA71180 Rice gene
C 7	15.4	85.6	1008	3	AAC56198 Eucalyptu
C 8	15.4	85.6	1061	6	AB199675 Mouse isc
9	15.4	85.6	1250	9	ADBO7415 Novel cod
10	15.4	85.6	1404	7	ACA42729 Protaroyt
11	15.4	85.6	1611	9	ADD49064 Human NOV
C 12	15.4	85.6	2196	7	ADA69886 Rice gene
C 13	15.4	85.6	2448	9	ADD29815 Human tum
C 14	15.4	85.6	2478	3	AAA79707 Eucalyptu
C 15	15.4	85.6	2559	9	ADD15216 Human ser
C 16	15.4	85.6	2787	5	ABV21138 Human pro
C 17	15.4	85.6	2929	5	ABV25833 Human pro
C 18	15.4	85.6	2929	5	ABV29359 Human pro
C 19	15.4	85.6	2929	5	ABV25524 Human pro
C 20	15.4	85.6	2929	5	ABV28091 Human pro
C 21	15.4	85.6	2929	5	ABV28883 Human pro
C 22	15.4	85.6	2929	5	ABV22253 Human pro
C 23	15.4	85.6	2929	5	ABV24150 Human pro

C 24	15.4	85.6	2929	5	ABV24860 Human pro
C 25	15.4	85.6	2929	5	ABV25159 Human pro
C 26	15.4	85.6	2929	5	ABV23047 Human pro
C 27	15.4	85.6	2929	5	ABV23269 Human pro
C 28	15.4	85.6	2929	5	ABV25226 Human pro
C 29	15.4	85.6	2929	5	ABV28062 Human pro
C 30	15.4	85.6	2929	5	ABV29113 Human pro
C 31	15.4	85.6	2929	5	ABV25353 Human pro
C 32	15.4	85.6	3104	7	ADA53342 Human cod
C 33	15.4	85.6	3179	4	AAD09560 Human tra
C 34	15.4	85.6	3364	4	AAK69788 Human imm
C 35	15.4	85.6	3317	6	AAK98307 Human pro
C 36	15.4	85.6	3917	6	AAK98308 Human pro
C 37	15.4	85.6	3918	6	AAK98309 Human pro
C 38	15.4	85.6	3918	6	AAK98317 Human pro
C 39	15.4	85.6	3918	6	AAK98311 Human pro
C 40	15.4	85.6	3918	6	AAK98306 Human pro
C 41	15.4	85.6	3918	6	AAK98316 Human pro
C 42	15.4	85.6	3918	6	AAK98315 Human pro
C 43	15.4	85.6	3918	6	AAK98314 Human pro
C 44	15.4	85.6	3918	6	AAK98313 Human pro
C 45	15.4	85.6	3918	6	AAK98318 Human pro

ALIGNMENTS

RESULT 1

ACC48302

ID ACC48302 standard; DNA; 20 BP.

XX ACC48302;

XX ACC48302;

DT 11-AUG-2003 (first entry)

XX

DE CpG oligodeoxynucleotide used for dendritic cell maturation.

XX

KW CpG oligodeoxynucleotide; dendritic cell; tumour; immunotherapy; vaccine;

KW cytostatic; immunostimulant; gene therapy; ss.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT misc_difference 1 /tag= a

FT /note= "N is any base (especially G) or no base"

FT misc_difference 2 /tag= b

FT /note= "N is any base (especially G) or no base"

XX

PN WO2003020884-A2.

XX

PD 13-MAR-2003.

XX

PF 13-AUG-2002; 2002WO-US025732.

XX

PR 14-AUG-2001; 2001US-03121902.

XX

PA {US\$ } US DEPT HEALTH & HUMAN SERVICES.

XX

PI Kliman DM, Gursel M, Verthelyi D;

XX

DR WPI; 2003-300874/29.

XX

PT Generating mature dendritic cells for tumor immunotherapy or as vaccines

PT for activating the immune system to treat diseases such as cancer,

PT comprises contacting a dendritic cell precursor with a D type

PT oligodeoxynucleotide.

XX

PS Disclosure; Page 26; 69pp; English.

XX

CC The present sequence is that of a D type CpG oligodeoxynucleotide that is

CC an example of claimed D type oligodeoxynucleotides (see ACC48294) of the

CC invention. Mature dendritic cells are obtained by contacting a dendritic
 CC cell precursor, such as a monocyte, with such an oligodeoxynucleotide.
 CC The method is useful for generating mature dendritic cells and enhancing
 CC T cell responses, thus enhancing antigen presentation. Mature dendritic
 CC cells are useful for tumour immunotherapy, for augmenting an immune
 CC response to an infectious agent or to a vaccine, and as vaccines to
 CC prevent future infection or to activate the immune system to treat
 CC diseases such as cancer. Mature dendritic cells may also be used to
 CC produce activated T lymphocytes

XX Sequence 20 BP; 1 A; 5 C; 11 G; 1 T; 0 U; 2 Other;

Query Match 100.0%; Score 18; DB 7; Length 20;

Best Local Similarity 100.0%; Pred. No. 2.3e+02;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TGCGCGCGCGCAGGGGG 18
 Db 3 TGCGCGCGCGCAGGGGG 20

RESULT 2

AAL10608/c
 ID AAL10608 standard; cDNA; 374 BP.

XX AC AAL10608;

XX DT 07-DEC-2001 (first entry)

XX DE Human breast cancer expressed polynucleotide 3065.

XX KW Human; breast cancer; cell marker; cytostatic; ss.

XX OS Homo sapiens.

XX PN WO200151628-A2.

XX PD 19-JUL-2001.

XX PF 10-JAN-2001; 2001WO-US000798.

XX PR 14-JAN-2000; 2000US-0176077P.

XX PR 14-MAR-2000; 2000US-0189167P.

XX PR 24-MAR-2000; 2000US-0192099P.

XX PR 29-MAR-2000; 2000US-0193480P.

XX PR 15-MAY-2000; 2000US-0205230P.

XX PR 09-JUN-2000; 2000US-0211315P.

XX PR 25-JUL-2000; 2000US-0220534P.

XX PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

XX PI Lillie J, Xu Y, Wang Y, Steinmann K;

XX DR WPI; 2001-451856/48.

XX PT New peptide useful as a marker for the diagnosis of breast cancer.

XX PS Claim 1; Page 569; 3695pp; English.

XX CC The invention relates to human breast cancer expressed polynucleotides
 CC (AAL07544-AAL26789) and methods of assessing whether a patient is
 CC afflicted with breast cancer by examining the correlation between the
 CC expression of certain markers and the cancerous state of breast cells.
 CC The polynucleotides and encoded polypeptides are potential markers for
 CC detecting, diagnosing, monitoring, characterising treating and
 CC potentially preventing breast cancer. The polynucleotides and encoded
 CC polypeptides are also useful for isolating compounds with cytostatic
 CC activity

XX SQ Sequence 374 BP; 69 A; 109 C; 122 G; 68 T; 0 U; 6 Other;

Query Match 85.6%; Score 15.4; DB 4; Length 374;

Best Local Similarity 94.1%; Pred. No. 1.9e+03;

Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GCGCGCGCGCAGGGGG 18

Db 304 GCGCGCGCGCATGGGG 288

RESULT 3

AAL17683/c
 ID AAL17683 standard; cDNA; 450 BP.

XX AC AAL17683;

XX DT 07-DEC-2001 (first entry)

XX DE Human breast cancer expressed polynucleotide 10140.

XX KW Human; breast cancer; cell marker; cytostatic; ss.

XX OS Homo sapiens.

XX PN WO200151628-A2.

XX PD 19-JUL-2001.

XX PF 10-JAN-2001; 2001WO-US000798.

XX PR 14-JAN-2000; 2000US-0176077P.

XX PR 14-MAR-2000; 2000US-0189167P.

XX PR 24-MAR-2000; 2000US-0192099P.

XX PR 29-MAR-2000; 2000US-0193480P.

XX PR 15-MAY-2000; 2000US-0205230P.

XX PR 09-JUN-2000; 2000US-0211315P.

XX PR 25-JUL-2000; 2000US-0220534P.

XX PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.

XX PI Lillie J, Xu Y, Wang Y, Steinmann K;

XX DR WPI; 2001-451856/48.

XX PT New peptide useful as a marker for the diagnosis of breast cancer.

XX PS Claim 1; Page 1809; 3695pp; English.

XX CC The invention relates to human breast cancer expressed polynucleotides
 CC (AAL07544-AAL26789) and methods of assessing whether a patient is
 CC afflicted with breast cancer by examining the correlation between the
 CC expression of certain markers and the cancerous state of breast cells.
 CC The polynucleotides and encoded polypeptides are potential markers for
 CC detecting, diagnosing, monitoring, characterising treating and
 CC potentially preventing breast cancer. The polynucleotides and encoded
 CC polypeptides are also useful for isolating compounds with cytostatic
 CC activity

XX SQ Sequence 450 BP; 83 A; 138 C; 146 G; 83 T; 0 U; 0 Other;

Query Match 85.6%; Score 15.4; DB 4; Length 450;

Best Local Similarity 94.1%; Pred. No. 1.9e+03;

Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GCGCGCGCGCAGGGGG 18

Db 260 GCGCGCGCGCATGGGG 244

RESULT 4

AAC41286/c

ID AAC41286 standard; DNA; 499 BP.

XX AC AAC41286;

XX DT 17-OCT-2000 (first entry)


```

PR 27-AUG-1999; 99US-0151080P.
PR 30-AUG-1999; 99US-0151303P.
PR 31-AUG-1999; 99US-0151438P.
PR 01-SEP-1999; 99US-0151930P.
PR 07-SEP-1999; 99US-0152363P.
PR 10-SEP-1999; 99US-0153070P.
PR 13-SEP-1999; 99US-0153758P.
PR 16-SEP-1999; 99US-0154018P.
PR 20-SEP-1999; 99US-0154779P.
PR 22-SEP-1999; 99US-0155113P.
PR 23-SEP-1999; 99US-0155486P.
PR 24-SEP-1999; 99US-0155659P.
PR 28-SEP-1999; 99US-0156458P.
PR 29-SEP-1999; 99US-0156596P.
PR 04-OCT-1999; 99US-0157117P.
PR 06-OCT-1999; 99US-0157753P.
PR 07-OCT-1999; 99US-0158029P.
PR 08-OCT-1999; 99US-0158232P.
PR 12-OCT-1999; 99US-0158369P.
PR 13-OCT-1999; 99US-0159293P.
PR 13-OCT-1999; 99US-0159295P.
PR 14-OCT-1999; 99US-0159328P.
PR 14-OCT-1999; 99US-0159330P.
PR 14-OCT-1999; 99US-0159331P.
PR 14-OCT-1999; 99US-0159637P.
PR 18-OCT-1999; 99US-0159638P.
PR 18-OCT-1999; 99US-0159584P.
PR 21-OCT-1999; 99US-0160741P.
PR 21-OCT-1999; 99US-0160767P.
PR 21-OCT-1999; 99US-0160768P.
PR 21-OCT-1999; 99US-0160770P.
PR 21-OCT-1999; 99US-0160814P.
PR 21-OCT-1999; 99US-0160815P.
PR 22-OCT-1999; 99US-0160980P.
PR 22-OCT-1999; 99US-0160981P.
PR 22-OCT-1999; 99US-0160989P.
PR 25-OCT-1999; 99US-0161404P.
PR 25-OCT-1999; 99US-0161405P.
PR 25-OCT-1999; 99US-0161406P.
PR 26-OCT-1999; 99US-0161359P.
PR 26-OCT-1999; 99US-0161360P.
PR 26-OCT-1999; 99US-0161361P.
PR 28-OCT-1999; 99US-0161320P.
PR 28-OCT-1999; 99US-0161392P.
PR 28-OCT-1999; 99US-0161393P.
PR 29-OCT-1999; 99US-0162142P.

Query Match 85.6%; Score 15.4; DB 3; Length 499;
Best Local Similarity 94.1%; Pred. No. 1.9e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GCGCGCGCGCGCGGGG 18
DB 166 GCGCGCGCGCGCGGGG 150

RESULT 5
AAA79481/c
ID AAA79481 standard; cDNA; 900 BP.
XX
AC AAA79481;
XX
DT 27-NOV-2000 (first entry)
XX
DE Eucalyptus grandis cell signalling involved polynucleotide SEQ ID NO:282.
XX
KW Eucalyptus grandis; Pinus radiata; Monterey pine; plant; modification;
XX plant cell signalling; modulation; transgenic plant; pathogen; growth;
XX environmental change; development; cell proliferation; differentiation;
XX elongation; survival; disease resistance; nutrient metabolism; ss.

PR 27-AUG-1999; 99US-0151080P.
PR 30-AUG-1999; 99US-0151303P.
PR 31-AUG-1999; 99US-0151438P.
PR 01-SEP-1999; 99US-0151930P.
PR 07-SEP-1999; 99US-0152363P.
PR 10-SEP-1999; 99US-0153070P.
PR 13-SEP-1999; 99US-0153758P.
PR 16-SEP-1999; 99US-0154018P.
PR 20-SEP-1999; 99US-0154779P.
PR 22-SEP-1999; 99US-0155113P.
PR 23-SEP-1999; 99US-0155486P.
PR 24-SEP-1999; 99US-0155659P.
PR 28-SEP-1999; 99US-0156458P.
PR 29-SEP-1999; 99US-0156596P.
PR 04-OCT-1999; 99US-0157117P.
PR 06-OCT-1999; 99US-0157753P.
PR 07-OCT-1999; 99US-0158029P.
PR 08-OCT-1999; 99US-0158232P.
PR 12-OCT-1999; 99US-0158369P.
PR 13-OCT-1999; 99US-0159293P.
PR 13-OCT-1999; 99US-0159295P.
PR 14-OCT-1999; 99US-0159328P.
PR 14-OCT-1999; 99US-0159330P.
PR 14-OCT-1999; 99US-0159331P.
PR 14-OCT-1999; 99US-0159637P.
PR 18-OCT-1999; 99US-0159638P.
PR 18-OCT-1999; 99US-0159584P.
PR 21-OCT-1999; 99US-0160741P.
PR 21-OCT-1999; 99US-0160767P.
PR 21-OCT-1999; 99US-0160768P.
PR 21-OCT-1999; 99US-0160770P.
PR 21-OCT-1999; 99US-0160814P.
PR 21-OCT-1999; 99US-0160815P.
PR 22-OCT-1999; 99US-0160980P.
PR 22-OCT-1999; 99US-0160981P.
PR 22-OCT-1999; 99US-0160989P.
PR 25-OCT-1999; 99US-0161404P.
PR 25-OCT-1999; 99US-0161405P.
PR 25-OCT-1999; 99US-0161406P.
PR 26-OCT-1999; 99US-0161359P.
PR 26-OCT-1999; 99US-0161360P.
PR 26-OCT-1999; 99US-0161361P.
PR 28-OCT-1999; 99US-0161320P.
PR 28-OCT-1999; 99US-0161392P.
PR 28-OCT-1999; 99US-0161393P.
PR 29-OCT-1999; 99US-0162142P.

Query Match 85.6%; Score 15.4; DB 3; Length 499;
Best Local Similarity 94.1%; Pred. No. 1.9e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GCGCGCGCGCGCGGGG 18
DB 166 GCGCGCGCGCGCGGGG 150

RESULT 6
ADA71180/c
ID ADA71180 standard; DNA; 969 BP.
XX
AC ADA71180;
XX
DT 20-NOV-2003 (first entry)
XX
DE Rice gene, SEQ ID 4503.
XX
KW Plant; bacterial infection; fungal infection; viral infection; rice;
XX gene; ds.
XX
OS Oryza sativa.
XX
PN WO2003000898-A1.
XX
PD 03-JAN-2003.
XX
PF 22-JUN-2001; 2001WO-IB001105.

```

XX Eucalyptus grandis.

XX WO200042171-A1.

XX 20-JUL-2000.

XX 11-JAN-2000; 2000WO-US000724.

XX 12-JAN-1999; 99US-00288986.

XX 01-NOV-1999; 99US-0162866P.

XX (GENE-) GENESIS RES & DEV CORP LTD.

XX Strabala TJ, Nieuwenhuizen NJ;

XX WPI; 2000-476052/41.

XX Isolated polynucleotide encoding a polypeptide involved in cell signaling used for generating transgenic plants with modified responses to external signals.

XX Claim 1; Page 149; 527pp; English.

XX AAA79263 to AAA79736 and AAB25100 to AAB25570 represent polynucleotide and protein sequences isolated from eucalyptus (Eucalyptus grandis) or pine (Pinus radiata also known as Monterey pine). The protein sequences are involved in cell signalling. The polynucleotide and protein sequences can be used to modify the response of plant cells to external signals e.g. environmental changes or pathogens during the growth and development of a plant. They can be used to modify cell proliferation, differentiation, elongation and survival, resistance to disease and nutrient metabolism. Examples of modifications which can be produced are altered fruit ripening and senescence of leaves and flowers e.g. to delay senescence and prolong the life of cut flowers or enhance senescence of reproductive organs to engineer sterile plants. Other modifications can be used to delay senescence in selected cell types or organs providing fruit and vegetables which have a longer shelf life between harvest and consumption, or to decrease branching frequency in forest tree species giving long stretches of valuable knot-free clear wood which can be used in solid timber furniture and veneers

XX Sequence 900 BP; 130 A; 375 C; 205 G; 130 T; 0 U; 0 Other;

XX Query Match 85.6%; Score 15.4; DB 3; Length 900;

XX Best Local Similarity 94.1%; Pred. No. 1.8e+03;

XX Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GCGCGCGCGCGCGGGG 18

DB 243 GCGCGCGCGCGCGGGG 227

RESULT 6

ADA71180/c

ID ADA71180 standard; DNA; 969 BP.

XX AC

XX ADA71180;

XX DT 20-NOV-2003 (first entry)

XX DE Rice gene, SEQ ID 4503.

XX KW Plant; bacterial infection; fungal infection; viral infection; rice;

XX gene; ds.

XX OS Oryza sativa.

XX PN WO2003000898-A1.

XX PD 03-JAN-2003.

XX PF 22-JUN-2001; 2001WO-IB001105.

XX 22-JUN-2001; 2001WO-IB001105.
XX (SYGN) SYNGENTA PARTICIPATIONS AG.
XX Chang H, Chen W, Cooper B, Glazebrook J, Goff SA, Hou Y;
XX Katagiri F, Quan S, Rao Y, Whitham S, Xie Z, Zhu T, Zou G;
XX WPI; 2003-175290/17.
XX Identifying at least one gene involved in plant resistance or response to
XX pathogenic infection for conferring resistance or tolerance to a plant to
XX bacterial, fungal or viral infection by determining or detecting plant
XX gene expression.
XX Claim 6; SEQ ID NO 4503; 899pp; English.
XX The present invention relates to a method (M1) for identifying genes
XX involved in plant resistance or response to pathogenic infection. M1
XX comprises identifying a gene whose expression is significantly altered in
XX the incompatible interaction of plant gene expression relative to
XX expression of the gene in an uninfected plant, in a mutant plant that
XX does not express a gene associated with response to pathogenic infection,
XX or in a corresponding incompatible or compatible interaction. (M1) is
XX useful for conferring resistance to resistance or tolerance to a plant to
XX bacterial, fungal or viral infection. The present sequence was used to
XX illustrate the invention.
XX Sequence 969 BP; 196 A; 312 C; 309 G; 150 T; 0 U; 2 Other;
XX Query Match 85.6%; Score 15.4; DB 7; Length 969;
XX Best Local Similarity 94.1%; Pred. No. 1.8e+03;
XX Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 2 GCCTCCGGCGGCGGCGG 18
Db 811 GCCTCCGGCGGCGGCGG 795
RESULT 7
AAC56198/c
ID AAC56198 standard; DNA; 1008 BP.
XX AAC56198;
XX 25-JAN-2001 (first entry)
XX Eucalyptus grandis transcription factor DNA sequence #329.
XX Plant; transcription factor; gene expression; eucalyptus; pine; acacia;
XX poplar; sweetgum; teak; mahogany; bZIP; G-box binding factor;
XX basic helix-loop-helix zipper; homeotic; homeodomain; homeobox; MADS;
XX homeodomain zipper; LIM domain; AP2; EREBs; zinc finger domain;
XX type 2 Cys2His2; CCAAT box element; MYB; ss.
XX Eucalyptus grandis.
XX WO200053724-A2.
XX 14-SEP-2000.
XX 09-MAR-2000; 2000WO-US006112.
XX 11-MAR-1999; 99US-00266513.
XX 18-AUG-1999; 99US-0149485P.
XX (GENE-) GENESIS RES & DEV CORP LTD.
XX (FLET-) FLETCHER CHALLENGE FORESTS LTD.
XX Wood M, McGrath A, Shenk MA, Glenn M;
XX WPI; 2000-579369/54.
XX

PT New isolated polynucleotide encoding a plant transcription factor for
PT producing a plant e.g. a woody plant, preferably eucalyptus or pine,
PT having modified gene expression or modified activity of a polypeptide.
XX Claim 1; Page 131; 747pp; English.
XX The present invention relates to novel plant transcription factors from
XX Eucalyptus grandis or Pinus radiata. The present sequence is the coding
XX sequence for one such transcription factor. The transcription factor may
XX be used to produce a plant having modified gene expression such as a
XX woody plant e.g. a eucalyptus, pine, acacia, poplar, sweetgum, teak, or
XX mahogany species or to modify the activity of a polypeptide in a plant.
XX The transcription factors of the present invention are members from the
XX following families of regulatory proteins: bZIP, bZIP family of G-box
XX binding factors, basic helix-loop-helix zipper,
XX homeotic/homeodomain/homeobox/MADS, homeodomain zipper, LIM domain, AP2
XX and EREBs, zinc finger domains of type 2 Cys2His2, CCAAT box elements and
XX MYB
XX Sequence 1008 BP; 175 A; 315 C; 331 G; 187 T; 0 U; 0 Other;
XX Query Match 85.6%; Score 15.4; DB 3; Length 1008;
XX Best Local Similarity 94.1%; Pred. No. 1.7e+03;
XX Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 2 GCCTCCGGCGGCGGCGG 18
Db 236 GCCTCCGGCGGCGGCGG 220
RESULT 8
ABI99675
ID ABI99675 standard; cDNA; 1061 BP.
XX ABI99675;
XX 07-MAR-2002 (first entry)
XX Mouse ischaemic condition related cDNA sequence SEQ ID NO:711.
XX Mouse; ischaemia; compressive ischaemia; occlusive ischaemia;
XX vasospastic ischaemia; ischaemic condition; ischaemic disease; ss.
XX Mus musculus.
XX WO200188188-A2.
XX 22-NOV-2001.
XX 18-MAY-2001; 2001WO-JF004192.
XX 18-MAY-2000; 2000JP-00145977.
XX (UYN1-) UNIV NIHON SCHOOL JURIDICAL PERSON.
XX Ishikawa K, Asai S, Takahashi Y, Nagata T, Ishii Y;
XX WPI; 2002-034733/04.
XX Examining the ischemic condition (e.g. occlusive ischemia) by measuring
XX expression levels of particular genes defined in the specification or by
XX determining the expression profile of a gene group comprising these
XX genes.
XX Claim 2; Page 1768-1769; 2690pp; English.
XX The present invention describes a method for examining ischaemic
XX conditions, comprising measuring the expression levels of particular
XX genes (i) in a test sample or determining the expression profile of a
XX gene group in the sample comprising genes selected from (i). The method
XX is useful for examining the ischaemic condition (e.g. compressive
XX ischaemia, occlusive ischaemia or vasospastic ischaemia) by measuring
XX expression levels of particular genes (ABI99202 to ABI99912, encoding the

CC protein sequences in ABB57020 to ABB57374) or by determining the
 CC expression profile of a gene group comprising these genes. The expression
 CC levels or expression profiles produced by these genes are used as an
 CC indicator when screening for ischaemic condition-improving drugs or
 CC therapeutics for ischaemic diseases. ABI99913 and ABI99914 represent PCR
 CC primers for a mouse ischaemic condition related sequence, which are used
 CC in the exemplification of the present invention

XX
 SQ Sequence 1061 BP; 177 A; 284 C; 405 G; 191 T; 0 U; 4 Other;

Query Match 85.6%; Score 15.4; DB 6; Length 1061;
 Best Local Similarity 94.1%; Pred. No. 1.7e+03;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GCGCGCGCGCGAGGGGG 18
 |||||
 Db 891 GCGCGCGCGCGAGGGGG 907

RESULT 9

ADE07415
 ID ADE07415 standard; DNA; 1250 BP.

AC ADE07415;

DT 29-JAN-2004 (first entry)

XX Novel coding sequence (useful for identifying genetic disorders) #481.

DE novel gene; novel protein; tissue marker; molecular weight marker;
 KW chromosome marker; genetic disorder; gene; ds.

XX Unidentified.

XX W02003054152-A2.

PN 03-JUL-2003.

XX 10-DEC-2002; 2002WO-US039555.

XX 10-DEC-2001; 2001US-0339739P.

PR 11-DEC-2001; 2001US-0339453P.

PR 14-MAR-2002; 2002US-0365091P.

PR 14-MAR-2002; 2002US-0365384P.

PR 12-APR-2002; 2002US-0372381P.

PR 12-APR-2002; 2002US-0372615P.

PR 22-APR-2002; 2002US-00128558.

PR 24-APR-2002; 2002US-0376045P.

XX (HYSB-) HYSEQ INC.

PA Targ YT, Asundi V, Goodrich RW, Ren F, Zhang J, Zhao QA, Wang J;

PI Ghosh M, Xue AJ, Wehrman T, Weng G, Zhou P, Drmanac RT, Wang Z;

PI Ma Y, Wang D, Chen R, Xu C, Boyle BJ;

XX WPI; 2003-569235/53.

DR P-PSDB; ADE08326.

XX New polynucleotides, useful for expressing recombinant proteins for

PT analysis, characterization or therapeutic use, or as markers for tissues

PT in which the corresponding protein is preferentially expressed.

XX Claim 1; SEQ ID NO 481; 1177pp; English.

XX The invention comprises the amino acid and coding sequences of novel

CC proteins. The DNA and protein sequences of the invention are useful as:

CC markers for tissues in which the corresponding protein is preferentially

CC expressed; as molecular weight markers on gels; as chromosome markers or

CC tags; to identify chromosomes or to map related gene positions; and to

CC compare with endogenous DNA sequences in patients to identify potential

CC genetic disorders. The present DNA sequence represents a gene of the

CC invention.

SQ Sequence 1250 BP; 202 A; 407 C; 419 G; 222 T; 0 U; 0 Other;

Query Match 85.6%; Score 15.4; DB 9; Length 1250;
 Best Local Similarity 94.1%; Pred. No. 1.7e+03;
 Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GCGCGCGCGCGAGGGGG 18
 |||||
 Db 72 GCGCGCGCGCGAGGGGG 88

RESULT 10

ACA42729

ID ACA42729 standard; DNA; 1404 BP.

XX ACA42729;

XX 19-JUN-2003 (first entry)

XX Prokaryotic essential gene #24386.

XX Antisense; ds; prokaryotic essential gene; cell proliferation;
 KW drug design; gene.

XX Pseudomonas aeruginosa.

XX W0200277183-A2.

XX 03-OCT-2002.

XX 21-MAR-2002; 2002WO-US009107.

XX 21-MAR-2001; 2001US-00815242.

PR 06-SEP-2001; 2001US-00948993.

PR 25-OCT-2001; 2001US-0342923P.

PR 08-FEB-2002; 2002US-00072851.

PR 06-MAR-2002; 2002US-0362699P.

XX (ELIT-) ELITRA PHARM INC.

XX Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JM;

PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;

XX WPI; 2003-029926/02.

DR P-PSDB; ABU38859.

XX New antisense nucleic acids, useful for identifying proteins or screening

PT for homologous nucleic acids required for cellular proliferation to

PT isolate candidate molecules for rational drug discovery programs.

XX Claim 14; SEQ ID NO 30599; 1766pp; English.

XX The invention relates to an isolated nucleic acid comprising any one of

CC the 6213 antisense sequences given in the specification where expression

CC of the nucleic acid inhibits proliferation of a cell. Also included are:

CC (1) a vector comprising a promoter operably linked to the nucleic acid

CC encoding a polypeptide whose expression is inhibited by the antisense

CC nucleic acid; (2) a host cell containing the vector; (3) an isolated

CC polypeptide or its fragment whose expression is inhibited by the

CC antisense nucleic acid; (4) an antibody capable of specifically binding

CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular

CC proliferation or the activity of a gene in an operon required for

CC the gene product or that has an activity against a biological pathway

CC required for proliferation, or that inhibits cellular proliferation; (8)

CC identifying a gene required for cellular proliferation or the biological

CC pathway in which a proliferation-required gene or its gene product lies

CC or a gene on which the test compound that inhibits proliferation of an

CC organism acts; (9) manufacturing an antibiotic; (10) profiling a

CC compound's activity; (11) a culture comprising strains in which the gene

CC product is overexpressed or underexpressed; (12) determining the extent

CC to which each of the strains is present in a culture or collection of

CC strains; or (13) identifying the target of a compound that inhibits the

CC proliferation of an organism. The antisense nucleic acids are useful for
 CC identifying proteins or screening for homologous nucleic acids required
 CC for cellular proliferation to isolate candidate molecules for rational
 CC drug discovery programs, or for screening homologous nucleic acids
 CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
 CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is one of the target
 CC prokaryotic essential genes. Note: The sequence data for this patent did
 CC not form part of the printed specification, but was obtained in
 CC electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

SQ Sequence 1404 BP; 166 A; 458 C; 484 G; 296 T; 0 U; 0 Other;

Query Match 85.6%; Score 15.4; DB 7; Length 1404;

Best Local Similarity 94.1%; Pred. No. 1.7e+03;

Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TGCGCCGCGCGCAGGGGG 17

Db 1154 TGCGCCGCGCGCAGGGGG 1170

RESULT 11

ADDA49064

ID ADD49064 standard; DNA; 1611 BP.

XX AC ADD49064;

XX DT 15-JAN-2004 (first entry)

XX DE Human NOV9b coding sequence, SEQ ID 37.

XX KW Antidiabetic; anorectic; cardiatic; hypotensive; antiarteriosclerotic;
 KW virucide; antibacterial; fungicide; protozoacide; neurotropic;
 KW neuroprotective; antiparkinsonian; anticonvulsant; osteopathic;
 KW antirheumatic; antiinflammatory; dermatological; antiasthmatic;
 KW antilepemic; gene therapy; NOV protein; metabolic disorder; diabetes;
 KW obesity; viral infection; bacterial infection; fungal infection;
 KW helminthic infection; protozoal infection; anorexia; cancer;
 KW cardiovascular disease; hypertension; atherosclerosis;
 KW neurodegenerative disorder; Alzheimer's disease; Parkinson's disease;
 KW epilepsy; immune disorder; osteoarthritis; haematopoietic disorder;
 KW inflammatory skin disorder; asthma; dyslipidemia; human; gene; ds.

XX OS Homo sapiens.

XX PN WO2003060149-A2.

XX PD 24-JUL-2003.

XX PF 06-JAN-2003; 2003WO-US000252.

XX PR 04-JAN-2002; 2002US-0345222P.

XX PR 14-JAN-2002; 2002US-0348693P.

XX PR 16-JAN-2002; 2002US-0349182P.

XX PR 17-JAN-2002; 2002US-0349733P.

XX PR 18-JAN-2002; 2002US-0350263P.

XX PR 24-JAN-2002; 2002US-0351977P.

XX PR 28-MAY-2002; 2002US-0383758P.

XX PR 05-JUN-2002; 2002US-0385969P.

XX PR 11-JUN-2002; 2002US-0387834P.

XX PR 17-JUL-2002; 2002US-0396407P.

XX PR 30-SEP-2002; 2002US-0415115P.

XX PR 03-JAN-2003; 2003US-00336603.

XX PA (CURA-) CURAGEN CORP.

XX PI Grosse KM, Alsbrook JP, Anderson DW, Burgess CE, Edinger SR;

XX PI Ellerman K, Furtak X, Gangolli EA, Gerlach VL, Gilbert JA;

XX PI Gunther E, Gorman L, Guo X, Ji W, Li L, Miller CE, Padigar M;

XX PI Fatturajan M, Rastelli L, MacDougall JR, Mishra VS, Smithson G;

XX PI Spytek KA, Stone DJ, Shenoy SG, Taupier RJ, Vernet CAM, Zhong M;

XX PI Malyankar UM, Millet I, Kekuda R;

XX

DR WPI; 2003-587288/55.

DR P-PSDB; ADD49065.

XX

PT New isolated NOVX polypeptides and polynucleotides, useful for
 PT preventing, diagnosing or treating NOVX-associated disorders, e.g.
 PT osteoarthritis, obesity, atherosclerosis, cancer, Parkinson's disease,
 PT asthma, or infections.

XX

PS Claim 20; Page 144; 311pp; English.

XX

CC The present invention relates to novel NOV proteins and their coding
 CC sequences (ADD49028-ADD49131). The proteins and coding sequences are
 CC useful in the manufacture of a medicament for treating a syndrome
 CC associated with a human disease, preferably a NOV-associated disorder
 CC such as metabolic disorders, diabetes, obesity, infectious diseases
 CC (viral, bacterial, fungal, helminthic, and protozoal), anorexia, cancer,
 CC cardiovascular diseases (hypertension, atherosclerosis),
 CC neurodegenerative disorders (Alzheimer's disease, Parkinson's disease,
 CC epilepsy, immune disorders (osteoarthritis), hematopoietic disorders,
 CC inflammatory skin disorders, asthma and various dyslipidemias. The coding
 CC sequences and proteins may also be used as targets for the identification
 CC of small molecules that modulate or inhibit e.g. neurogenesis, cell
 CC differentiation, cell proliferation, haematopoiesis, wound healing and
 CC angiogenesis, in gene therapy, in generation of antibodies that bind
 CC immunospecifically to NOV substances for use in therapeutic or diagnostic
 CC methods.

XX

SQ Sequence 1611 BP; 448 A; 403 C; 434 G; 326 T; 0 U; 0 Other;

Query Match 85.6%; Score 15.4; DB 9; Length 1611;

Best Local Similarity 94.1%; Pred. No. 1.7e+03;

Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GCGCCGCGCGCAGGGGG 18

Db 116 GCGCCGCGCGCAGGGGG 132

RESULT 12

ADA69886/c

ID ADA69886 standard; DNA; 2196 BP.

XX AC ADA69886;

XX DT 20-NOV-2003 (first entry)

XX DE Rice gene, SEQ ID 3209.

XX DE Plant; bacterial infection; fungal infection; viral infection; rice;

XX KW gene; ds.

XX OS Oryza sativa.

XX PN WO2003000898-A1.

XX PD 03-JAN-2003.

XX PF 22-JUN-2001; 2001WO-IB001105.

XX PR 22-JUN-2001; 2001WO-IB001105.

XX PA (SYGN) SYNGENTA PARTICIPATIONS AG.

XX PI Chang H, Chen W, Cooper B, Glazebrook J, Goff SA, Hou Y;

XX PI Katagiri F, Quan S, Tao Y, Whitham S, Xie Z, Zhu T, Zou G;

XX DR WPI; 2003-175290/17.

XX

PT Identifying at least one gene involved in plant resistance or response to
 PT pathogenic infection for conferring resistance or tolerance to a plant to
 PT bacterial, fungal or viral infection by determining or detecting plant
 PT gene expression.

XX Claim 6; SEQ ID NO 3209; 899pp; English.
PS
CC The present invention relates to a method (M1) for identifying genes
CC involved in plant resistance or response to pathogenic infection. M1
CC comprises identifying a gene whose expression is significantly altered in
CC the incompatible interaction of plant gene expression relative to
CC expression of the gene in an uninfected plant, in a mutant plant that
CC does not express a gene associated with response to pathogenic infection,
CC or in a corresponding incompatible or compatible interaction. (M1) is
CC useful for conferring resistance to resistance or tolerance to a plant to
CC bacterial, fungal or viral infection. The present sequence was used to
CC illustrate the invention.
XX
XX
SQ Sequence 2196 BP; 481 A; 542 C; 607 G; 563 T; 0 U; 3 Other;
Query Match 85.6%; Score 15.4; DB 7; Length 2196;
Best Local Similarity 94.1%; Pred. No. 1.6e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2 GCGCGGCGCGAGGGGG 18
DB 356 GCGCGGCGCGAGGGGG 340
RESULT 13
ADD29815
ID ADD29815 standard; mRNA; 2448 BP.
XX AC ADD29815;
XX 15-JAN-2004 (first entry)
XX Human tumour suppressor mRNA SEQ ID NO:311.
XX
XX SS; human; tumour suppressor; cancer; cancer; cytostatic; gene therapy.
XX Homo sapiens.
XX OS
XX WO2003058201-A2.
XX PN
XX 17-JUL-2003.
XX PD
XX 31-DEC-2002; 2002WO-US041825.
XX PF
XX 31-DEC-2001; 2001US-0345317P.
XX PR
XX (QUAR-) QUARK BIOTECH INC.
XX (CLEV-) CLEVELAND CLINIC FOUND.
XX PI
XX Feinstein E, Gudkov AV;
XX WPI; 2003-598393/56.
XX DR
XX Diagnosing cancer comprises determining the polypeptide or polynucleotide
XX levels e.g., hepatic lipase, in a sample from a subject, where a higher
XX level compared to that in a subject free of cancer is indicative of
XX cancer.
XX
XX Disclosure; SEQ ID NO 311; 272pp; English.
XX
XX The invention relates to a novel method for diagnosing a cancer in a
XX subject. The method comprises determining, in a sample from the subject,
XX the level of at least one polypeptide, where a higher level of the
XX polypeptide compared to the level of the polypeptide in a subject free of
XX cancer is indicative of cancer. The polypeptide is selected from any of
XX the polypeptides encoded by the polynucleotides listed in the
XX specification and polypeptides which are at least 70% homologous to the
XX polypeptides. The method of the invention has cytostatic activity, and
XX may have a use in gene therapy. The method is useful in identifying
XX markers specific for one or several types of cancer, depending on the
XX tissue origin, which may be used in numerous diagnostic and prognostic
XX applications as well as cancer type-specific targets for therapeutic

CC intervention. The compounds that modulate the activity of a tumour
CC suppressor gene are useful in the treatment of cancer or as anti-cancer
CC drugs. The present sequence represents a polynucleotide of the invention.
XX
SQ Sequence 2448 BP; 573 A; 728 C; 609 G; 522 T; 0 U; 16 Other;
Query Match 85.6%; Score 15.4; DB 9; Length 2448;
Best Local Similarity 94.1%; Pred. No. 1.6e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2 GCGCGGCGCGAGGGGG 18
DB 490 GCGCGGCGCGAGGGGG 506
RESULT 14
AAA79707/c
ID AAA79707 standard; cDNA; 2478 BP.
XX AC AAA79707;
XX 27-NOV-2000 (first entry)
XX DT
XX DE Eucalyptus grandis cell signalling involved polynucleotide SEQ ID NO:859.
XX KW Eucalyptus grandis; Pinus radiata; Monterey pine; plant; modification;
XX plant cell signalling; modulation; transgenic plant; pathogen; growth;
XX environmental change; development; cell proliferation; differentiation;
XX elongation; survival; disease resistance; nutrient metabolism; ss.
XX OS Eucalyptus grandis.
XX PN WO200042171-A1.
XX 20-JUL-2000.
XX 11-JAN-2000; 2000WO-US000724.
XX PF
XX 12-JAN-1999; 99US-00228985.
XX PR
XX 01-NOV-1999; 99US-0162868P.
XX PA (GENE-) GENESIS RES & DEV CORP LTD.
XX Strabala TJ, Nieuwenhuizen NJ;
XX WPI; 2000-476052/41.
XX DR
XX Isolated polynucleotide encoding a polypeptide involved in cell signaling
XX used for generating transgenic plants with modified responses to external
XX signals.
XX
XX Claim 1; Page 415-416; 527pp; English.
XX
XX AAA79263 to AAA79736 and AAB25100 to AAB25570 represent polynucleotide
XX and protein sequences isolated from eucalyptus (Eucalyptus grandis) or
XX pine (Pinus radiata also known as Monterey pine). The protein sequences
XX are involved in cell signalling. The polynucleotide and protein sequences
XX can be used to modify the response of plant cells to external signals
XX e.g. environmental changes or pathogens during the growth and development
XX of a plant. They can be used to modify cell proliferation,
XX differentiation, elongation and survival, resistance to disease and
XX nutrient metabolism. Examples of modifications which can be produced are
XX altered fruit ripening and senescence of leaves and flowers e.g. to delay
XX senescence and prolong the life of cut flowers or enhance senescence of
XX reproductive organs to engineer sterile plants. Other modifications can
XX be used to delay senescence in selected cell types or organs providing
XX fruit and vegetables which have a longer shelf life between harvest and
XX consumption, or to decrease branching frequency in forest tree species
XX giving long stretches of valuable knot-free clear wood which can be used
XX in solid timber furniture and veneers
XX
XX Sequence 2478 BP; 518 A; 756 C; 671 G; 533 T; 0 U; 0 Other;
SQ

Query Match 85.6%; Score 15.4; DB 3; Length 2478;
Best Local Similarity 94.1%; Pred. No. 1.6e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GCGCGCGCGCGCGGGG 18
| | | | | | | | | | | | | | | | | | | | | |
Db 625 GCGCGCGCGCGCGGGG 641

Search completed: July 2, 2004, 08:31:38
Job time : 137.89 secs

RESULT 15
ADD15216
ID ADD15216 standard; DNA; 2559 BP.
AC ADD15216;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human serotonin 5-HT2 receptor DNA.
XX
KW human; ds; mental disorder; differential gene expression; psychosis;
KW schizophrenia; mood disorder; bipolar; major depression; neuroleptic;
KW antidepressant; gene therapy.
XX
OS Homo sapiens.
XX
PN WO2003039490-A2.
XX
PD 15-MAY-2003.
XX
PF 12-NOV-2002; 2002WO-US036683.
XX
PR 09-NOV-2001; 2001US-0339252P.
XX
PA (UYTB-) UNIV OFFICE TECHNOLOGY LICENSING STAMPOR.
XX
PI Akil H, Bunney WE, Burke S, Choudary PV, Cox DR, Evans S;
PI Jones EG, Li J, Lopez JF, Myers RM, Thompson R, Vawter MP;
PI Watson SJ;
XX
DR WPI; 2003-441464/41.
XX
PT Determining a predisposition to mental disorders utilizing differential
PT gene expression, useful for diagnosing, and/or treating mood disorders or
PT psychosis, including bipolar and major depression disorders and
PT schizophrenia.
XX
PS Example 3; SEQ ID NO 24; 85pp; English.
XX
CC This invention relates to a novel method for determining a predisposition
CC to mental disorders by utilizing differential gene expression.
CC Specifically, it refers to the differential gene expression of brain
CC region specific nucleic acids that can be used to determine a prevalence
CC of mental disorders with a gender bias. Accordingly, it comprises
CC contacting a patient's biological sample with a reagent (e.g. antibody)
CC that selectively associates with a polynucleotide given in the
CC specification, and detecting the level of reagent that associates to
CC determine whether the subject has, or is predisposed for, a mental
CC disorder. As such, the present invention describes a method and
CC compositions that are useful for diagnosing, and/or treating mental
CC disorders, such as psychosis e.g. schizophrenia or a mood disorder
CC including bipolar and major depression disorders. These compositions have
CC neuroleptic and antidepressant activities and can be used to treat the
CC aforementioned conditions via gene therapy routes. This polynucleotide
CC sequence is a brain specific gene (with gender bias) that is
CC differentially expressed in individuals predisposed to a mental disorder,
CC used in an exemplification of the invention.
XX
SQ Sequence 2559 BP; 579 A; 787 C; 627 G; 566 T; 0 U; 0 Other;

Query Match 85.6%; Score 15.4; DB 9; Length 2559;
Best Local Similarity 94.1%; Pred. No. 1.6e+03;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 2, 2004, 07:38:45 ; Search time 1348.02 Seconds
(without alignments)
398.746 Million cell updates/sec

Title: US-10-068-160-18

Perfect score: 18

Sequence: 1 tgcgcgcgagcaggggg 18

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapert 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

```

EST:*
1: em_estba.*
2: em_esthum.*
3: em_estin.*
4: em_estmu.*
5: em_estov.*
6: em_estpl.*
7: em_estro.*
8: em_hic.*
9: gb_est1.*
10: gb_est2.*
11: gb_hic.*
12: gb_est3.*
13: gb_est4.*
14: gb_est5.*
15: em_estfun.*
16: em_estom.*
17: em_gss_hum.*
18: em_gss_inv.*
19: em_gss_pln.*
20: em_gss_vit.*
21: em_gss_fun.*
22: em_gss_mam.*
23: em_gss_mus.*
24: em_gss_pro.*
25: em_gss_rod.*
26: em_gss_phg.*
27: em_gss_vrl.*
28: gb_gss1.*
29: gb_gss2.*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	17	94.4	320	9	AA662789
C 2	17	94.4	565	28	BH797911 1008096D0
C 3	17	94.4	870	29	CG254815
C 4	17	94.4	877	29	CG238619

C	5	17	94.4	907	29	CC662082
	6	17	94.4	929	29	CG254827
	7	17	94.4	964	29	CC662091
	8	17	94.4	972	29	CC615817
	9	16.4	91.1	520	13	BQ307583
	10	16.4	91.1	1208	14	CD507147
	11	16.4	91.1	1241	14	CD255841
	12	16	88.9	322	14	CK245128
	13	16	88.9	595	10	BP140016
	14	16	88.9	691	10	BNS22625
	15	15.6	86.7	1063	29	CNS040FA
	16	15.4	85.6	58	9	AA613423
	17	15.4	85.6	176	29	CE366192
	18	15.4	85.6	239	10	BB484225
	19	15.4	85.6	245	14	CF569017
	20	15.4	85.6	277	14	CA483093
	21	15.4	85.6	349	13	BU038662
	22	15.4	85.6	369	13	CA150251
	23	15.4	85.6	375	13	BY315784
	24	15.4	85.6	419	12	BJ499495
	25	15.4	85.6	437	10	BB637116
	26	15.4	85.6	445	12	BG814485
	27	15.4	85.6	557	28	BH201166
	28	15.4	85.6	583	13	CA154272
	29	15.4	85.6	583	29	AG145391
	30	15.4	85.6	585	14	CD462917
	31	15.4	85.6	589	28	BZ123626
	32	15.4	85.6	590	9	AJ398997
	33	15.4	85.6	641	13	BQ397448
	34	15.4	85.6	647	29	AG036372
	35	15.4	85.6	659	14	CF483179
	36	15.4	85.6	669	12	BP510258
	37	15.4	85.6	670	12	B1955910
	38	15.4	85.6	730	29	CG182165
	39	15.4	85.6	731	13	BU220035
	40	15.4	85.6	734	29	CC695433
	41	15.4	85.6	742	12	EG707732
	42	15.4	85.6	757	29	CNS02N12
	43	15.4	85.6	802	28	BH982312
	44	15.4	85.6	808	10	BF530495
	45	15.4	85.6	813	28	BZ551296

ALIGNMENTS

RESULT 1
AA662789/c
LOCUS
DEFINITION nu99a09.s1 NCI-CGAP Pr-22 Homo sapiens cDNA clone IMAGE121808 3', similar to gb:Y12794_cds1 V-ERBA RELATED PROTEIN BAR-2 (HUMAN); mRNA sequence.
AA662789
AA662789.1 GI:2616780
EST.
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
REFERENCE
AUTHORS
TITLE NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TUMOR Gene Index
JOURNAL
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html

Trace considered overall poor quality
Seq primer: -40ml3 fwd. RT from Amersham
High quality sequence stop: 1.

FEATURES

source

1. 320
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:1218808"
/sex="male"
/tissue_type="normal prostate"
/lab_host="DH103"

/clone_lib="NCL CGAP Pr22"
/note="Organ: prostate; Vector: pT73D-Pac (Pharmacia)
with a modified polylinker; 1st strand cDNA was prepared
from normal prostate bulk tissue, and was then primed with
a Not I - oligo(dT) primer. Double-stranded cDNA was
ligated to Eco RI adaptors (Pharmacia), digested with Not
I and cloned into the Not I and Eco RI sites of the
modified pT73 vector. Library is normalized, and was
constructed by Bento Soares and M. Fatima Bonaldo. "

ORIGIN

Query Match 94.4%; Score 17; DB 9; Length 320;
Best Local Similarity 100.0%; Pred. No. 4.8e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GCGCCGATCGAGGGGG 18

|||||

Db 68 GCGCCGATCGAGGGGG 52

RESULT 2

BH797911

LOCUS

DEFINITION BH797911 565 bp DNA linear GSS 25-APR-2002
1008096D04.x1 1008 - RescueMu Grid I Zea mays genomic, genomic
survey sequence.

ACCESSION

VERSION

BH797911.1

GI:120307382

KEYWORDS

GSS.

SOURCE

ORGANISM

Zea mays

Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.

REFERENCE

Walbot,V.

TITLE

JOURNAL

COMMENT

Maize genomic sequences found using engineered RescueMu transposon
Contact: Walbot V
Unpublished (2001)
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
Possible ligation site so sequence was trimmed. Post-ligation
sequence submitted separately.
Plate: 1008096 row: 26
Class: transposon-tagged.

FEATURES

source

1. 565
/organism="Zea mays"
/mol_type="genomic DNA"
/cultivar="mixed background W23/Al88/B73"
/db_xref="taxon:4577"
/tissue_type="leaf"
/dev_stage="adult"
/lab_host="DH103"
/clone_lib="1008 - RescueMu Grid I"
/note="Organ: leaf; Vector: RescueMu (engineered from

pBlueScript backbone); Site 1: BamHI; Site 2: BglII;
RescueMu is a 4.9 kb, modified maize Mu transposon
designed to allow plasmid rescue from total genomic DNA.
Mu elements insert preferentially into transcription
units. For more information on RescueMu, go to the web
site www.zmndb.iastate.edu and follow the links for
'RescueMu.' Grid I was grown at Berkeley in 2001. DNA was
extracted from leaf punches, double digested using BamHI
and BglII, and ligated to form circular plasmids. DH10B
cells were transformed and then screened on LB plates with
ampicillin."

ORIGIN

Query Match 94.4%; Score 17; DB 28; Length 565;
Best Local Similarity 100.0%; Pred. No. 5.3e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCGCCCGATCGAGGGGG 17

|||||

Db 521 TCGCCCGATCGAGGGGG 537

RESULT 3

CG254815/c

LOCUS

DEFINITION

CG254815

ACCESSION

VERSION

CG254815.1

GI:34158597

KEYWORDS

GSS.

SOURCE

ORGANISM

Zea mays

Zea mays

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Other GSSs: CG1DX07TV

Contact: Cathy Whitelaw

TIGR

9712 Medical Center Drive, Rockville, MD 20850, USA

Tel: 301-838-5843

Fax: 301-838-0208

Email: whitelaw@tigr.org

Seq primer: TR

Class: sheared ends.

Location/Qualifiers

1. 870

/organism="Zea mays"

/mol_type="genomic DNA"

/strain="B73"

/db_xref="taxon:4577"

/clone="ZMMB0740A14"

/clone_lib="ZM_0.7_1.5_KB"

/note="Vector: pBCSK-; Site 1: HincII; 0.7-1.5 kb
methylation filtered genomic DNA library"

ORIGIN

Query Match

Best Local Similarity

Matches

17; Conservative

0; Mismatches

0; Indels

0; Gaps

0;

QY

1 TCGCCCGATCGAGGGGG

17

|||||

Db

420 TCGCCCGATCGAGGGGG

404

RESULT 4

CG238619/c

LOCUS	CG238619	877 bp	DNA	linear	GSS 22-AUG-2000
DEFINITION	CG1AQ39TH ZM 0.7 1.5 KB Zea mays genomic clone ZMMBMA0719G05, genomic survey sequence.				
ACCESSION	CG238619				
VERSION	CG238619.1	GI:34138505			
KEYWORDS	GSS.				
SOURCE	Zea mays				
ORGANISM	Zea mays				
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.				
AUTHORS	1 (bases 1 to 877) Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T., Citek, R.W., Nunberg, A., Robbins, D. and Lakey, N.				
TITLE	Consortium for Maize Genomics				
JOURNAL	Unpublished (2002)				
COMMENT	Other GSSs: OG1AQ39TV Contact: Cathy Whitelaw				
FEATURES	TIGR 9712 Medical Center Drive, Rockville, MD 20850, USA Tel: 301-838-5843 Fax: 301-838-0208 Email: whitelaw@tigr.org Seq primer: TR Class: sheared ends.				
source	1..877 Location/Qualifiers /organism="Zea mays" /mol_type="genomic DNA" /strain="B73" /db_xref="taxon:4577" /clone="ZMMBMA0719G05" /clone_lib="ZM 0.7 1.5 KB" /note="Vector: pCISK; Site 1: HincII; 0.7-1.5 kb methylation filtered genomic DNA library"				
ORIGIN	Query Match 94.4%; Score 17; DB 29; Length 877; Best Local Similarity 100.0%; Pred. No. 5.7e+03; Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0				
Qy	1 TGCGCCGATGCAGGGG 17 				
Db	246 TGCGCCGATGCAGGGG 230 				
RESULT 5	CC662082 907 bp DNA linear GSS 19-JUN-2000				
LOCUS	CGYBN59TH ZM 0.7 1.5 KB Zea mays genomic clone ZMMBMA0496J20,				
DEFINITION	genomic survey sequence.				
ACCESSION	CC662082				
VERSION	CC662082.1	GI:32065965			
KEYWORDS	GSS.				
SOURCE	Zea mays				
ORGANISM	Zea mays				
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.				
AUTHORS	1 (bases 1 to 907) Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T., Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T., Citek, R.W., Nunberg, A., Robbins, D. and Lakey, N.				
TITLE	Consortium for Maize Genomics				
JOURNAL	Unpublished (2002)				
COMMENT	Other GSSs: OGBV58TV Contact: Cathy Whitelaw				
FEATURES	TIGR 9712 Medical Center Drive, Rockville, MD 20850, USA Tel: 301-838-5843 Fax: 301-838-0208 Email: whitelaw@tigr.org				

```

CC662091
LOCUS       CC662091       964 bp      DNA      linear      GSS 19-JUN-2003
DEFINITION   OGVEN58TV ZM 0.7 1.5 KB Zea mays genomic clone ZM58Ma0496J20,
              genomic survey sequence.
ACCESSION    CC662091
VERSION      CC662091.1 GI:32065976
KEYWORDS     GSS.
SOURCE       Zea mays
ORGANISM     Zea mays
REFERENCE    1 (bases 1 to 964)
AUTHORS      Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,
              Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T.,
              Citek, R.W., Nunberg, A., Robbins, D. and Lakey, N.
              Consortium for Maize Genomics
              Unpublished (2002)
              Other GSSs: OGVEN58TH
              Contact: Cathy Whitelaw
TIGR         9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208
Email: whitelaw@tigr.org
Seq primer:  TF
Class: sheared ends.
FEATURES             Location/Qualifiers
     source           1..964
                     /organism="Zea mays"
                     /mol_type="genomic DNA"
                     /strain="B73"
                     /db_xref="taxon:4577"
                     /clone="ZM58Ma0496J20"
                     /clone_lib="ZM 0.7 1.5 KB"
                     /note="Vector: pBCSK-; Site 1: HincII; 0.7-1.5 kb
                     methylation filtered genomic DNA library"
ORIGIN
Query Match       94.4%; Score 17; DB 29; Length 964;
Best Local Similarity 100.0%; Pred. No. 5.7e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCGCCGCGATGCAGGGGG 17
|||||
Db 733 TCGCCGCGATGCAGGGGG 749

RESULT 8
CC615817
LOCUS       CC615817       972 bp      DNA      linear      GSS 18-JUN-2003
DEFINITION   OGLAP15TV ZM 0.7 1.5 KB Zea mays genomic clone ZM58Ma0310D06,
              genomic survey sequence.
ACCESSION    CC615817
VERSION      CC615817.1 GI:31977238
KEYWORDS     GSS.
SOURCE       Zea mays
ORGANISM     Zea mays
REFERENCE    1 (bases 1 to 972)
AUTHORS      Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,
              Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T.,
              Citek, R.W., Nunberg, A., Robbins, D. and Lakey, N.
              Consortium for Maize Genomics
              Unpublished (2002)
              Other GSSs: OGLAP15TH
              Contact: Cathy Whitelaw
TIGR         9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-5843
Fax: 301-838-0208

```

```

Email: whitelaw@tigr.org
Seq primer: TF
Class: sheared ends.
FEATURES             Location/Qualifiers
     source           1..972
                     /organism="Zea mays"
                     /mol_type="genomic DNA"
                     /strain="B73"
                     /db_xref="taxon:4577"
                     /clone="ZM58Ma0310D06"
                     /clone_lib="ZM 0.7 1.5 KB"
                     /note="Vector: pBCSK-; Site 1: HincII; 0.7-1.5 kb
                     methylation filtered genomic DNA library"
ORIGIN
Query Match       94.4%; Score 17; DB 29; Length 972;
Best Local Similarity 100.0%; Pred. No. 5.8e+03;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCGCCGCGATGCAGGGGG 17
|||||
Db 401 TCGCCGCGATGCAGGGGG 417

RESULT 9
BQ307583
LOCUS       BQ307583       520 bp      mRNA      linear      EST 16-MAY-2002
DEFINITION   MR0-BT4507-220601-201-h03 BT4507 Homo sapiens cDNA, mRNA sequence.
ACCESSION    BQ307583
VERSION      BQ307583.1 GI:20844024
KEYWORDS     EST.
SOURCE       Homo sapiens (human)
ORGANISM     Homo sapiens
REFERENCE    1 (bases 1 to 520)
AUTHORS      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
              Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
              Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
              Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.,
              Brunstein, A., deOliveira, P.S., Bucher, P., Jongeneel, C.V.,
              O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
              Simpson, A.J.J.
              Shotgun sequencing of the human transcriptome with ORF expressed
              sequence tags
              Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
              20202663
              MEDLINE
              PUBMED
              10737800
              Contact: Simpson A.J.G.
              Laboratory of Cancer Genetics
              Ludwig Institute for Cancer Research
              Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
              Brazil
              Tel: +55-11-2704922
              Fax: +55-11-2707001
              Email: asimpson@ludwig.org.br
              This sequence was derived from the FAPESP/LICR Human Cancer Genome
              Project. This entry can be seen in the following URL
              (http://www.ludwig.org.br/scripts/gethtml2.pl?ti=MR0at2=MR0-BT4507-
              220601-201-h03&t3=2001-06-22&t4=1)
              Seq primer: puc 18 forward
              High quality sequence stop: 124.
              Location/Qualifiers
              1..520
              /organism="Homo sapiens"
              /mol_type="mRNA"
              /db_xref="taxon:9606"
              /dev_stage="Adult"
              /clone_lib="BT4507"
              /note="Organ: breast; Vector: puc18; Site 1: SmaI; Site 2:
              SmaI; A mini-library was made by cloning products derived
              from ORESTES PCR (U.S. Letters Patent application No.
              196,716 - Ludwig Institute for Cancer Research) profiles
              into the pUC 18 vector. Reverse transcription of tissue

```

mRNA and cDNA amplification were performed under low stringency conditions."

ORIGIN

Query Match 91.1%; Score 16.4; DB 13; Length 520;
 Best Local Similarity 94.4%; Pred. No. 9.2e+03;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TCGCCCGATCGAGGGGG 18
 |||||
 Db 383 TCGCCCGCTCGAGGGGG 400

RESULT 10

CD507147 1208 bp mRNA linear EST 12-JUN-2003
 CDA83-C07-yld-s SHGC-CDA Gasterosteus aculeatus cDNA clone
 CDA83-C07 3', mRNA sequence.

ACCESSION

CD507147 GI:31437716

VERSION

EST.

KEYWORDS

Gasterosteus aculeatus (three spined stickleback)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 Acanthomorpha; Acanthopterygii; Percomorpha; Gasterosteiformes;
 Gasterosteidae; Gasterosteus.

REFERENCE

1 (bases 1 to 1208)
 Kingsley, D.M., Feichel, C., Balabhadra, S., Grimwood, J., Dickson, M.,
 Schmutz, J. and Myers, R.M.

TITLE

Expressed sequence tags from *Gasterosteus aculeatus*

JOURNAL

Unpublished (2003)

COMMENT

HHMI and Department of Developmental Biology
 Stanford University School of Medicine
 Beckman Center B300, 279 Campus Drive, Stanford, CA 94305-5329, USA
 Tel: 650 725 5954
 Fax: 650 725 7739
 Email: kingsley@cngm.stanford.edu

FEATURES

source

1..1208
 /organism="Gasterosteus aculeatus"
 /mol_type="mRNA"
 /strain="Salinas river, CA"
 /db_xref="taxon:69293"
 /clone="CDA83-C07"
 /sex="mixed male and female"
 /tissue_type="heads and internal organs combined"
 /dev_stage="adult"
 /clone_lib="SHGC-CDA"
 /notes="Vector: lambda ZAP Express/pBK-CMV; Site 1: EcoRI
 (5' adaptor); Site 2: XhoI (3' linker primer). The mixed
 organ cDNA library was generated using the ZAP-cDNA method
 by Stratagene. First strand cDNA synthesis was primed with
 a 50 bp linker primer containing an oligo dT sequence
 preceded by a synthetic XhoI site. 5 prime adaptors were
 used containing an EcoRI cohesive end. The finished cDNAs
 were inserted in to the ZAP express vector
 unidirectionally in the sense orientation with respect to
 the lacZ promoter of pBK-CMV. An amplified library was
 prepared from approximately 3 million primary clones in
 the lambda ZAP Express vector. In vivo excision was then
 used to generate individual pBK-CMV phagemid clones for
 EST sequencing."

ORIGIN

Query Match 91.1%; Score 16.4; DB 14; Length 1208;
 Best Local Similarity 94.4%; Pred. No. 1.1e+04;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TCGCCCGATCGAGGGGG 18
 |||||
 Db 336 TCGCCCGATCGAGGGGG 353

RESULT 11

CD255841/c

LOCUS

DEFINITION

AGENCY: 14156934 NICHG_XGC_Brnl Xenopus laevis cDNA clone

IMAGE: 6954538 5', mRNA sequence.

ACCESSION

CD255841

VERSION

CD255841.1 GI:31016307

KEYWORDS

EST.

SOURCE

ORGANISM

Xenopus laevis (African clawed frog)

Xenopus laevis

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 Xenopodinae; Xenopus.

REFERENCE

1 (bases 1 to 1241)

NIH-MGC <http://mgc.nci.nih.gov/>.

Unpublished (1999)

CONTACT: Daniela S. Gerhard, Ph.D.

Office of Cancer Genomics

National Cancer Institute / NIH

Bldg. 31 Rm10A07 Bethesda, MD 20892

Email: cgabs-r@mail.nih.gov

Tissue Procurement:

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: LLAM14578 Row: j Column: 09

High quality sequence start: 94

High quality sequence stop: 384.

Location/Qualifiers

1..1241

/organism="Xenopus laevis"

/mol_type="mRNA"

/db_xref="taxon:8355"

/clone="IMAGE:6954538"

/dev_stage="adult"

/lab_host="DH10B (phage-resistant)"

/clone_lib="NICHG XGC Brnl"

/note="Organ: brain; Vector: pCMV-SPORT6; Site 1: NotI;
 Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
 Average insert size 1.5 kb. Constructed by Life
 Technologies. Note: This is a Xenopus Gene Collection
 (XGC) library."

ORIGIN

Query Match 91.1%; Score 16.4; DB 14; Length 1241;
 Best Local Similarity 94.4%; Pred. No. 1.1e+04;
 Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TCGCCCGATCGAGGGGG 18
 |||||
 Db 855 TCGCCCGATCGAGGGGG 838

RESULT 12

CK245128

LOCUS

DEFINITION

EST728765 potato callus cDNA library, normalized and full-length

Solanum tuberosum cDNA clone FOCAB91 3' end, mRNA sequence.

ACCESSION

CK245128

VERSION

CK245128.1 GI:39791385

KEYWORDS

EST.

SOURCE

ORGANISM

Solanum tuberosum (potato)

Solanum tuberosum

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamiales; Solanales; Solanaceae; Solanum.
1 (bases 1 to 322)
Buell, C.R., Hart, A., Zismann, V., Karamycheva, S.A. and Baker, B.
Generation of ESTs from potato callus tissue
Unpublished (2003)
Other_ESTs: EST728763 EST728764
Contact: Robin Buell
The Institute for Genomic Research
9712 Medical Center Dr, Rockville, MD 20850, USA
Email: potato-array@tigr.org
Clones can be requested from TIGR via potato@tigr.org
Seq primer: GPA ATA CGA CTC ACT ATA GGG C.
Location/Qualifiers
1..322
/organism="Solanum tuberosum"
/mol_type="mRNA"
/cultivar="Kennebec"
/db_xref="taxon:4113"
/clone="POCAB91"
/tissue_type="callus"
/lab_host="DH10B-Tona"
/clone_lib="potato callus cDNA library, normalized and
full-length"
/note="Vector: pCMVSPORT6.1; Site 1: EcoRI; Site 2: NotI;
supplier: RNA was isolated from Solanum tuberosum var.
Kennebec callus tissue grown on solid media."

Query Match 88.9%; Score 16; DB 14; Length 322;
Best Local Similarity 100.0%; Pred. No. 1.3e+04;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 3 CGCCGATGCAGGGGG 18
|||||
DB 228 CGCCGATGCAGGGGG 243
|||||

RESULT 13
BF140016/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
595 bp mRNA linear EST 24-OCT-2000
601791154F1 NCI_CGAP_Lu30 Mus musculus cDNA clone IMAGE:4021788 5'
mRNA sequence.
BF140016
BF140016.1 GI:10979056
EST.
Mus musculus (house mouse)
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NIH-MGC http://mgc.nci.nih.gov/.
1 (bases 1 to 595)
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: NCI-CGAP clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM9277 row: 1 column: 13
High quality sequence stop: 584.
Location/Qualifiers
1..595
/organism="Mus musculus"
/mol_type="mRNA"
/strain="Czech II"
/db_xref="taxon:10090"
/clone="IMAGE:4021788"
/tissue_type="tumor, metastatic to mammary"

FEATURES
source

1 **REFERENCE**
AUTHORS Roest Croliiuss H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C., Bernot, A., Fizesac, C., Winkler, P., Brottier, P., Quetier, F., Saurin, W. and Weissenbach, J.
TITLE Estimate of human gene number provided by genome-wide analysis using Tetraodon nigroviridis DNA sequence
JOURNAL Nat. Genet. 25 (2), 235-238 (2000)
MEDLINE 20296653
PUBMED 10835645

2 **REFERENCE**
AUTHORS Roest Croliiuss H., Jaillon, O., Dasilva, C., Ozouf-Coataz, C., Fizesac, C., Fischer, C., Bouneau, L., Billault, A., Quetier, F.,

Search completed: July 2, 2004, 13:33:08
Job time : 1351.14 secs

Result No.	Score	Query %		DB	ID	Description
		Match	Length			
1	16	88.9	963	4	US-09-252-991A-7939	Sequence 7939, Appl
2	16	88.9	1050	4	US-09-252-991A-7799	Sequence 7799, Appl
3	14.8	82.2	246	4	US-09-382-552-59	Sequence 59, Appl
4	14.8	82.2	426	4	US-09-252-991A-3760	Sequence 3760, Appl
5	14.8	82.2	774	4	US-09-489-039A-1478	Sequence 1478, Appl
6	14.8	82.2	885	4	US-09-252-991A-16564	Sequence 16564, Appl
7	14.8	82.2	1110	4	US-09-489-039A-6568	Sequence 6568, Appl
8	14.8	82.2	1169	4	US-09-620-312D-951	Sequence 951, Appl
9	14.8	82.2	1230	4	US-09-489-039A-6246	Sequence 6246, Appl
10	14.8	82.2	1351	4	US-09-252-991A-16454	Sequence 16454, Appl
11	14.8	82.2	1356	3	US-09-318-448-42	Sequence 42, Appl
12	14.8	82.2	1369	4	US-09-252-991A-15036	Sequence 15036, Appl
13	14.8	82.2	1273	3	US-09-318-448-45	Sequence 45, Appl
14	14.8	82.2	1275	3	US-09-318-448-41	Sequence 41, Appl
15	14.8	82.2	1473	4	US-09-252-991A-13784	Sequence 13784, Appl
16	14.8	82.2	1500	4	US-09-252-991A-13688	Sequence 13688, Appl
17	14.8	82.2	1749	4	US-09-516-914-22	Sequence 22, Appl
18	14.8	82.2	1908	3	US-09-318-448-36	Sequence 36, Appl
19	14.8	82.2	1253	4	US-09-252-991A-3804	Sequence 3804, Appl
20	14.8	82.2	2289	4	US-09-489-039A-2837	Sequence 2837, Appl
21	14.8	82.2	2355	4	US-09-252-991A-3845	Sequence 3845, Appl
22	14.8	82.2	2451	4	US-09-489-039A-3349	Sequence 3349, Appl
23	14.8	82.2	2523	4	US-09-489-039A-3473	Sequence 3473, Appl
24	14.8	82.2	3359	4	US-09-023-655-1229	Sequence 1229, Appl
25	14.8	82.2	4167	4	US-09-252-991A-3666	Sequence 3666, Appl
26	14.8	82.2	5771	4	US-09-833-381-307	Sequence 307, Appl
27	14.8	82.2	5915	4	US-09-382-553-3	Sequence 3, Appl

; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-7799

Query Match 88.9%; Score 14.8; DB 4; Length 1050;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 CGCGCGCGCAGGGGG 18
|||||
DB 1010 CGCGCGCGCAGGGGG 1025

RESULT 3

US-09-382-552-59

; Sequence 59, Application US/09382552

; Patent No. 6673909

; GENERAL INFORMATION:

; APPLICANT: Brown, Jr., Robert H.

; APPLICANT: Liu, Jing

; APPLICANT: Aoki, Masashi

; APPLICANT: Ho, Meng

; APPLICANT: Matsuda-Asada, Chie

; TITLE OF INVENTION: DYSFERLIN, A GENE MUTATED IN DISTAL MYOPATHY AND LIMB

; FILE REFERENCE: 00786/399002

; CURRENT APPLICATION NUMBER: US/09/382,552

; CURRENT FILING DATE: 1999-08-25

; EARLIER APPLICATION NUMBER: US 60/097,927

; NUMBER OF SEQ ID NOS: 233

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 59

; LENGTH: 246

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-382-552-59

Query Match

Best Local Similarity 82.2%; Score 14.8; DB 4; Length 246;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TGCGCGCGCGCAGGGGG 18
|||||
DB 163 TGCGCGCGCGCAGGGGG 180

RESULT 4

US-09-252-991A-3760

; Sequence 3760, Application US/09252991A

; Patent No. 6551795

; GENERAL INFORMATION:

; APPLICANT: Marc J. Rubenfield et al.

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

; FILE REFERENCE: 107196.136

; CURRENT APPLICATION NUMBER: US/09/252,991A

; CURRENT FILING DATE: 1999-02-18

; PRIOR APPLICATION NUMBER: US 60/074,788

; PRIOR FILING DATE: 1998-02-18

; PRIOR APPLICATION NUMBER: US 60/094,190

; PRIOR FILING DATE: 1998-07-27

; NUMBER OF SEQ ID NOS: 33142

; SEQ ID NO 3760

; LENGTH: 426

; TYPE: DNA

; ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-3760

Query Match

Best Local Similarity 82.2%; Score 14.8; DB 4; Length 426;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TGCGCGCGCGCAGGGGG 18

DB 124 TGCGCGCGCGCAGGGGG 141
|||||

RESULT 5

US-09-489-039A-1478

; Sequence 1478, Application US/09489039A

; Patent No. 6610836

; GENERAL INFORMATION:

; APPLICANT: Gary Breton et. al

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA

; FILE REFERENCE: 2709.2004001

; CURRENT APPLICATION NUMBER: US/09/489,039A

; CURRENT FILING DATE: 2000-01-27

; PRIOR APPLICATION NUMBER: US 60/117,747

; PRIOR FILING DATE: 1999-01-29

; NUMBER OF SEQ ID NOS: 14342

; SEQ ID NO 1478

; LENGTH: 774

; TYPE: DNA

; ORGANISM: Klebsiella pneumoniae

US-09-489-039A-1478

Query Match

Best Local Similarity 82.2%; Score 14.8; DB 4; Length 774;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TGCGCGCGCGCAGGGGG 18
|||||

DB 570 TGCGCTGGCGCAGGGGG 587

RESULT 6

US-09-252-991A-16564/c

; Sequence 16564, Application US/09252991A

; Patent No. 6551795

; GENERAL INFORMATION:

; APPLICANT: Marc J. Rubenfield et al.

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

; FILE REFERENCE: 107196.136

; CURRENT APPLICATION NUMBER: US/09/252,991A

; CURRENT FILING DATE: 1999-02-18

; PRIOR APPLICATION NUMBER: US 60/074,788

; PRIOR FILING DATE: 1998-02-18

; PRIOR APPLICATION NUMBER: US 60/094,190

; PRIOR FILING DATE: 1998-07-27

; NUMBER OF SEQ ID NOS: 33142

; SEQ ID NO 16564

; LENGTH: 885

; TYPE: DNA

; ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-16564

Query Match

Best Local Similarity 82.2%; Score 14.8; DB 4; Length 885;

Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 TGCGCGCGCGCAGGGGG 18
|||||

DB 311 TGCGCGCGCGCAGGGGG 294

RESULT 7

US-09-489-039A-6658/c

; Sequence 6658, Application US/09489039A

; Patent No. 6610836

; GENERAL INFORMATION:

; APPLICANT: Gary Breton et. al

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA

; FILE REFERENCE: 2709.2004001

; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 6658
; LENGTH: 1110
; TYPE: DNA
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-6658

Query Match 82.2%; Score 14.8; DB 4; Length 1110;
Best Local Similarity 88.9%; Pred. No. 5.9e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TGGCGCGCGCAGGGGGG 18
|||||
Db 1031 TGGCGCTGCGCAAGGGGG 1014

RESULT 8

US-09-620-312D-951
; Sequence 951, Application US/09620312D
; Patent No. 6569662
; GENERAL INFORMATION:
; APPLICANT: Tang, Y. Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Zhang, Jie
; APPLICANT: Ren, Feiyan
; APPLICANT: Chen, Rui-hong
; APPLICANT: Zhao, Qing A.
; APPLICANT: Wehrman, Tom
; APPLICANT: Xue, Aidong J.
; APPLICANT: Yang, Yonghong
; APPLICANT: Wang, Jian-Rui
; APPLICANT: Zhou, Ping
; APPLICANT: Ma, Yuning
; APPLICANT: Wang, Dunrui
; APPLICANT: Wang, Zhiwei
; APPLICANT: John Tillinghast
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: No. 6569662a1 Nucleic Acids and
; FILE REFERENCE: Polypeptides
; CURRENT APPLICATION NUMBER: US/09/620,312D
; CURRENT FILING DATE: 2000-07-19
; PRIOR APPLICATION NUMBER: 09/552,317
; PRIOR FILING DATE: 2000-04-25
; PRIOR APPLICATION NUMBER: 09/488,725
; PRIOR FILING DATE: 2000-01-21
; NUMBER OF SEQ ID NOS: 1105
; SOFTWARE: pt_FL_genes Version 1.0
; SEQ ID NO 951
; LENGTH: 1169
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (258)..(821)
US-09-620-312D-951

Query Match 82.2%; Score 14.8; DB 4; Length 1169;
Best Local Similarity 88.9%; Pred. No. 5.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TGGCGCGCGCAGGGGGG 18
|||||
Db 124 TGGCGCGCGCGGGGGG 141

RESULT 9

US-09-489-039A-6246/c

; Sequence 6246, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 6246
; LENGTH: 1230
; TYPE: DNA
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-6246

Query Match 82.2%; Score 14.8; DB 4; Length 1230;
Best Local Similarity 88.9%; Pred. No. 5.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TGGCGCGCGCAGGGGGG 18
|||||
Db 62 TGGCGCGCGCAGGGGG 45

RESULT 10

US-09-252-991A-16454/c
; Sequence 16454, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 16454
; LENGTH: 1251
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-16454

Query Match 82.2%; Score 14.8; DB 4; Length 1251;
Best Local Similarity 88.9%; Pred. No. 5.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 TGGCGCGCGCAGGGGGG 18
|||||
Db 693 TGGCGCGCGCATGGGCG 676

RESULT 11

US-09-318-448-42
; Sequence 42, Application US/09318448
; Patent No. 6210950
; GENERAL INFORMATION:
; APPLICANT: Johnson, William G.
; APPLICANT: Stenroos, Edward S.
; TITLE OF INVENTION: METHODS FOR DIAGNOSING, PREVENTING, AND TREATING
; TITLE OF INVENTION: DEVELOPMENTAL DISORDERS
; FILE REFERENCE: 601-1-057
; CURRENT APPLICATION NUMBER: US/09/318,448
; CURRENT FILING DATE: 1999-05-25
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 42

Query Match 82.2%; Score 14.8; DB 3; Length 1273;
Best Local Similarity 88.9%; Pred. No. 5.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0

Search completed: July 2, 2004, 13:37:41
Job time : 29.2073 secs

Query Match 82.2%; Score 14.8; DB 3; Length 1273;
Best Local Similarity 88.9%; Pred. No. 5.8e+02;
Matches 16; Conservative 0; Mismatches 2; Indels 0

Sequence 5, Application US/10666022
Publication No. US20040105872A1
GENERAL INFORMATION:
APPLICANT: The Government of the United States of America, as represented by the
APPLICANT: Secretary of the Department of Health and Human Services
APPLICANT: Kinnman, Dennis W.
APPLICANT: Vertheim, Daniela
TITLE OF INVENTION: METHOD OF TREATING AND PREVENTING INFECTIONS IN IMMUNOCOMPROMISED
SUBJECTS WITH IMMUNOSTIMULATORY CPG
FILE REFERENCE: 4239-66899
CURRENT APPLICATION NUMBER: US/10/666,022
CURRENT FILING DATE: 2003-09-17
PRIOR APPLICATION NUMBER: US 60/411,944
PRIOR FILING DATE: 2002-09-18
NUMBER OF SEQ ID NOS: 181
SOFTWARE: PatentIn version 3.1
SEQ ID NO 5
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: synthetic
FEATURE:
NAME/KEY: misc feature
LOCATION: {1}..(20)
OTHER INFORMATION: n is a, c, g, or t, or no nucleotide
US-10-666-022-5

Query Match 100.0%; Score 18; DB 17; Length 20;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TCGCGCGCGCGCAGGGGG 18
DB 3 TCGCGCGCGCGCAGGGGG 20

RESULT 3
US-10-437-963-58926/c
Sequence 58926, Application US/10437963
Publication No. US20040123343A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 58926
LENGTH: 687
TYPE: DNA
ORGANISM: Oryza sativa
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT4530_60597C.1
US-10-437-963-58926

Query Match 91.1%; Score 16.4; DB 17; Length 687;
Best Local Similarity 94.4%; Pred. No. 2e+02;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TCGCGCGCGCGCAGGGGG 18
DB 204 TCGCGCGCGCGCAGGGGG 187

RESULT 4
US-10-437-963-55777/c
Sequence 55777, Application US/10437963
Publication No. US20040123343A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 55777
LENGTH: 2052
TYPE: DNA
ORGANISM: Oryza sativa
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT4530_57751C.1
US-10-437-963-55777

Query Match 88.9%; Score 16; DB 17; Length 2052;
Best Local Similarity 100.0%; Pred. No. 2.2e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GCGCGCGCGCAGGGGG 17
DB 272 GCGCGCGCGCAGGGGG 257

RESULT 5
US-10-437-963-3377/c
Sequence 3377, Application US/10437963
Publication No. US20040123343A1
GENERAL INFORMATION:
APPLICANT: La Rosa, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Zhou, Yihua
APPLICANT: Cao, Yongwei
APPLICANT: Wu, Wei
APPLICANT: Boukharov, Andrey A.
APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21(53221)B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 3377
LENGTH: 369
TYPE: DNA
ORGANISM: Oryza sativa
FEATURE:
OTHER INFORMATION: Clone ID: PAT_MRT4530_10359C.1
US-10-437-963-3377

Query Match 85.6%; Score 15.4; DB 17; Length 369;
Best Local Similarity 94.1%; Pred. No. 6.4e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GCGCGCGCGCAGGGGG 18
DB 280 GCGCGCGCGCAGGGGG 264

RESULT 6

RESULT 10

US-10-437-963-22077
; Sequence 22077, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping

; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated with
; FILE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 22077
; LENGTH: 616
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_27287C.1

US-10-437-963-22077

Query Match 85.6%; Score 15.4; DB 17; Length 616;
Best Local Similarity 94.1%; Pred. No. 5.6e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GCGCGCGCGCAGCGGGG 18

DB 282 GCGCGCGCGCAGCGGGG 298

RESULT 11

US-10-198-846-7873/c
; Sequence 7873, Application US/10198846
; Publication No. US20030099974A1
; GENERAL INFORMATION:
; APPLICANT: Lillie, James
; APPLICANT: Xu, Yongyao
; APPLICANT: Wang, Youzhen
; APPLICANT: Steinmann, Kathleen

; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
; TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF BREAST CANCER
; FILE REFERENCE: MRI-049
; CURRENT APPLICATION NUMBER: US/10/198,846
; CURRENT FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/306,220
; PRIOR FILING DATE: 2001-07-18
; NUMBER OF SEQ ID NOS: 14084
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7873
; LENGTH: 664
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 16, 432, 474, 499, 500, 504, 516, 522, 523, 524, 531, 547,
; LOCATION: 548, 556, 558, 566, 567, 569, 578, 593, 594, 597, 612, 614,
; LOCATION: 620, 621, 628, 634, 637
; OTHER INFORMATION: n = A,T,C or G

US-10-198-846-7873

Query Match 85.6%; Score 15.4; DB 15; Length 664;
Best Local Similarity 94.1%; Pred. No. 5.4e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GCGCGCGCGCAGCGGGG 18

QY

DB 295 GCGCGCGCGCATGGGG 279

RESULT 12

US-10-259-165-431/c
; Sequence 431, Application US/10259165
; Publication No. US20030135888A1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Tong
; APPLICANT: Wang, Xun
; APPLICANT: Chang, Hur-song
; APPLICANT: Briggs, Steven P.
; APPLICANT: Cooper, Bret
; APPLICANT: Glazebrook, Jane
; APPLICANT: Goff, Stephen A.
; APPLICANT: Katagiri, Fumiyaki
; APPLICANT: Kreps, Joel
; APPLICANT: Moughamer, Todd
; APPLICANT: Provart, Nicholas
; APPLICANT: Rickes, Darrell
; TITLE OF INVENTION: GENES THAT ARE MODULATED BY POSTTRANSCRIPTIONAL GENE SILENCING

; FILE REFERENCE: 70030-NP
; CURRENT APPLICATION NUMBER: US/10/259,165
; CURRENT FILING DATE: 2002-09-26
; PRIOR APPLICATION NUMBER: US 60/370,620
; PRIOR FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/368,327
; PRIOR FILING DATE: 2002-03-27
; PRIOR APPLICATION NUMBER: US 60/325,277
; PRIOR FILING DATE: 2001-09-26
; NUMBER OF SEQ ID NOS: 782
; SOFTWARE: PatentList.pl version 3.0.4 (C) 2001 Syngenta
; SEQ ID NO 431
; LENGTH: 681
; TYPE: DNA
; ORGANISM: Oryza sativa
; US-10-259-165-431

Query Match 85.6%; Score 15.4; DB 15; Length 681;
Best Local Similarity 94.1%; Pred. No. 5.4e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 TGCGCGCGCGCAGCGGGG 17

DB 637 TGCGCGCGCGCAGCGGGG 621

RESULT 13

US-10-259-165-99/c
; Sequence 99, Application US/10259165
; Publication No. US20030135888A1
; GENERAL INFORMATION:
; APPLICANT: Zhu, Tong
; APPLICANT: Wang, Xun
; APPLICANT: Chang, Hur-song
; APPLICANT: Briggs, Steven P.
; APPLICANT: Cooper, Bret
; APPLICANT: Glazebrook, Jane
; APPLICANT: Goff, Stephen A.
; APPLICANT: Katagiri, Fumiyaki
; APPLICANT: Kreps, Joel
; APPLICANT: Moughamer, Todd
; APPLICANT: Provart, Nicholas
; APPLICANT: Rickes, Darrell
; TITLE OF INVENTION: GENES THAT ARE MODULATED BY POSTTRANSCRIPTIONAL GENE SILENCING

; FILE REFERENCE: 70030-NP
; CURRENT APPLICATION NUMBER: US/10/259,165
; CURRENT FILING DATE: 2002-09-26
; PRIOR APPLICATION NUMBER: US 60/370,620
; PRIOR FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/368,327
; PRIOR FILING DATE: 2002-03-27

```
; PRIOR APPLICATION NUMBER: US 60/325,277
; PRIOR FILING DATE: 2001-09-26
; NUMBER OF SEQ ID NOS: 782
; SOFTWARE: PatentList.pl version 3.0.4 (C) 2001 Syngenta
; SEQ ID NO 99
; LENGTH: 684
; TYPE: DNA
; ORGANISM: Oryza sativa
US-10-259-165-99

Query Match      85.6%; Score 15.4; DB 15; Length 684;
Best Local Similarity 94.1%; Pred. No. 5.4e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TGGCCGCGCGCAGGGGG 17
   |||||
Db 637 TGGCCGCGCACAGGGGG 621

RESULT 14
US-10-198-846-11115/C
; Sequence 11115, Application US/10198846
; Publication No. US20030099974A1
; GENERAL INFORMATION:
; APPLICANT: Lillie, James
; APPLICANT: Xu, Yongyao
; APPLICANT: Wang, Youzhen
; APPLICANT: Steinmann, Kathleen
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
; TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF BREAST CANCER
; FILE REFERENCE: MRI-049
; CURRENT APPLICATION NUMBER: US/10/198,846
; CURRENT FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/306,220
; PRIOR FILING DATE: 2001-07-18
; NUMBER OF SEQ ID NOS: 14084
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11115
; LENGTH: 745
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1
; OTHER INFORMATION: n = A,T,C or G
US-10-198-846-11115

Query Match      85.6%; Score 15.4; DB 15; Length 745;
Best Local Similarity 94.1%; Pred. No. 5.3e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GCGCCGCGCGCAGGGGG 18
   |||||
Db 297 GCGCCGCGCGCATGGGG 281
```

```
RESULT 15
US-10-425-114-2950
; Sequence 2950, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
```

```
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 2950
; LENGTH: 785
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700237916_FLI
US-10-425-114-2950

Query Match      85.6%; Score 15.4; DB 13; Length 785;
Best Local Similarity 94.1%; Pred. No. 5.2e+02;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 TGGCCGCGCGCAGGGGG 17
   |||||
Db 113 TGGCCGCGCGCAGGGAG 129

Search completed: July 2, 2004, 13:58:25
Job time : 138.732 secs
```